

173647

STIC-Biotech/ChemLib

From: Shaw, Amanda Marie  
Sent: Wednesday, December 07, 2005 11:54 AM  
To: STIC-Biotech/ChemLib  
Subject: sequence search for 10/713/137

Please search:

- 1) SEQ ID NO: 2 and 3 (each of these sequences is 24 nucleotides in length). Please limit the search results to nucleic acids that are of a length of 50 nucleotides or less.
- 2) SEQ ID NO: 1 (258 nucleotides in length)

The CRF has been entered:

[http://expoweb1:8001/cgi-bin/expo/BioInfo/bioquery.pl?APPL\\_ID=10713137](http://expoweb1:8001/cgi-bin/expo/BioInfo/bioquery.pl?APPL_ID=10713137)

Please provide a printout of the first 40 results.

Thank you,

Amanda Shaw  
Patent Examiner  
Art Unit 1634  
Remsen 2E78  
Mailbox: REM 2C70  
571-272-8668

CRF

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
.STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

**THIS PAGE BLANK (USP10)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 15:51:35 ; Search time 2143 Seconds  
(without alignments)  
6843.495 Million cell updates/sec

Title: US-10-713-137-1  
Perfect score: 258  
Sequence: 1 cagcgaggatggcaagca.....ttgtcccgatggtgcac 258

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*

1: gb.ba:\*  
2: gb.in:\*  
3: gb.env:\*  
4: gb.cm:\*  
5: gb.ov:\*  
6: gb.pat:\*  
7: gb.ph:\*  
8: gb.pr:\*  
9: gb.ro:\*  
10: gb.sts:\*  
11: gb.sy:\*  
12: gb.un:\*  
13: gb.vi:\*  
14: gb.htg:\*  
15: gb.pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	257.6	99.8	47758	8	DQ060518 Homo sapi
2	257.6	99.8	116026	14	AC131306 Homo sapi
3	257.6	99.8	136599	8	AC130289 Homo sapi
4	257.6	99.8	156907	8	AL354047 Homo sapi
5	246.6	95.6	259	6	CS101221 Sequence
6	236.8	91.8	602	8	X85766 H. sapiens N
7	176.4	68.4	257	8	AF375649 Ateles be
8	120.4	46.7	1152	6	BD097464 Method fo
9	120.4	46.7	3462	6	BD097463 Method fo
10	120.4	46.7	3595	8	HUMNOSIND
11	120.4	46.7	3855	8	HU05810 Human induc
12	120.4	46.7	3946	6	AX067221 Sequence
13	120.4	46.7	3946	8	HSU20141 Human induc
14	120.4	46.7	3963	8	HUMITONOS
15	120.4	46.7	4062	6	AR124185 Human mRNA
16	120.4	46.7	4062	6	CQ776352 Sequence
17	120.4	46.7	4062	6	CQ776469 Sequence
18	120.4	46.7	4062	6	AR270915 Sequence

19	120.4	46.7	4062	8	HSU31511 Human induc
20	120.4	46.7	4145	6	I15516 Sequence 1
21	120.4	46.7	4145	6	I61175 Sequence 1
22	120.4	46.7	4145	8	L09210 Homo sapien
23	120.4	46.7	4164	6	A39980 Sequence 1
24	120.4	46.7	4164	6	AR380862 Sequence 1
25	120.4	46.7	4164	8	HSINOSA
26	120.4	46.7	4467	6	CQ723665 Sequence
27	120.4	46.7	35764	11	AY046510 Adenovira
28	118.8	46.0	4150	6	AX067222 Sequence
29	118.8	46.0	4150	8	AF068236 Homo sapi
30	116	45.0	179504	14	AC158064 Homo sapi
31	102.8	39.8	2838	4	AF223942 Ovis arie
32	100.2	38.8	648	10	BV410321 S29P690F
33	99.6	38.6	647	4	SSU59390 Sus scrofa
34	98.8	38.3	38817	9	AF427516 Mus muscu
35	98.8	38.3	178443	9	AL592185 Mouse DNA
36	98.8	38.3	236456	14	AC036147 Mus muscu
37	98.4	38.1	163	9	RNO230468 Rattus no
38	98.4	38.1	110000	14	AC105495 Rattus no
39	98.4	38.1	240200	14	AC103040 Rattus no
40	98.4	38.1	314746	14	AC106421 Rattus no
41	98	38.0	3970	9	AF027180 Cavia por
42	94.8	36.7	413	9	AY297461 Mesocric
43	94.8	36.7	3441	9	RATNOSA Rattus norv
44	94.8	36.7	3442	9	AY211532 Rattus no
45	94.8	36.7	3444	9	RNU26686 Rattus norv

## ALIGNMENTS

RESULT 1	DQ060518	Homo sapiens nitric oxide synthase 2A (inducible, hepatocytes)	47758 bp	DNA	linear	PRI 23-MAY-2005
LOCUS	DQ060518	(NOS2A) gene, complete cds.				
ACCESSION	DQ060518					
VERSION	DQ060518.1	GI:66268800				
KEYWORDS						
SOURCE		Homo sapiens (human)				
ORGANISM		Homo sapiens				
REFERENCE						
AUTHORS		Livingston,R.J., Rieder,M.J., Shaffer,T., Bertucci,C., Baier,C.N., Rajkumar,N., Willia,H.T., Daniels,M., Downing,T.K., Stanaway,I.B., Nguyen,C.P., Gildersleeve,H., Cassidy,C.M., Johnson,E.J., Swanson,J.E., McFarland,I., Yool,B., Park,C. and Nickerson,D.A.				
TITLE		Direct Submission				
JOURNAL		Submitted (13-MAY-2005) Genome Sciences, University of Washington, 1705 NE Pacific, Seattle, WA 98195, USA				
COMMENT		To cite this work please use: NIEHS-SNPs, Environmental Genome Project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).				
FEATURES						
source		Location/Qualifiers				
		1..47758				
		/organism="Homo sapiens"				
		/mol_type="genomic DNA"				
		/db_xref="taxon:9606"				
repeat_region		153..211				
		/rpt_family="MIR"				
		/rpt_type="dispersed"				
variation		343				
		/frequency="0.10"				
		/replace="t"				
repeat_region		510..585				
		/rpt_family="ERV1"				
		/rpt_type="dispersed"				
variation		541				
		/frequency="0.02"				
		/replace="a"				





```

variation      4899      /gene="NOS2A"
                /frequency="0.01"
                /replace="a"
variation      4954      /gene="NOS2A"
                /frequency="0.33"
                /replace="a"
variation      4963      /gene="NOS2A"
                /frequency="0.01"
                /replace="t"
                /rpt_family="MIR"
repeat_region 5002..5219 /rpt_type="dispersed"

Query Match      99.8%; Score 257.6; DB 8; Length 47758;
Best Local Similarity 99.6%; Pred. No. 2.3e-49;
Matches 257; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAGACGACTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
DB 21382 CAGCGGAGTGATGGCAGACGACTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 21441
QY 61 GGTACACAGATGCCAGATGCCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTCAG 120
DB 21442 GGTACACAGATGCCAGATGCCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTCAG 21501
QY 121 GTACCCGGCCAGCTCAGCCRCGGCCATTGGGGCGGGAGCCCCGGTGGTAGGCGAGTG 180
DB 21502 GTACCCGGCCAGCTCAGCCRCGGCCATTGGGGCGGGAGCCCCGGTGGTAGGCGAGTG 21561
QY 181 ACAGAGTGAGCCAGAGAGACAGCAGCCGGGCTTACAGACTCACAGGGCCGCTCTT 240
DB 21562 ACAGAGTGAGCCAGAGAGACAGCAGCCGGGCTTACAGACTCACAGGGCCGCTCTT 21621
QY 241 GTTCCCAGCTGTGCATC 258
DB 21622 GTTCCCAGCTGTGCATC 21639

RESULT 2
AC131306
LOCUS
DEFINITION
AC131306.1 GI:232325231
VERSION
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
1 (bases 1 to 116026)
Birren,B., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 17, clone RP11-1145F2 map 17, WORKING DRAFT
SEQUENCE, 11 unordered pieces.
2 (bases 1 to 116026)
Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
Cook,A., Cooke,P., DeIrellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faroo,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kella,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schuback,R., Seaman,S., Severy,P.,

```

```

Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (20-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L27556
Center clone name: 1145_F2
----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 111511 bases at least Q40
Consensus quality: 113602 bases at least Q30
Consensus quality: 114471 bases at least Q20
Insert size: 182000; agarose-fp
Quality coverage: 15.7 in Q20 bases; agarose-fp
Quality coverage: 24.8 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.
*
* 1896: contig of 1896 bp in length
* 1897: gap of 100 bp
* 1997: contig of 989 bp in length
* 2986: gap of 100 bp
* 3085: contig of 1464 bp in length
* 4549: contig of 100 bp
* 4550: gap of 100 bp
* 4550: gap of 100 bp
* 4650: contig of 1324 bp in length
* 5073: gap of 100 bp
* 5974: gap of 100 bp
* 6074: contig of 1823 bp in length
* 7896: gap of 100 bp
* 7897: contig of 1791 bp in length
* 9787: gap of 100 bp
* 9788: contig of 2703 bp in length
* 12590: contig of 100 bp
* 12591: gap of 100 bp
* 1466: contig of 2076 bp in length
* 14767: gap of 100 bp
* 14867: contig of 12028 bp in length
* 26894: gap of 100 bp
* 26895: gap of 100 bp
* 44060: contig of 17066 bp in length
* 44061: gap of 100 bp
* 44161: contig of 71866 bp in length.
*
Location/Qualifiers
1. .116026
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosomes="17"
/map="17"
/clone_lib="RP11-1145F2"
/clone="RP11-1145F2"
1. .1896
/clone="assembly_fragment"
/clone_end="SF6"
vector_side="left"
1897. .1996
misc_feature
gap

```





```

RESULT 4
HS66C13/c
LOCUS
DEFINITION Homo sapiens chromosome 17 from PAC RPCI-1 66C13 map 17p11.2 region
VERSION D17S842-D17S953, complete sequence.
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Ramser, J., Mueller, I., Sudbrak, R., Kosiura, A., Langer, I.,
Steffens, C., Klein, M., Heilmann, K., Schuelzchen, S., Starke, A.,
Thompson, C., Radelof, U., Francis, F., Seraneki, P., Poustka, A.,
Lehrach, H. and Reinhardt, R.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 156907)
MOLGENR.
Direct Submission
Submitted (28-APR-2000) MOLGENR, Abt. Lehrach, Max Planck Institut
Fuer Molekulare Genetik, Ihnestrasse 73, Berlin, 14195 Germany
On Jun 19, 2001 this sequence version replaced gi:13752107.
Clone received from the Resource Centre of the Human Genome Project
at the Max-Planck-Institute for Molecular Genetics
contig 01 1. 156907.
FEATURES
source
1. 156907
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="17"
/map="17p11.2"
/clone="PAC RPCI-1 66C13"
/clone_lib="RPC11,3-5 Human PAC library, originating
institute: Roswell Park Cancer Institute, creator: Pieter
de Jong, P. Ioannou"
/note="region between markers D17S842-D17S953"
misc_feature 1
/note="SP6_end:PAC RPCI-1 66C13"
misc_feature 156907
/note="T7_end:PAC RPCI-1 66C13"
ORIGIN
Query Match 99.8%; Score 257.6; DB 8; Length 156907;
Best Local Similarity 99.6%; Pred. No. 1.9e-49;
Matches 257; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAGCGGAGTGATGCAAGCAGCACTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 87933 CAGCGGAGTGATGCAAGCAGCACTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 87874
Qy 61 GGCTACCAAGATGCAGATGGCAGATCAGAGGGACCTGCGCAACGTGGAATTCACCTCAG 120
Db 87873 GGCTACCAAGATGCAGATGGCAGATCAGAGGGACCTGCGCAACGTGGAATTCACCTCAG 87814
Qy 121 GTACCCGGCCAGCTCAGCCRCGCGCATTTGGGCGGGAGCCCGTGTGAGCGAGTG 180
Db 87813 GTACCCGGCCAGCTCAGCCRCGCGCATTTGGGCGGGAGCCCGTGTGAGCGAGTG 87754
Qy 181 ACAGAGTGGAGCCAGAGGAGACACGAGCCCGGGCTTACAGACTTCACAGGGCCCGCTT 240
Db 87753 ACAGAGTGGAGCCAGAGGAGACACGAGCCCGGGCTTACAGACTTCACAGGGCCCGCTT 87694
Qy 241 GTTCCCAAGCTGTGCATC 258
Db 87693 GTTCCCAAGCTGTGCATC 87676
ORIGIN
Query Match 95.6%; Score 246.6; DB 6; Length 259;
Best Local Similarity 99.2%; Pred. No. 1.7e-46;
Matches 257; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
Qy 1 CAGCGGAGTGATGCAAGCAGCACTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 1 CAGCGGAGTGATGCAAGCAGCACTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Qy 61 GGCTACCAAGATGCAGATGGCAGATCAGAGGGACCTGCGCAACGTGGAATTCACCTCAG 120
Db 61 GGCTACCAAGATGCAGATGGCAGATCAGAGGGACCTGCGCAACGTGGAATTCACCTCAG 120
Qy 121 GTACCCGGCCAGCTCAGCC-RCCGGCCATTTGGGCGGGAGCCCGTGTGAGCGAGT 179
Db 121 GTACCCGGCCAGCTCAGCCAGCCGCCCATTTGGGCGGGAGCCCGTGTGAGCGAGT 180
Qy 180 GACAGAGTGGAGCCAGAGAGACACGAGCCCGGGCTTACAGACTTCACAGGGCCCGCTT 239
Db 181 GACAGAGTGGAGCCAGAGAGACACGAGCCCGGGCTTACAGACTTCACAGGGCCCGCTT 240
Qy 240 TGTTCCTCCAGCTGTGCATC 258
Db 241 TGTTCCTCCAGCTGTGCATC 259
ORIGIN
Query Match 99.6%; Score 602 bp DNA linear PRI 19-AUG-1996
HNS02E89
LOCUS
DEFINITION H. sapiens NOS2 gene, exon 8 and 9.
ACCESSION X85766
VERSION X85766.1 GI:1130725
KEYWORDS nitric oxide synthase; NOS2.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Xu, W., Charles, I.G., Liu, L., Moncada, S. and Emson, P.
TITLE Molecular cloning and structural organization of the human
inducible nitric oxide synthase gene (NOS2)
JOURNAL Biochem. Biophys. Res. Commun. 219 (3), 784-788 (1996)
PUBMED 8645258
REFERENCE 2 (bases 1 to 602)
AUTHORS Xu, W.
TITLE Direct Submission
JOURNAL Submitted (21-MAR-1995) W. Xu, Babraham Institute, MRC Group, Dept
of Neurobiology, Cambridge CB2 4AT, UK
COMMENT Sequence overlapping with that under the acc#X73029.

```

JOURNAL	Submitted (02-MAY-2001) Departamento de Bioquimica, Universidade de Sao Paulo, Rua Professor Lineu Prestes, 748/bloco 12/sala 1200, Sao Paulo, SP 05508-900, Brazil
FEATURES	Location/Qualifiers
source	1..257
	/organism="Ateles belzebuth chamek"
	/mol_type="genomic DNA"
	/sub_species="chamek"
	/db_xref="taxon:118643"
	/chromosome="14"
gene	<1..>257
mRNA	/gene="NOS2A"
	<1..>66
CDS	/gene="NOS2A"
	/product="nitric oxide synthase 2A"
	<1..>66
	/gene="NOS2A"
	/codon_start=1
	/product="nitric oxide synthase 2A"
	/protein_id="AAL31486.1"
	/db_xref="GI:16923453"
	/translation="YAGYQMPDGSIRGDPANVEFTQ"
ORIGIN	
Query Match	68.4%; Score 176.4; DB 8; Length 257;
Best Local Similarity	91.2%; Pred. No. 2.4e-30;
Matches	186; Conservative 1; Mismatches 17; Indels 0; Gaps 0;
QY	55 TATGCTGGCTACCATGCCAGATGCCAGATCAGAGGGAGCCCTGCCAACTGGAATTC 114
Db	1 TATGCTGGCTACCATGCCAGATGCCAGATCAGAGGGAGCCCTGCCAACTGGAATTC 60
QY	115 ACTCAGGTACCCGGCCAGCCCTCAGCCRCGCGCATTTGGGGGGGAGCCCGCTGTGTGAG 174
Db	61 ACTCAGGTACCCAAACCCAGCCCTCGGCCCGGAGAGCCCGCTGTGTGAG 120
QY	175 CGAGTGACAGAGTGGAGCCAGAGAGACACGCGCCCGGGCTTACAGACTCACAGGGGCC 234
Db	121 CGAGTGACAGAGTGGAGCCAGAGAGACACGCGCCCGGGCTTACAGACTCAGAGGGGCC 180
QY	235 CGTCTGTGTTCCCGAGCTGTGCATC 258
Db	181 TGTCGTGTTCCCGAGCTGTGCATC 204
RESULT 8	
BD097464	1152 bp DNA linear PAT 27-AUG-2002
LOCUS	
DEFINITION	Method for screening of inhibitors of inducible nitrogen oxide synthetase activation.
ACCESSION	BD097464
VERSION	BD097464.1 GI:22643038
KEYWORDS	WO 0166791-A/2.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 1152)
AUTHORS	Ishii,Y., Ueda,Y., Iwami,M., Arakawa,H. and Not,Y.
TITLE	Method for screening of inhibitors of inducible nitrogen oxide synthetase activation
JOURNAL	Patent: WO 0166791-A 2 13-SEP-2001;
	FUJISAWA PHARMACEUTICAL CO LTD,YOSHINORI ISHII,YOSHIKO UEDA,MORITA IWAMI,HIROYUKI ARAKAWA,YOSHITADA NOTSU
COMMENT	OS Homo sapiens (human)
	PN WO 0166791-A/2
	PD 13-SEP-2001
	PF 09-MAR-2001 WO 2001JP001865
	PR 10-MAR-2000 JP 00P 72480
	PI YOSHINORI ISHII,YOSHIKO UEDA,MORITA IWAMI,HIROYUKI ARAKAWA, PI YOSHITADA NOTSU
	PC C12Q1/25,C12N15/52,G01N33/50,G01N33/15

FEATURES	Location/Qualifiers
source	1..602
	/organism="Homo sapiens"
	/mol_type="genomic DNA"
	/db_xref="taxon:9606"
	/chromosome="17"
	/map="q11.2"
	/clone="COS 4"
	/sex="male"
	/cell_line="PLT6B"
	/cell_type="fibroblasts"
	/clone_lib="PLT6B cosmid library"
gene	137..602
exon	/gene="NOS2"
	137..278
	/genes="NOS2"
	/product="inducible nitric oxidase synthase"
exon	number=8
	548..602
	/genes="NOS2"
	/product="inducible nitric oxidase synthase"
	number=9
ORIGIN	
Query Match	91.8%; Score 236.8; DB 8; Length 602;
Best Local Similarity	94.6%; Pred. No. 2.7e-44;
Matches	244; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
QY	1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGTCTCATCGCTATGCT 60
Db	159 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGTCTCATCGCTATGCT 218
QY	61 GGCTACCATGATGCCAGTGCAGCATCAGAGGGAGCCCTGCCAACCTGGAATTCACCTCAG 120
Db	219 GGCTACCATGATGCCAGTGCAGCATCAGAGGGAGCCCTGCCAACCTGGAATTCACCTCAG 278
QY	121 GTACCCGGCCAGCTCAGCCRCGCGCATTTGGGGGGGAGCCCGTGTGTGAGCGAGTG 180
Db	279 GTACCCGGCCAGCTCAGCCRCGCGCATTTGGGAGCGGGAGCCCGTGTGTGAGTG 338
QY	181 ACAGATGGAGCCAGAGGAGACACCGAGCCCGGGCTTACAGACTCAGAGGGCCCGTCTT 240
Db	339 ACAGATGGAGCCAGAGGAGAACCGAGCCAGGCTCTCACAGACTCAGAGGGCCCGTGT 398
QY	241 GTTCCCCAGCTGTGCATC 258
Db	399 GTTCCCCAGCTGTGCATC 416
RESULT 7	
AF375649	257 bp DNA linear PRI 14-NOV-2001
LOCUS	
DEFINITION	Ateles belzebuth chamek nitric oxide synthase 2A (NOS2A) gene, partial cds.
ACCESSION	AF375649
VERSION	AF375649.1 GI:16923452
KEYWORDS	
SOURCE	Ateles belzebuth chamek (Chamek spider monkey)
ORGANISM	Ateles belzebuth chamek
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae; Ateleinae; Ateles.
REFERENCE	1 (bases 1 to 257)
AUTHORS	Suarez,H.N., Lima,C.R., Lemos,B., Bonvicino,C.R., Moreira,M.A. and Canavez,F.C.
TITLE	Gene assignment in Ateles paniscus chamek (Platyrrhini, Primates). Allocation of 18 markers of human syntenic groups 1, 2, 7, 14, 15, 17 and 22
JOURNAL	Chromosome Res. 9 (8), 631-639 (2001)
PUBMED	11778686
REFERENCE	2 (bases 1 to 257)
AUTHORS	Canavez,F.C.
TITLE	Direct Submission

CC		Method for screening of inhibitors of inducible nitrogen oxide																													
CC		synthetase																													
FH	Key	activation	Location/Qualifiers																												
			1. .1152 /organism='Homo sapiens (human)'. /db_xref='taxon:9606'																												
FT		source																													
FT		1. .1152 /organism='Homo sapiens' /mol_type='genomic DNA' /db_xref='taxon:9606'																													
FEATURES																															
source																															
ORIGIN																															
Query Match		46.7%; Score 120.4; DB 6; Length 1152;																													
Best Local Similarity		99.2%; Pred. No. 1.4e-17;																													
Matches 121;		Conservative 0; Mismatches 1; Indels 0; Gaps 0;																													
Qy	Db	1	CAGCGGAGTGATGCCAAGCAGCAGCTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60																												
379	Db	1	CAGCGGAGTGATGCCAAGCAGCAGCTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 438																												
Qy	Db	61	GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCTGCCAAGCTGGGAATTCACCTCAG 120																												
439	Db	1	GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCTGCCAAGCTGGGAATTCACCTCAG 498																												
121	Qy	GT	122																												
499	CT	500																													
RESULT 9																															
BD097463																															
LOCUS																															
DEFINITION		3462 bp DNA linear PAT 27-AUG-2002																													
synthetase activation.		Method for screening of inhibitors of inducible nitrogen oxide																													
ACCESSION		BD097463																													
VERSION		BD097463.1 GI:22643037																													
KEYWORDS		WO 0166791-A/1.																													
SOURCE		Homo sapiens (human)																													
ORGANISM		Homo sapiens																													
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;																													
AUTHORS		Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;																													
TITLE		Hominidae; Homo.																													
JOURNAL		1 (bases 1 to 3462)																													
COMMENT		Ishii,Y., Ueda,Y., Iwami,M., Arakawa,H. and Not,Y.																													
synthetase activation		Method for screening of inhibitors of inducible nitrogen oxide																													
Patent:		WO 0166791-A 1 13-SEP-2001;																													
FUJISAWA PHARMACEUTICAL CO LTD, YOSHINORI ISHII, YOSHIKO UEDA, MORITA																															
IWAMI, HIROYUKI ARAKAWA, YOSHITADA NOTSU																															
OS		Homo sapiens (human)																													
PN		WO 0166791-A/1																													
PD		13-SEP-2001																													
PF		09-MAR-2001 WO 2001JP001865																													
PI		10-MAR-2000 JP 00P 72480																													
YOSHINORI ISHII, YOSHIKO UEDA, MORITA IWAMI, HIROYUKI ARAKAWA, PI																															
YOSHITADA NOTSU																															
PC		C12Q1/25, C12N15/52, G01N33/50, G01N33/15																													
Method for screening of inhibitors of inducible nitrogen oxide																															
CC																															
synthetase																															
activation																															
FH	Key	synthetase	Location/Qualifiers																												
			1. .3462 /organism='Homo sapiens (human)'. /db_xref='taxon:9606'																												
FT		source																													
FT		1. .3462 /organism='Homo sapiens' /mol_type='genomic DNA' /db_xref='taxon:9606'																													
FEATURES																															
source																															
ORIGIN																															

Query Match		46.7%; Score 120.4; DB 6; Length 3462;									
Best Local Similarity		99.2%; Pred. No. 1.2e-17;									
Matches		121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY	DB	1	CAGCGGAGTGATGCCAAGCAGCAGCTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60								
745	DB	1	CAGCGGAGTGATGCCAAGCAGCAGCTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 804								
QY	DB	61	GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCTGCCAAAGCTGGAATTCATCTCAG 120								
805	DB	1	GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCTGCCAAAGCTGGAATTCATCTCAG 864								
QY	DB	121	GT 122								
865	DB	CT	866								
RESULT 10											
HUMNOSIND											
LOCUS		Homo sapiens inducible nitric oxide synthase mRNA, complete cds.									
DEFINITION		3595 bp mRNA linear PRI 30-SEP-1993									
ACCESSION		L24553									
VERSION		L24553.1 GI:404048									
KEYWORDS		nitric oxide synthase.									
SOURCE		Homo sapiens (human)									
ORGANISM		Homo sapiens									
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.									
AUTHORS		1 (bases 1 to 3595)									
TITLE		Sherman,P.A., Laubach,V.E., Reep,B.R. and Wood,E.R.									
JOURNAL		Purification and cDNA sequence of an inducible nitric oxide synthase from a human tumour cell line									
COMMENT		Biochemistry (1993) In press									
FEATURES		Original source text: Homo sapiens (library: ATCC ccl221)									
source		colorectal adenocarcinoma cDNA to mRNA.									
CDS		Location/Qualifiers									
		1..3595									
		/organism="Homo sapiens"									
		/mol_type="mRNA"									
		/db_xref="taxon:9606"									
		/cell_line="DLD-1"									
		/tissue_type="colorectal adenocarcinoma"									
		/tissue_lib="ATCC ccl221"									
		77..3538									
		/note="inducible"									
		/codon_start=1									
		/product="nitric oxide synthase"									
		/protein_id="AAA36375.1"									
		/db_xref="GI:404049"									
		/translation="MACPWKFLPKTKFHOYAMNGEKDINNVEKAPCATSSPVTQDDL KAGHLTKCRSKSPQLVETGKSPESLVKLDATPLSSPRHRIKNWGSMTFODTLHH KAKGLTQCRSKSPQLVETGKSPESLVKLDAT									

```
Query Match          46.7%; Score 120.4; DB 8; Length 3595;
Best Local Similarity 99.2%; Pred. No. 1.2e-17;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGACTTCGCGGGTGTGGAATGCTCAGCTCATCGCTATGCT 60
    |||
DB 821 CAGCGGAGTGATGGCAAGCAGACTTCGCGGGTGTGGAATGCTCAGCTCATCGCTATGCT 880

QY 61 GCCTACCAAGTCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
    |||
DB 881 GCCTACCAAGTCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 940

QY 121 GT 122
DB 941 CT 942

RESULT 11
HSU05810          3855 bp mRNA linear PRI 07-DEC-1994
LOCUS             Human inducible nitric oxide synthase mRNA, complete cds.
DEFINITION        U05810
ACCESSION         U05810.1 GI:452487
VERSION           Homo sapiens (human)
KEYWORDS          Homo sapiens
SOURCE            Homo sapiens
ORGANISM          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE         1 (bases 1 to 3855)
AUTHORS           Maier R., Bilbe G., Rediske J. and Lotz M.
TITLE             Inducible nitric oxide synthase from human articular chondrocytes:
                  cDNA cloning and analysis of mRNA expression
JOURNAL           Biochim. Biophys. Acta 1208 (1), 145-150 (1994)
PUBMED            7522054
REFERENCE         2 (bases 1 to 3855)
AUTHORS           Maier R.
TITLE             Direct Submission
JOURNAL           Submitted (28-JAN-1994) Rainer Maier, Medicine, University of
                  California, San Diego, 9500 Gilman Drive, La Jolla, CA 92093-0663,
                  USA
FEATURES           Location/Qualifiers
                   1..3855
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_type="articular chondrocytes"
                   1..194
                     /codon_start=1
                     /product="inducible nitric oxide synthase"
                     /protein_id="AA56666.1"
                     /db_xref="GI:452488"
                     /translation="MACPMKFLFKTFHOYAMNGEGINNVKAPCATSPVTDLDL
OYHNLKSQNESPOLVETGKSPESLKLDPPLSSPRHRIKNWGSQMTFQDTLHH
KAGILTCRSKSLGSLGIMTPKSLTRGRDKPTPDBELLQAIEFVNOYVGSLEAKIE
EHLARVEAVTKETITVLTQTDGLIFATKQARNAPRCIGRIQNSNLQVDFARSCL
TAREMFEHTCHRVYSTNNGNRSATVPFQSDGKHDPVWNAQLIRVAGYQMPDGS
IRGDPANVFETQICIDLGWKPKRFEDVPLVLAQNGRDPPELFEIPDLVLVAMEHP
KYVPRRELKHWALPAVANMLLEVGLFPGCPFGNGWTGTEIGVRDFCDVQRNII
EYVGRWGLKTHKLSLWKDQAVEINIAVLHSFQKQNTVIMDHSAESFMKYMONE
YSRGCGPADWLVPPMSGSTIPFHEQMLNVLSPFYXOYVEAKWTHVQDEKRP
KREITPLKVLKAVLFACLMRKTMASRVKRVITLFAFETGKSEALAWDLGALFSCAP
PKVCMKRLVLSCLBEERLLLVTTSTFGNGDCPGNGEKLLKSLFMLELNKNFRYAVF
GLGSMYRPFCAFDIDQKLSHLGASQLTPMGSDGLSQEDAFPSWAVQTFKAACE
TFDVRCKHQIOLPKLVTSTWDPHHYRLVQSDPLDLKSLSSMHAKXVFTWRLKSR
QNLQSTSSRATILVLSCEGOGNLVLPGEHLGVCNQPALVQCIILRRVVDGPTPH
QVRLBALDESGYWSDRRLPCSLSQALTYFLDITPTQLLLQKLAQVATEPER
QRLEALCQPSSEYSKWFTNSPTFLEVLSEFPSSLRVASGILLQLPKLKRFTYSISPR
DHTPTTILHTLVAVVYTHTRDQGLPHHGCSTWLSLKPDPVPCFVRNAGFHLPEL
PSHPICILIGTGIAIPFRSGFWQORLHDSQHKVGRGRTLVFCRRPDDHDHYQEML
EMAQKGLVHAVHTAYSLRPLGPKPKVYVQDILRQOLASEVLRLVHLKEPGLHYVQGDVMA
RDVAHTLKQLVAAKLNEEQVEDYFFQLKSKRYHEDIFGAVFPPEAKKDRVAVQPS
```





```
QY 61 GGTACCATGATCCAGATGGCAGCATCAGAGGGAGCCCTGCCAACGTGGAATTCACCTCAG 120
Db 819 GGTACCATGATCCAGATGGCAGCATCAGAGGGAGCCCTGCCAACGTGGAATTCACCTCAG 878
QY 121 GT 122
Db 879 CT 880

RESULT 15
AR124185
LOCUS AR124185 4062 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 11 from patent US 6171856.
ACCESSION AR124185
VERSION AR124185.1 GI:14109546
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4062)
AUTHORS Thigpen,A., Hohmeier,H.-E., Newgard,C.B., Unger,R.H.,
Shimabukuro,M., Chen,G., Rhodes,C.J., Hugl,S.R. and Cousin,S.
TITLE Methods and compositions relating to no-mediated cytotoxicity
JOURNAL Patent: US 6171856-A 11 09-JAN-2001;
FEATURES
source
1. 4062
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 46.7%; Score 120.4; DB 6; Length 4062;
Best Local Similarity 99.2%; Pred. No. 1.2e-17;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 850 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 909
QY 61 GGTACCATGATCCAGATGGCAGCATCAGAGGGAGCCCTGCCAACGTGGAATTCACCTCAG 120
Db 910 GGTACCATGATCCAGATGGCAGCATCAGAGGGAGCCCTGCCAACGTGGAATTCACCTCAG 969
QY 121 GT 122
Db 970 CT 971

RESULT 16
QY76352
LOCUS QY76352 4062 bp DNA linear PAT 11-MAR-2004
DEFINITION Sequence 38 from Patent EP1394274.
ACCESSION QY76352
VERSION QY76352.1 GI:45379742
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuwara,K.
TITLE Methods of testing for bronchial asthma or chronic obstructive
JOURNAL Patent: EP 1394274-A 38 03-MAR-2004;
FEATURES
source
1. 4062
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 46.7%; Score 120.4; DB 6; Length 4062;
Best Local Similarity 99.2%; Pred. No. 1.2e-17;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 850 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 909
QY 61 GGTACCATGATCCAGATGGCAGCATCAGAGGGAGCCCTGCCAACGTGGAATTCACCTCAG 120
Db 910 GGTACCATGATCCAGATGGCAGCATCAGAGGGAGCCCTGCCAACGTGGAATTCACCTCAG 969
QY 121 GT 122
Db 970 CT 971

RESULT 17
QY76469
LOCUS QY76469 4062 bp DNA linear PAT 11-MAR-2004
DEFINITION Sequence 155 from Patent EP1394274.
ACCESSION QY76469
VERSION QY76469.1 GI:45379859
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuwara,K.
TITLE Methods of testing for bronchial asthma or chronic obstructive
JOURNAL Patent: EP 1394274-A 155 03-MAR-2004;
FEATURES
source
1. 4062
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 46.7%; Score 120.4; DB 6; Length 4062;
Best Local Similarity 99.2%; Pred. No. 1.2e-17;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 850 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 909
QY 61 GGTACCATGATCCAGATGGCAGCATCAGAGGGAGCCCTGCCAACGTGGAATTCACCTCAG 120
Db 910 GGTACCATGATCCAGATGGCAGCATCAGAGGGAGCCCTGCCAACGTGGAATTCACCTCAG 969
QY 121 GT 122
Db 970 CT 971

RESULT 18
AR270915
LOCUS AR270915 4062 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 1478 from patent US 6500938.
ACCESSION AR270915
VERSION AR270915.1 GI:29702149
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4062)
AUTHORS Au-Young,J. and Seilhamer,J.J.
TITLE Composition for the detection of signaling pathway gene expression
JOURNAL Patent: US 6500938-A 1478 31-DEC-2002;
Incyte Genomics, Inc.; Palo Alto, CA;
```

```
Best Local Similarity 99.2%; Pred. No. 1.2e-17;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 850 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 909
QY 61 GGTACCATGATCCAGATGGCAGCATCAGAGGGAGCCCTGCCAACGTGGAATTCACCTCAG 120
Db 910 GGTACCATGATCCAGATGGCAGCATCAGAGGGAGCCCTGCCAACGTGGAATTCACCTCAG 969
QY 121 GT 122
Db 970 CT 971

RESULT 17
QY76469
LOCUS QY76469 4062 bp DNA linear PAT 11-MAR-2004
DEFINITION Sequence 155 from Patent EP1394274.
ACCESSION QY76469
VERSION QY76469.1 GI:45379859
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuwara,K.
TITLE Methods of testing for bronchial asthma or chronic obstructive
JOURNAL Patent: EP 1394274-A 155 03-MAR-2004;
FEATURES
source
1. 4062
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 46.7%; Score 120.4; DB 6; Length 4062;
Best Local Similarity 99.2%; Pred. No. 1.2e-17;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 850 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 909
QY 61 GGTACCATGATCCAGATGGCAGCATCAGAGGGAGCCCTGCCAACGTGGAATTCACCTCAG 120
Db 910 GGTACCATGATCCAGATGGCAGCATCAGAGGGAGCCCTGCCAACGTGGAATTCACCTCAG 969
QY 121 GT 122
Db 970 CT 971

RESULT 18
AR270915
LOCUS AR270915 4062 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 1478 from patent US 6500938.
ACCESSION AR270915
VERSION AR270915.1 GI:29702149
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4062)
AUTHORS Au-Young,J. and Seilhamer,J.J.
TITLE Composition for the detection of signaling pathway gene expression
JOURNAL Patent: US 6500938-A 1478 31-DEC-2002;
Incyte Genomics, Inc.; Palo Alto, CA;
```

WOX;	
FEATURES	Location/Qualifiers
source	1..4062
	/organism="unknown"
	/mol_type="genomic DNA"
ORIGIN	
Query Match	46.7%; Score 120.4; DB 6; Length 4062;
Best Local Similarity	99.2%; Pred.No. 1.2e-17;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1 CAGCGGAGTGATGGCAAGCAGCAGCTTCCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 60
Db	850 CAGCGGAGTGATGGCAAGCAGCAGCTTCCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 909
Qy	61 GGCTACCATGCGCAGATGGCAGATCAGAGGGGACCTGCCAACGTGGAATTCACATCAG 120
Db	910 GGCTACCATGCGCAGATGGCAGATGGCAGATCAGAGGGGACCTGCCAACGTGGAATTCACATCAG 969
Qy	121 GT 122
Db	970 CT 971
RESULT 19	
LOCUS	HSU31511 4062 bp mRNA linear PRI 11-MAR-1997
DEFINITION	Human inducible nitric oxide synthase (NOS) mRNA, complete cds.
ACCESSION	U31511
VERSION	U31511.1 GI:951320
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
	Hominidae; Homo.
REFERENCE	1 (bases 1 to 4062)
AUTHORS	Park, C.S., Park, R. and Krishna, G.
TITLE	Constitutive expression and structural diversity of inducible isoform of nitric oxide synthase in human tissues
JOURNAL	Life Sci. 59 (3), 219-225 (1996)
PUBMED	869932
REFERENCE	2 (bases 1 to 4062)
AUTHORS	Park, C., Gianotti, C., Park, R. and Krishna, G.
TITLE	Direct Submision
JOURNAL	Submitted (11-JUL-1995) Chang-Shin Park, Lab. of Molecular Immunology, NHLBI, 9000 Rockville Pike, Bethesda, MD 20892-1760, USA
FEATURES	Location/Qualifiers
source	1..4062
	/organism="Homo sapiens"
	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/chromosome="17"
	/map="17cen-q11.2"
gene	1..4062
	/gene="NOS"
CDS	106..3567
	/gene="NOS"
	/note="inducible isoform"
	/codon_start=1
	/product="nitric oxide synthase"
	/protein_id="AAB49041.1"
	/db_xref="GI:951321"
	/translations="MACPWWKFLFKTFHQYAMNGEKDINNVERKAPCATSSPVTDQDL QYNLSQQNESPOLVETGKSPESLVKLDATPLSSPRHVRKNWGGSGMTFODTLHH KAGKILCRSKSCIGSMTPKSLTRGPRDKPTDPELLPOAIEFVNYYGSPFKEAKIE EHLARVAVTKELTETTYQLTGDELIFATQAWRNAPRIGRIQWNLQVFDARCS TAREMFHICRHVYRTNNGIRSAITVFFQSDGRKDFRWNAQLIRIAGYQMPGS IRGDPANVEFTQLCCDIGWPKYGRFDVPLVLQNGRDPDLFEIPDDLVLVAMEHP IYEWFELEKLWALPVALNMLEVGFPGCFPNQWYMGTEIGVRDFCDVQRNII EEVGRMGLETHKLASLWKQAVVEINIAVLHSFQKQNVIMDHSAESFMKYMONE YRSRGGCCPADWILVPPMSGSIITPVPHQEMLVLSPPFYIYQVEAWKTHVQDEKRRP

		polyA_site			
		/gene="NOS"			
		/note="16 A nucleotides"			
ORIGIN					
Query Match		46.7%; Score 120.4; DB 8; Length 4062;			
Best Local Similarity		99.2%; Pred. No. 1.2e-17;			
Matches 121; Conservative		0; Mismatches 1; Indels 0; Gaps 0;			
Qy	1	CAGCGGAGTGATGGCAAGCAGCAGCTTCCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT	60		
Db	850	CAGCGGAGTGATGGCAAGCAGCAGCTTCCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT	909		
Qy	61	GGCTACCATGCGCAGATGGCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG	120		
Db	910	GGCTACCATGCGCAGATGGCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG	969		
Qy	121	GT 122			
Db	970	CT 971			
RESULT 20					
I15516		4145 bp		DNA	linear PAT 02-APR-1996
DEFINITION		Sequence 1 from patent US 5468630.			
ACCESSION		I15516			
VERSION		I15516.1 GI:1250424			
KEYWORDS		.			
SOURCE		Unknown.			
ORGANISM		Unclassified.			
REFERENCE		1 (bases 1 to 4145)			
AUTHORS		Billiar,T.R., Nusseier,A.K., Geller,D.A. and Simmons,R.L.			
TITLE		cDNA clone for human inducible nitric oxide synthase and process for preparing same			
JOURNAL		Patent: US 5468630-A 1 21-NOV-1995;			
FEATURES		Location/Qualifiers			
source		1..4145			
		/organism="unknown"			
		/mol_type="unassigned DNA"			
ORIGIN					
Query Match 46.7%; Score 120.4; DB 6; Length 4145;					
Best Local Similarity 99.2%; Pred. No. 1.2e-17;					
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
Qy	1	CAGCGGAGTGATGGCAAGCAGCAGCTTCCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT	60		
Db	951	CAGCGGAGTGATGGCAAGCAGCAGCTTCCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT	1010		
Qy	61	GGCTACCATGCGCAGATGGCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG	120		
Db	1011	GGCTACCATGCGCAGATGGCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG	1070		
Qy	121	GT 122			
Db	1071	CT 1072			
RESULT 21					



QYHNLSKQONESPOPLVETGKSPESLVKLDATPLSPRHVRIKNMGSGMTFODTLHH  
KAKGILTCRSKSLGSIIMTPKSLTRGRDXTPTDELLPOAIEFVNQYGSFKAEKIE  
EHLARVAVTKIEITTYQITGDELIFATKQARNAPRCIGRIQNSLNQVDFARSCS  
TAREMFHICRHVRYSTNNGNIRSAITVFFQPSDGRDGRFVWNAQLIRYAGYQMPDGS  
IRGDPANVEFTQLCIDLGWPKYGRFDVPLVLQANGRDPELFEIPDLVLEAMBHP  
KEYWRELELKWALPAVANMLLEVGLEFPGCCFNQWYMGTEIGVRDFCDVQRYNII  
EEVRRMGLETHKLASLWKQDAVVEINIAVLHSFQKONVTIMDHSAAESFMKYMONE  
YRSRGGCPADWILVPPMGSITPVFQHEMLNVLSPFYVQVEAWKTHVQDEKRRP  
KRREIPBLKVLKAVLFACMLMRKTASRVRTILPATETYSKSEALWDLGALSCAFN  
PKVYMDKYLSCLBEERLLVVTSTFGNGDCPENGEGKJXSLFMLKELNNKFRYAVF  
GLSSMYPRFCAFAHDIDQKLSHLGASQLTPMGEGDELSGOEDAFRSWAVQTPKAACE  
TFDVRGKHQIPIKLYTSNVTWDPHHYLVQDSQPLDLKSLGSMHAKNVFTWRLKSR  
ONLQSPSTSRATILVELSCDGOGLNVLPGHILGVCPCGNOPALVQGLIRVVDGPTPH  
QTVREALDESQSVWSDKLPCLSLQALTYFLDITPTPTQLLQKLAQVATEEER  
ORLEALCQSEYSKWKFTNSPTFLEVEEFPSSURVSAGFLLSQPLILKPRFYSISSR  
DHTPTETHLTVAVVYTHTRDQGPLHGVCSWTWNSLKPDQDPVPCFVRNAGSHLPED  
PSHPICLIGPTGIAPRSFQWRQLHDSQHKVGRGRTLVFGCRRPDEDHIIYOEEML  
EMAQKGVILHVAHTAYSRLPGKPKVYVODILRQQLASEVLRLHKEPGLHVCVDVRMA  
RDVAHTLQKLVAAKLNBEQVEDYFFQLKSQKRYHEDI FGAVPFYEAKKDRVAVQPS  
SLEMSAL"

ORIGIN

Query Match 46.7%; Score 120.4; DB 6; Length 4164;  
Best Local Similarity 99.2%; Pred. No. 1.2e-17;  
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 CAGCGGAGTGATGCAACGACGACTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
Db 970 CAGCGGAGTGATGCAACGACGACTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1029  
  
Qy 61 GGCTACCAGATGCCAGATGCGCAGCATCAGAGGGACCCCTGCCACGTTGGAATTCACCTCAG 120  
Db 1030 GGCTACCAGATGCCAGATGCGCAGCATCAGAGGGACCCCTGCCACGTTGGAATTCACCTCAG 1089

Qy 121 GT 122  
Db 1090 CT 1091

RESULT 24  
AR380862  
LOCUS AR380862  
DEFINITION Sequence 1407 from patent US 6607879.  
ACCESSION AR380862  
VERSION AR380862.1 GI:40088496  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 4164)  
AUTHORS Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.  
TITLE Compositions for the detection of blood cell and immunological response gene expression  
JOURNAL Patent: US 6607879-A 1407 19-AUG-2003;  
Incyte Corporation; Palo Alto, CA  
FEATURES  
source Location/Qualifiers  
1..4164  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 46.7%; Score 120.4; DB 6; Length 4164;  
Best Local Similarity 99.2%; Pred. No. 1.2e-17;  
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 CAGCGGAGTGATGCAACGACGACTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
Db 970 CAGCGGAGTGATGCAACGACGACTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1029  
  
Qy 61 GGCTACCAGATGCCAGATGCGCAGCATCAGAGGGACCCCTGCCACGTTGGAATTCACCTCAG 120  
Db 1030 GGCTACCAGATGCCAGATGCGCAGCATCAGAGGGACCCCTGCCACGTTGGAATTCACCTCAG 1089

Qy 121 GT 122  
Db 1090 CT 1091  
  
RESULT 25  
HSINOSA  
LOCUS HSINOSA  
DEFINITION H. sapiens mRNA for nitric oxide synthase.  
ACCESSION X73029  
VERSION X73029.1 GI:441452  
KEYWORDS nitric oxide synthase.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Charles I. G., Palmer R.M., Hickery,M.S., Bayliss,M.T., Chubb,A.P., Hall,V.S., Moss,D.W. and Moncada,S.  
TITLE Cloning, characterization, and expression of a cDNA encoding an inducible nitric oxide synthase from the human chondrocyte  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 90 (23), 11419-11423 (1993)  
PUBMED 7504305  
REFERENCE 2 (bases 1 to 4164)  
AUTHORS Charles,I.  
TITLE Direct Submission  
JOURNAL Submitted (23-APR-1993) I. Charles, Wellcome Research Laboratories, Ble. 113, Dept. of Cekk Biology, Langley Park, Beckenham, Kent, BR3 3BS, UK

FEATURES

source Location/Qualifiers  
1..4164  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/cell\_type="chondrocyte"  
1..4164  
/gene="INOS"  
226..3687  
/gene="INOS"  
/codon\_start=1  
/product="nitric oxide synthase"  
/protein\_id="CAA51512.1"  
/db\_xref="GI:441453"  
/db\_xref="GOA:P35228"  
/db\_xref="UniProt/Swiss-Prot:P35228"  
/translation="MACPKFKFTKFKHYAMNGEKDINNVEKAPCATSSPVTDLL QYHNLSKQONESPOPLVETGKSPESLVKLDATPLSPRHVRIKNMGSGMTFODTLHH KAKGILTCRSKSLGSIIMTPKSLTRGRDXTPTDELLPOAIEFVNQYGSFKAEKIE EHLARVAVTKIEITTYQITGDELIFATKQARNAPRCIGRIQNSLNQVDFARSCS TAREMFHICRHVRYSTNNGNIRSAITVFFQPSDGRDGRFVWNAQLIRYAGYQMPDGS IRGDPANVEFTQLCIDLGWPKYGRFDVPLVLQANGRDPELFEIPDLVLEAMBHP KEYWRELELKWALPAVANMLLEVGLEFPGCCFNQWYMGTEIGVRDFCDVQRYNII EEVRRMGLETHKLASLWKQDAVVEINIAVLHSFQKONVTIMDHSAAESFMKYMONE YRSRGGCPADWILVPPMGSITPVFQHEMLNVLSPFYVQVEAWKTHVQDEKRRP KRREIPBLKVLKAVLFACMLMRKTASRVRTILPATETYSKSEALWDLGALSCAFN PKVYMDKYLSCLBEERLLVVTSTFGNGDCPENGEGKJXSLFMLKELNNKFRYAVF GLSSMYPRFCAFAHDIDQKLSHLGASQLTPMGEGDELSGOEDAFRSWAVQTPKAACE TFDVRGKHQIPIKLYTSNVTWDPHHYLVQDSQPLDLKSLGSMHAKNVFTWRLKSR ONLQSPSTSRATILVELSCDGOGLNVLPGHILGVCPCGNOPALVQGLIRVVDGPTPH QTVREALDESQSVWSDKLPCLSLQALTYFLDITPTPTQLLQKLAQVATEEER ORLEALCQSEYSKWKFTNSPTFLEVEEFPSSURVSAGFLLSQPLILKPRFYSISSR DHTPTETHLTVAVVYTHTRDQGPLHGVCSWTWNSLKPDQDPVPCFVRNAGSHLPED PSHPICLIGPTGIAPRSFQWRQLHDSQHKVGRGRTLVFGCRRPDEDHIIYOEEML EMAQKGVILHVAHTAYSRLPGKPKVYVODILRQQLASEVLRLHKEPGLHVCVDVRMA RDVAHTLQKLVAAKLNBEQVEDYFFQLKSQKRYHEDI FGAVPFYEAKKDRVAVQPS SLEMSAL"

Query Match 46.7%; Score 120.4; DB 8; Length 4164;  
Best Local Similarity 99.2%; Pred. No. 1.2e-17;  
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 CAGCGGAGTGATGCAACGACGACTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
Db 970 CAGCGGAGTGATGCAACGACGACTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1029  
  
Qy 61 GGCTACCAGATGCCAGATGCGCAGCATCAGAGGGACCCCTGCCACGTTGGAATTCACCTCAG 120  
Db 1030 GGCTACCAGATGCCAGATGCGCAGCATCAGAGGGACCCCTGCCACGTTGGAATTCACCTCAG 1089

```

QY 1 CAGCGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 970 CAGCGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1029
QY 61 GGCTACCAAGTCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTAG 120
Db 1030 GGCTACCAAGTCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTAG 1089
QY 121 GT 122
Db 1090 CT 1091

RESULT 26
LOCUS CQ723665 4467 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 9599 from Patent WO02068579.
ACCESSION CQ723665
VERSION CQ723665.1 GI:42284522
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 9599 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
source
location/Qualifiers
1..4467
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 46.7%; Score 120.4; DB 6; Length 4467;
Best Local Similarity 99.2%; Pred. No. 1.1e-17;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 745 CAGCGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 804
QY 61 GGCTACCAAGTCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTAG 120
Db 805 GGCTACCAAGTCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTAG 864
QY 121 GT 122
Db 865 CT 866

RESULT 27
LOCUS AY046510 35764 bp DNA linear SYN 17-SEP-2001
DEFINITION Adenoviral expression vector Ad-hiNOS, complete sequence.
ACCESSION AY046510
VERSION AY046510.1 GI:15636799
KEYWORDS Adenoviral expression vector Ad-hiNOS
SOURCE Adenoviral expression vector Ad-hiNOS
ORGANISM Adenoviral expression vector Ad-hiNOS
other sequences; artificial sequences; vectors.
REFERENCE 1 (bases 1 to 35764)
AUTHORS Shapiro,R., Gao,W., Tzeng,E., Robbins,P.D., Timoty,B.R. and
Gambotto,A.
TITLE Construction and characterization of a clinical grade adenoviral
vector encoding the human iNOS cDNA
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 35764)

```

---

```

AUTHORS Shapiro,R., Gao,W., Tzeng,E., Robbins,P.D., Timoty,B.R. and
Gambotto,A.
TITLE Direct Submission
JOURNAL Submitted (18-JUL-2001) Surgery, University of Pittsburgh, 300
Technology Drive, Pittsburgh, PA 15219, USA
FEATURES
source
location/Qualifiers
1..35764
/organism="Adenoviral expression vector Ad-hiNOS"
/mol_type="genomic DNA"
/db_xref="taxon:170704"
/Note="recombinant human adenovirus type 5 encoding human
iNOS; derived from padlox shuttle vector and donor
adenoviral vector psi5"
repeat_region
1..103
/Note="terminal repeat"
/rpt_type=inverted
misc_feature
193..354
/Note="packaging site"
gene
1264..4725
/Note="iNOS"
1264..4725
/Note="iNOS"
CDS
/codon_start=1
/product="inducible nitric oxide synthase"
/protein_id="AAL02120.1"
/db_xref="GI:15636800"
/translation="MACPWKFLFTKFKHYAMGKEDINNVEKAPCATSSPTQDDL
QYHNLKQONESPOLVETGKSPESLVKLDATPLSSPRHVRICKNGSGMTFQDITLHH
KAKGLITCRSKSLGSIINTPKSLTRGPRDKTPPDELLPOALEFVNOYGSFKEAKIE
BHLARVEATKEIETTYQTGDELLIFATKOAMRNAPRCIGRIQWSNLQVDFDASKIS
TAREMFEHICRHVRYSTNGNIRSAITVFPQSDGKHDFVWNAQLIRYAGQMDPGS
IRGDPANVFETQLCIDLGKPKYGRFVVPLVQLANGRDPELFEIPDLVLAAMEHP
KYEMPRELEKWAYALPAVANMLLEVGLFEPGCPNGWYMGTEIFGIDVQVRYNII
EVEGREGLETHKLASLKDQAVRINIAVHSFPOKQNTVMDHSAAESPMKYQNE
YRSRGCPADWILVPPMSGSIPTVFHQMNLNVLSPFYQVEAKTHVQDEKRRP
KRREIPKLVKAVLFAFLMKRTWASRVRTILPATETGSEBALWDLGALFSCAFN
PKVCMDKYRLSCLEBEERLLLVSTFGNGDCPGNGEKLKSLFLMELNNKFRVAVF
GLGSSMYPRCAFADHIDQKLSHLGASLTQPMGEDELSDGQEDASWAVQTFKAAEC
TFDVRGKQHIQIPKLYTSNTVDPHYRLVODSOPLDLSKALSSMHAKNVFTMRILKS
QNLQSTSSRATILVELSCDQGLNLYLPGHLYGVCNPNALVQILERVVDGTPPH
QTRLEDDDESQSYWSDKRLPPCSLSQALTYSPDITTPPTQLLQKLQAVATESPER
QRLEALCFPSEYKWKFTNSPTFLVLEBEPSELRSVAGFLUGLQFLIKRPFYSISSR
DHTPTTEHLTVAVVYHTGDSQGLHGVCSWTLSNLSKPDQDPVPCFVRNASAPHILPE
PSHCILIGPGTGIVPFRSFQOORLHDSQHKVGGRMTLVFGCRPRDSDHITYEBEML
EMAOGLVHAVHTAYSRLPGKPKVYQDILROQLASEVLRLVHLKPEGHLYVCGDVRMA
RDVATLQALVAALKLNEEQVEDYFFQLKSKRYHEDIFGAVFPVEAKKDRVAVQPS
SLEMSAL"
polyA_signal
4932..4936
/Note="SV40 early polyadenylation signal"
polyA_signal
4961..4965
/Note="SV40 polyadenylation signal"
protein_bind
5044..5077
/bound_moiety="LoxP"
repeat_region
35661..35764
/Note="terminal repeat"
/rpt_type=inverted

ORIGIN
Query Match 46.7%; Score 120.4; DB 11; Length 35764;
Best Local Similarity 99.2%; Pred. No. 8.4e-18;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 2008 CAGCGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 2067
QY 61 GGCTACCAAGTCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTAG 120
Db 2068 GGCTACCAAGTCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTAG 2127
QY 121 GT 122
Db 2128 CT 2129

```

RESULT 28  
AX067222  
LOCUS  
DEFINITION  
Sequence 3 from Patent WO0078946.  
AX067222  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
Keller,E.T., Gravenstein,S. and Hall,D.M.  
Treatment of viral influenza with antisense oligonucleotides  
Patent: WO 0078946-A 3 28-DEC-2000;  
JOURNAL  
Eastern Virginia Medical School (US)  
Location/Qualifiers  
FEATURES  
source  
1. .4150  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 46.0%; Score 118.8; DB 6; Length 4150;  
Best Local Similarity 98.4%; Pred. No. 2.7e-17;  
Matches 120; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 CAGCGGAGTATGCGACGACGACGCTCCGGGTGGGAATGCTCAGCTCCTCCGCTATGCT 60  
Db 979 CAGCGGAGTATGCGACGACGACGCTCCGGGTGGGAATGCTCAGCTCCTCCGCTATGCT 1038  
Qy 61 GGCTACAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAG 120  
Db 1039 GGCTACAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAG 1098  
Qy 121 GT 122  
Db 1099 CT 1100  
RESULT 29  
AF068236  
LOCUS  
DEFINITION  
Homo sapiens inducible nitric oxide synthase (NOS) mRNA, complete  
cda.  
AF068236  
VERSION  
AF068236.1 GI:3192916  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 4150)  
Luss,H., Li,R.-K., Shapiro,R.A., Tzeng,E., McGowan,F.X.,  
Yoneyama,T., Hatakayama,K., Geller,D.A., Mickle,D.A.G.,  
Simmons,R.L. and Billiar,T.R.  
Dedifferentiated human ventricular cardiac myocytes express  
inducible nitric oxide synthase mRNA but not protein in response to  
IL-1, TNF, IFNgamma, and LPS  
J. Mol. Cell. Cardiol. 29 (4), 1153-1165 (1997)  
9160867  
2 (bases 1 to 4150)  
Luss,H., Li,R.-K., Shapiro,R.A., Tzeng,E., McGowan,F.X.,  
Yoneyama,T., Hatakayama,K., Geller,D.A., Mickle,D.A.G.,  
Simmons,R.L. and Billiar,T.R.  
Direct Submission  
Submitted (26-MAY-1998) Pharmacology, Westf.Wilhelms-Univ.,  
JOURNAL Domagstr. 12, Munster D-48149, Germany  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
FEATURES  
Location/Qualifiers

source  
1. .4150  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/cell\_type="cardiac myocytes"  
gene  
1. .4150  
/gene="NOS"  
CDS  
235..3696  
/gene="NOS"  
/note="NOS II"  
/codon\_start=1  
/product="inducible nitric oxide synthase"  
/protein\_id="AAC19133.1"  
/db\_xref="GI:3192917"  
/translation="MACPKFLFKTKHQYAMNGEKDINNVEKAPCATSSPTVQDDL  
QYHNSKQNESQPLVETGKKSPELVKLDATPLSSPRHVRINKNGSGMTFDTLHH  
KAKGILTCRSKSLGIMTPKSLTRGPRDKPTPDELLPOAIEFVNYQYGSFGEAKIE  
EHLARVEAVTKEIETTGTQGTDELIFATKQARNAPRCIGRIQNSNLQVFPARCS  
TAREMPEHLCHRVYSTNGNIRSAITVFPQSDGKHDFRVNNAQILHYAGYOMPDS  
IRGDPANVEFTQCIDLGNKPKYGRFVDVPLVLAQNGRDELFELIPDLVLEVAMEHP  
KYEVPRELSLKTALPAVAMLLVEGLLEFPFGCPNGYMGTEIGVRDFCDVQRNII  
EEVRRMGLETHKLASLWKDAQVEINIAVLHSFQKQNTIMDHHSTAESFMKYMNE  
YRSRGCCPADWIWLVPPMSGSIPTVPHQEMLVNLSFYYQYQVEAKTHLVQDEKRRP  
KRREIPLKVLVAVLFACMLMRKTMAASRVRTILFATETGKSEALAWDLGALFSCAFN  
PKVVCNDKYRLSLCEERLLVVTSTFGNGDCPENGKELKSLFMLKELNKKRYAYE  
GLGSSWYPRFCAPAHIDIKLHSLGASQLTPMGEGDELSQEDAFPSWAVQTPKAAE  
TFDVRGKHQIQPKLYTSNVTWDPHHYRLVQDSQPLDLKSLSSMHAKNVFTWRLKSR  
QNLQSPSTSRATILVELSCEDGGQNLVLPGEHLGVCQGNQALVQGILERVVDGPTPH  
QTVRLBALDESGSYWVSDKRLPPCSLSQALTYFLDITPTPTQLLQKLAQVATEEPR  
ORLEALCQPSSEYKWKNTSPTELEVEFPSPRSVAGFLLSQLPLKPFYFYSISR  
DHPTEHLTVAVVTYTRDGGGPHHGVCSWLNSLKPDQVPVCFVRNAGSGHLPED  
PSHPCILIGFGTGIAPFRSFWQRLHDSQHKVGRGMILVFCRRPDEDHIIQVEEML  
ENWAKGHAVHTAYSRLPKPKYVVDILRQQLASEVLRLVHLKPEGHLYVCGDVRMA  
ROVAHTLKQLVAAKLKLNBEQVEDYFOLKSQRYHEDIFGAVFPVEAKKDRVAVQPS  
SLEMSAL"  
ORIGIN  
Query Match 46.0%; Score 118.8; DB 8; Length 4150;  
Best Local Similarity 98.4%; Pred. No. 2.7e-17;  
Matches 120; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 CAGCGGAGTATGCGACGACGACGCTCCGGGTGGGAATGCTCAGCTCCTCCGCTATGCT 60  
Db 979 CAGCGGAGTATGCGACGACGACGCTCCGGGTGGGAATGCTCAGCTCCTCCGCTATGCT 1038  
Qy 61 GGCTACAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAG 120  
Db 1039 GGCTACAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAG 1098  
Qy 121 GT 122  
Db 1099 CT 1100  
RESULT 30  
AC158064/c  
LOCUS  
DEFINITION  
Bos taurus clone CH240-54J11, WORKING DRAFT SEQUENCE, 16 unordered  
pieces.  
AC158064  
AC158064.2 GI:68266847  
VERSION  
HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP.  
KEYWORDS  
SOURCE  
Bos taurus (cow)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Bovinae; Bos.  
1 (bases 1 to 179504)  
Muzny,D.Marie., Metzker,M.Lee., Abramson,S., Adams,C., Alder,J.,  
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,  
Anyalebechi,V., Aoyagi,M., Ayodeji,M., Baca,E., Baden,H.,  
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,  
Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,

Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Frazer, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Georegeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hoques, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowitz, C., Kratt, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Louseged, H., Lozado, R.J., Lu, X., Ma, J., Maheeshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, E., Mathiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Muidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaelim, O., Okwuonu, G., Olarnpungagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajls, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steidle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczky, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weitas, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Direct Submission  
Unpublished  
2 (bases 1 to 179504)  
Worley, K.C.

Direct Submission  
Submitted (04-MAR-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 179504)  
Cow Genome Sequencing Consortium.

Direct Submission  
Submitted (01-JUL-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Jun 28, 2005 this sequence version replaced gi:60498836.  
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
Center: Baylor College of Medicine

Center code: BCM  
Web site: http://www.hgsc.bcm.tmc.edu/  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: FDEA  
Center clone name: CH240-54J11  
----- Summary Statistics  
Assembly program: Atlas 3.0;  
Consensus quality: 174250 bases at least Q40  
Consensus quality: 175616 bases at least Q30  
Consensus quality: 176727 bases at least Q20  
Estimated insert size: 174799; sum-of-contigs estimation  
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation  
-----  
\* NOTE: Estimated insert size may differ from sequence length  
\* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 16 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\* 1 1552: contig of 1552 bp in length  
\* 1553 1602: gap of 50 bp  
\* 11784: contig of 10182 bp in length  
\* 11785 1834: gap of 50 bp  
\* 58179: contig of 46345 bp in length  
\* 58180 58174: gap of 395 bp  
\* 102955 102955: contig of 44381 bp in length  
\* 102956 103005: gap of 50 bp  
\* 103006 111668: contig of 8663 bp in length  
\* 111669 111718: gap of 50 bp  
\* 111719 120506: contig of 8788 bp in length  
\* 120507 120557: gap of 50 bp  
\* 125884 125933: contig of 5327 bp in length  
\* 125934 129689: contig of 3756 bp in length  
\* 129690 129739: gap of 50 bp  
\* 129740 144940: contig of 15200 bp in length  
\* 144940 145284: gap of 345 bp  
\* 145285 171600: contig of 26316 bp in length  
\* 171601 171700: gap of unknown length  
\* 171701 172740: contig of 1040 bp in length  
\* 172741 172840: gap of unknown length  
\* 172841 173900: contig of 1060 bp in length  
\* 173901 174000: gap of unknown length  
\* 174001 175179: contig of 1179 bp in length  
\* 175180 175279: gap of unknown length  
\* 175280 176330: contig of 1051 bp in length  
\* 176331 176430: gap of unknown length  
\* 176431 178072: contig of 1642 bp in length  
\* 178073 178172: gap of unknown length  
\* 178173 179504: contig of 1332 bp in length.  
\* 179504 Location/Qualifiers  
1..179504  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9913"  
/clone="CH240-54J11"  
1553..1602  
/estimated\_length=50  
11785..11784  
/estimated\_length=50  
58180..58174  
/estimated\_length=395  
102956..103005  
/estimated\_length=50  
111669..111718  
/estimated\_length=50  
120507..120556  
/estimated\_length=50

FEATURES  
Source

gap  
gap  
gap  
gap  
gap  
gap

```

gap      125884..125933
/estimated_length=50
gap      128690..129739
/estimated_length=50
gap      144940..145284
/estimated_length=345
gap      171601..171700
/estimated_length=unknown
gap      172741..172840
/estimated_length=unknown
gap      173901..174000
/estimated_length=unknown
gap      175180..175279
/estimated_length=unknown
gap      176331..176430
/estimated_length=unknown
gap      178073..178172
/estimated_length=unknown

ORIGIN
Query Match      45.0%; Score 116; DB 14; Length 179504;
Best Local Similarity 89.3%; Pred. No. 6.7e-17;
Matches 125; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY      1 CAGCGGAGTGATGCAAGCAGCATCTCCGGGTGGGAATGCTCAGCTCATCCGCTATGCT 60
Dbb      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
44076 CAGCGGAGCGATGGGAAGCATGACTTCCGGGTCTGGAAACGCCAGCTCATCCGCTATGCC 44017

QY      61 GGCTACCATGATGCCAGATGCGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
Dbb      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
44016 GGCTACCATGATGCCAGATGCGCAGCATCAGAGGGGACCCCGCCAACTGGAGTTCACACAG 43957

QY      121 GTACCGGCCCGCAGCTCAGC 140
Dbb      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
43956 GTACCGACCCAGCTTTGGC 43937

```

```

RESULT 31
LOCUS      AF223942
DEFINITION Ovis aries inducible nitric oxide synthase mRNA, partial cds.
ACCESSION AF223942
VERSION    AF223942.1 GI:6980067
KEYWORDS   Ovis aries (sheep)
SOURCE      Ovis aries
ORGANISM    Ovis aries
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Caprinae; Ovis.
REFERENCE   1 (bases 1 to 2838)
AUTHORS     Mershon,J.L., Baker,R.S. and Clark,K.E.
TITLE       Estrogen increases iNOS expression in the ovine coronary artery
JOURNAL     Am. J. Physiol. Heart Circ. Physiol. 283 (3), H1169-H1180 (2002)
PUBMED      12181148
REFERENCE   2 (bases 1 to 2838)
AUTHORS     Mershon,J.L. and Clark,K.E.
TITLE       Direct Submission
JOURNAL     Submitted (12-JAN-2000) Department of Obstetrics and Gynecology,
            University of Cincinnati Medical Center, 231 Bethesda Ave,
            Cincinnati, OH 45267-0526 USA
FEATURES    Location/Qualifiers
            1..2838
                /organism="Ovis aries"
                /mol_type="mRNA"
                /db_xref="taxon:9940"
                <1..>2838
                /note="iNOS"
                /codon_start=3
                /product="inducible nitric oxide synthase"
                /protein_id="AA034710.1"
                /db_xref="GI:6980068"
                /translation="GTGTLTGDELIFATKQAWRNAPRCIGRIOWNSLQVDFARSCSTA
                GEMEHLICRHYRYATNNGNIRSAITVFPQRSDGKHDFRVNNAQLIRVAGYQMPDGSIR

```

```

GDPASVEFTQCIDLWGKPKFSRFDVLPVLQADGRDPBLFEIPPDVLVLEVPMEHPRY
EWFRELEKMYALPAVANMLLEVGLFEGPCENGWGMTEVGRDFCDVQRYNILEE
VGRMGLETHKLSLWKRVAEINVAVLSHQKQNVITMDHHSAAESFNKYQNEYR
SGGCPADWILWVPFISGSIITPVHOEMNLIIISPYITQVEAWKTHWQDERRPQR
REIRFKYLKAVFFASVLMQKAMSSVRATILFATETGRSETLAQDLGALFSCAFNPK
VLCDQYRLSHLEEEQLLVVTSFNGDSPGNGEKLKSLMLKELTNKFRYAVFGL
GSSMPQFCFAFHDIDKLSQASQALAPTGEGLSGQBEAFPSWAVOTFKAACETP
DVSQKHIEIPKLYTSSVTWDPHYELVODSEPLDLNKLSSMHAKPVFTMRKSOON
LQSPKSRITLLVELSCGSOAPSILPGHILGVFPNCQNALVQGLILERVVDGPAPQOP
MRLETCENGSYWVKDRPPLPPCSQALTHFLDITTPPTQLLRKLAQLATEISRRDL
LETLCQPSYNDKNGKFTNPTFLEVEFPFSLRVSASFLLSQPLKPRYYISSESRDL
TPEILHTVAVLTITRDQGPLHGVCTWLSLKPQDPVPCFVSASGQFQPEDESR
RPCILIGPGTGIAPPSFWQORLHEAHKGLQGRMTLVFGRRRPEEDHLYWEMLEEM
ARKGVLEHVHTAYSRLPDQPKVYVODILRQRLAGEVLRVLHBEQGHLYVCGDYRMARD
VAHSLKQLMATALSLNEEQVEDYFOLKNQK"

ORIGIN
Query Match      39.8%; Score 102.8; DB 4; Length 2838;
Best Local Similarity 90.2%; Pred. No. 1.4e-13;
Matches 110; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY      1 CAGCGAGTGATGGCAAGCAGCATCTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Dbb      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
219 CAGCGAGCGATGGGAAGCATGACTTCCGGGTCTGGAAATGCCAGCTCATCCGCTATGCC 278

QY      61 GGCTACCATGATGCCAGATGCGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
Dbb      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
279 GGCTACCATGATGCCAGATGCGCAGCATCAGAGGGGACCCCGCCAGTTCAGGATTCACACAG 338

QY      121 GT 122
Dbb      339 CT 340

RESULT 32
LOCUS      BV410321/c
DEFINITION S229P690FE2.T0 GermanShepherd Canis familiaris STS genomic,
            sequence tagged site.
ACCESSION   BV410321
VERSION     BV410321.1 GI:57784102
KEYWORDS    STS.
SOURCE      Canis familiaris (dog)
ORGANISM    Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1 (bases 1 to 648)
AUTHORS     Lindblad-Toh,K.
TITLE       The genome sequence of Canis familiaris
JOURNAL     Unpublished (2004)
COMMENT      Contact: Kerstin Lindblad-Toh
            Whitehead Institute for Biomedical Research, Center for Genome
            Research
            320 Charles Street, Cambridge, MA 02141, USA
            Tel: 6172521477
            Fax: 6172580903
            Email: keri@genome.wi.mit.edu
            Primer A: No sequence submitted
            Primer B: No sequence submitted
            STS size: 648
            Protocol:
            WGS-discovery (WGS):
            Paired-end low-coverage whole genome shotgun reads were generated
            from 9 breeds
            (German Shepherd, Rottweiler, Bedlington Terrier, Beagle, Labrador
            Retriever, English
            Shepherd, Italian Greyhound, Alaskan Malamute and the Portuguese
            Water Dog -100,000 each)
            and five other canids (Chinese, Alaskan, Indian and Spanish Gray
            Wolf as well as the
            Californian Coyote).

```







```
165136..165284,166050..166244,168294..168894)
/locus_tag="Nos2"
/product="nitric oxide synthase 2, inducible, macrophage"
/notes="match: ESTs: Em:AA512708.1 Em:BE372884.1
Em:BG974882.1 Em:BY174336.1 Em:BY175860.1 Em:BY176421.1
Em:BY202059.1 Em:BY724147.1 Em:BY747653.1 Em:CD555051.1
match: cDNAa: Em:AF065921.2 Em:AF065922.2 Em:AF065923.2
Em:AV090567.1 Em:BC062378.1 Em:D12520.1 Em:M84373.1
Em:M92649.1 Em:U43428.1"
Join(130908..131017,137214..137283,138391..138510,
140220..140368,143992..144154,145003..145134,
146201..146342,146440..146579,148619..148793,
148888..148989,153300..153494,153872..153954,
154279..154423,154509..154613,156487..156536,
156853..157027,157723..157855,158254..158332,
158596..158777,159735..159898,161443..161650,
163535..163622,163980..164101,165136..165284,
166050..166244,168294..168392)
/locus_tag="Nos2"
/standard_names="OTTMUSP00000000202"
/notes="match: proteins: Sw:O19114 Sw:P29477 Tr:AAH62378
Tr:AA124076 Tr:O97604 Tr:Q8R410 Tr:Q9BDH6 Tr:Q9N175"
/codon_start=1
/product="nitric oxide synthase 2, inducible, macrophage"
/protein_id="CAI25275.1"
/db_xref="GI:56208296"
/db_xref="InterPro:IPR001094"
/db_xref="InterPro:IPR001433"
/db_xref="InterPro:IPR001709"
/db_xref="InterPro:IPR003097"
/db_xref="InterPro:IPR004030"
/db_xref="InterPro:IPR008254"
/translation="MACPWKFLFKVKSQSDLKKEKQINNKKVTKPCAVLSPTIQDDP
KSHQSGPOLITGAQNVPESLDKLHVTSPQYVRIKNWGSGEILHDTLHKHATSDF
TCKSKSLGSIWNPXSLTRGPRDKPTPLELLPHAI EFINOYGSFKEAKTEHLARL
EAVTKEITGYQLTIDELIPATKMANRNAPRCIGRIQWNLQVDFARNCSQAQEMF
QHICRHIFATNNGNIRGAIVFPQSRDQGDGDFRLWNSQLINRAGYQPDGTIRGDA
TLEFTQCIDLGWKPRYGRDFVLPLQDQGDPEVFEIPDLVLEVTMEHPKPYEFQ
ELGKWPALPAAVNNLVEGLLEFPACFPNGMYMGTEIGVRDFCDTRYNILEEYGR
MGLETHYALSLMDKRAVTEINVAVLHSGKQNVITMDHHTASESPMKMQNEFYRARG
CPADWLVPPVSGSITPVFHOELNLYLSPPYYQIIPWKTHIWONEKLRRPREIR
FRVIVKATVPMKMKWASVRATLVFATETGSEALARDLATLFSYANKVKVCM
DYKASTLEEQLLLVITSTFGNDCPCNQTLKSLFMLELNLHTFRYAVFLGSSM
YQFCAPAHIDIDKLSHLGASQALPTGSDLSQEDAFPSWAVTFRAACETFDVRS
KHQIQIPKFTSNATWEPQYRLIQSPPELDNLRALSIHAKNVFTMLKSNQNLQSE
KSRITLLVQLTFEGSRGSPYLGHELGIFPGNQALVQGLERVTVDCTPHQTVCLE
VLDESGSYWVKDRLLPPCSLSOALTVDITPTTQLOLHLKARFATDTRORLEAL
CQPSYNDKFSNNTEFEVLEFPFLHVPRAFLLSQPLPKPRYSISSSQDHTPSE
VHLTVAVTIRQGGPDLHGVCSTWIRNLKPDPVFCFVRSVSGQPLPDPSPQPCI
LIGPGTGAFFRSFQWRKLVHDSQHKLGKGRMSLVFCRHPHEEDHLYDEEMQVWRK
VLQVHTGVSRLPFGPKPVYVDILOKLANEVLVSLHGEQGHLYICGRVWARDVATT
LKKVLKLNLSSEQVEDYFOLKSKRYHEDIFGAVFSYGAKGSALEEPKATRL"
168842..168847
/locus_tag="Nos2"
/locus_tag="RP23-341J22.2-001"
16863
/locus_tag="Nos2"
/locus_tag="RP23-341J22.2-001"
16866
/locus_tag="Nos2"
/locus_tag="RP23-341J22.2-001"
16870
/locus_tag="Nos2"
/locus_tag="RP23-341J22.2-001"
16885
/locus_tag="Nos2"
/locus_tag="RP23-341J22.2-001"
Join(AL592551.10:198515..198683,
AL592551.10:206760..206848,AL592551.10:210272..210473,
AL592551.10:212034..212144,complement(176638..176673),
AL592551.10:212034..212144,complement(176638..176673),
complement(176084..176134),complement(175517..175558),
complement(174638..174726),complement(174332..174494),
complement(171614..172181))
/locus_tag="RP23-12113.3-001"
/product="lectin, galactose binding, soluble 9"
/notes="match: ESTs: Em:AI042899.1 Em:AI043229.1
Em:AI530150.1 Em:AW541736.2 Em:BI647345.1 Em:BI647383.1
Em:BI657219.1 Em:BM243207.2
match: cDNAs: Em:BC003754.1 Em:U55060.1"
complement(171618)
/locus_tag="Lgals9"
/locus_tag="RP23-12113.3-001"
complement(171642..171647)
/locus_tag="Lgals9"
/locus_tag="RP23-12113.3-001"
Join(AL592551.10:198630..198683,
AL592551.10:206760..206848,AL592551.10:210272..210473,
AL592551.10:212034..212144,complement(178354..178433),
complement(176638..176673),complement(176084..176134),
complement(175517..175558),complement(174638..174726),
complement(174332..174494),complement(172035..172181))
/locus_tag="Lgals9"
/locus_tag="RP23-12113.3-002"
Join(AL592551.10:198630..198683,
AL592551.10:206760..206848,AL592551.10:210272..210473,
AL592551.10:212034..212144,complement(178354..178433),
complement(176638..176673),complement(176084..176134),
complement(175517..175558),complement(174638..174726),
complement(174332..174494),complement(172035..172181))
/locus_tag="Lgals9"
/locus_tag="RP23-12113.3-002"
/product="lectin, galactose binding, soluble 9"
Query Match 38.3%; Score 98.8; DB 9; Length 178443;
Best Local Similarity 78.7%; Pred. No. 6,1e-13;
Matches 129; Conservative 1; Mismatches 33; Indels 1; Gaps 1;
QY 1 CAGCGAGTGATGGCAACGACGACTTCGCGGTGTGGAAATGCTCAGCTCATCGCTATGCT 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 146223 CAGCGAGTGACGGCAAAATGCTTCAAGGCTTGGAAATTCAGAGCTCATCGGTACGCT 146282
QY 61 GGCTACCATGAGTCCAGATGGCAGCATCAGAGGACCTGCCAAGCTGGAATTCATCTCAG 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 146283 GGCTACCATGAGTCCGATGGCAGCATCAGAGGAGATGCTGCCACTTGAGATTACCCAG 146342
QY 121 GTACCGCGCCAGCTCAGCCRCGCGCATTTGGGCGGGGAGCC 164
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 146343 GTA-CTGACTCAGCTCTCTAGATCCCTGTGGCGAGGGAGCCC 146385
RESULT 36
AC036147
LOCUS 236456 bp DNA linear HTG 27-FEB-2003
DEFINITION Mus musculus chromosome 11 clone RP23-240G13 map 11, WORKING DRAFT
SEQUENCE, 10 unordered pieces.
ACCESSION AC036147
VERSION AC036147.4 GI:28570424
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 236456)
AUTHORS Birren,B., Nusbaum,C. and Lander,E.
```

**TITLE**  
**JOURNAL**  
**REFERENCE**  
**AUTHORS**

Mus musculus chromosome 11, clone RP23-240G13  
Unpublished  
2 (bases 1 to 236456)  
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,  
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,  
Boguslavskiy,L., Bouckgalter,B., Brown,A., Burkett,G.,  
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,  
Collamore,A., Cooke,P., DeAtellano,K., Dewar,K., Diaz,J.S.,  
Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,  
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,  
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,  
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,  
Klein,J., LaRoque,K., Lamazares,R., Landers,T., Lehoczy,J.,  
Levine,R., Liu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,  
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,  
Meldrum,J., Meneus,L., Mihova,T., Miranda,C., Mienga,V., Morrow,J.,  
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,  
O'Neill,D., Olivari,T.M., Oliver,J., Peterson,K., Pierre,N.,  
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,  
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,  
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,  
Testaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,  
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,  
Young,G., Zainoun,J., Zimmer,A. and Zody,M.

**TITLE**  
**JOURNAL**  
**REFERENCE**  
**AUTHORS**

Direct Submission  
Submitted (07-APR-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
3 (bases 1 to 236456)

Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,  
Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,  
Boguslavskiy,L., Bouckgalter,B., Camarata,J., Chang,J., Choepel,Y.,  
Collamore,A., Cook,A., Cooke,P., Corum,B., DeArelino,K.,  
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,  
Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,  
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,  
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,  
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,  
Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., Maclean,C.,  
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,  
Meldrum,J., Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J.,  
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,  
O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,  
Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,  
Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,  
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,  
Talamas,J., Testaye,S., Theodore,J., Topham,K., Travers,M.,  
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,  
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L8876

Center clone name: 240\_G\_13

----- Summary Statistics

Sequencing vector: M13; M7815; 40% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.960731  
Consensus quality: 23217 bases at least Q40  
Consensus quality: 234384 bases at least Q30  
Consensus quality: 235022 bases at least Q20  
Insert size: 230000; agarose-fp  
Insert size: 235556; sum-of-contigs

Quality coverage: 12.2 in Q20 bases; agarose-fp  
Quality coverage: 12.0 in Q20.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 10 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

\* 1 33985: contig of 33985 bp in length  
\* 33986 34085: gap of 100 bp  
\* 34086 35130: contig of 1045 bp in length  
\* 35131 35230: gap of 100 bp  
\* 35231 38166: contig of 2936 bp in length  
\* 38167 38266: gap of 100 bp  
\* 38267 41660: contig of 3394 bp in length  
\* 41661 41760: gap of 100 bp  
\* 41761 55510: contig of 13750 bp in length  
\* 55511 68417: contig of 12807 bp in length  
\* 68418 68517: gap of 100 bp  
\* 68518 141054: contig of 72537 bp in length  
\* 141055 141154: gap of 100 bp  
\* 141155 167738: contig of 26584 bp in length  
\* 167739 167838: gap of 100 bp  
\* 167839 203042: contig of 35204 bp in length  
\* 203043 203142: gap of 100 bp  
\* 203143 236456: contig of 33314 bp in length.

**FEATURES**  
**Location/Qualifiers**

source  
1..236456  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/chromosomes="11"  
/map="11"  
/clone="RP23-240G13"  
/clone\_lib="RPCI-23 Female Mouse BAC"  
misc\_feature  
1..33985  
/notes="assembly\_fragment"  
clone end:SP6  
vector side:left  
33986..34085  
/estimated\_length=100  
misc\_feature  
34086..35130  
/notes="assembly\_fragment"  
35131..35230  
/estimated\_length=100  
misc\_feature  
35231..38166  
/notes="assembly\_fragment"  
38167..38266  
/estimated\_length=100  
misc\_feature  
38267..41660  
/notes="assembly\_fragment"  
41661..41760  
/estimated\_length=100  
misc\_feature  
41761..55510  
/notes="assembly\_fragment"  
55511..68417  
/estimated\_length=100  
misc\_feature  
68418..68517  
/estimated\_length=100  
misc\_feature  
68518..141054  
/notes="assembly\_fragment"  
141055..141154  
/estimated\_length=100  
misc\_feature  
141155..167738  
/notes="assembly\_fragment"  
167739..167838  
/estimated\_length=100  
misc\_feature  
167839..203042

Matches 108; Conservative 0; Mismatches 16; Indels 0; Gaps 0

QY 1 CACGGAGTATGGCAGACAGACTTCGGGTGTGGAATGCTAGCTCATCGCTATGCT 60  
 Db 38 CACGGAGCGATGGGAGCAGTACTTCGGATCTGGAATTCCTAGCTCATCGGTACGCT 97

QY 61 GGTACACAGATGCCAGATGCGAGCATCAGAGGGGACCTGCCAACGTTGGAATTCACCTAG 120  
 Db 98 GGTACACAGATGCCCGATGGCCATCAGAGGGGATCTGCGACCTTGGAGTTACCCAG 157

QY 121 GTAC 124  
 Db 158 GTAC 161

RESULT 38  
 AC105495 0  
 WPCOMMENT

Sequence split into 5 fragments LOCUS AC105495 Accession AC105495

Fragment Name	Begin	End
AC105495_0	1	110000
AC105495_1	100001	210000
AC105495_2	200001	310000
AC105495_3	300001	410000
AC105495_4	400001	430182

LOCUS AC105495 430182 bp DNA linear HTG 11-OCT-2000  
 DEFINITION Rattus norvegicus clone CH230-216J16, WORKING DRAFT SEQUENCE, 11  
 unordered pieces.

ACCESSION AC105495  
 VERSION AC105495.5 GI:23603886  
 KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS\_FULLTOP.  
 SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 430182)  
 Muzny, D., Maric, M., Metzker, M., Lee, A., Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalabechi, V., Ayoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biwalto, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., De Souza, L., Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denison, S., Deyam, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, W., Gebregregoris, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S., Hodgson, A., Hogues, M., Hollins, B., Jacob, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacobs, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Kapathy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshaw, L., Loulseged, H., Lozano, R., Lu, X., Ma, J., Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Manthey, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Nwackelme, O., Okwuonu, G., Olarnpusagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plapper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puzos, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,

Rives, C., Rodkey, T., Rojas, A., Rose, M., Ruiz, R., Ruiz, S. J.,  
 Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,  
 Shetty, J., Shvartsbeyn, A., Sisson, I., Sittler, C. D., Smajls, D.,  
 Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,  
 Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,  
 Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,  
 Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J.,  
 Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, P.,  
 Williams, G., Wilson, R., Wleczyk, R., Wooden, H., Worley, K.,  
 Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,  
 Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von  
 Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O.,  
 Weinstock, G. and Gibbs, R. A.  
 Direct Submission  
 Unpublished  
 2 (bases 1 to 430182)  
 Worley, K. C.  
 Direct Submission  
 Submitted (09-JAN-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 430182)  
 Rat Genome Sequencing Consortium.  
 Direct Submission  
 Submitted (11-OCT-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 On Oct 9, 2002 this sequence version replaced gi:21736362.  
 The sequence in this assembly is a combination of BAC based reads  
 and whole genome shotgun sequencing reads assembled using Atlas  
 (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described  
 in the feature table below represents a scaffold in the Atlas  
 assembly (a 'contig-scaffold'). Within each contig-scaffold,  
 individual sequence contigs are ordered and oriented, and separated  
 by sized gaps filled with Ns to the estimated size. The sequence  
 may extend beyond the ends of the clone and there may be sequence  
 contigs within a contig-scaffold that consist entirely of whole  
 genome shotgun sequence reads. Both end sequences and whole genome  
 shotgun sequence only contigs will be indicated in the feature  
 table.

----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: hgsc-help@bcm.tmc.edu  
 ----- Project Information  
 Center project name: GNBL  
 Center clone name: CH230-216J16  
 ----- Summary Statistics  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 252209 bases at least Q40  
 Consensus quality: 254267 bases at least Q30  
 Consensus quality: 255370 bases at least Q20  
 Estimated insert size: 257492; sum-of-contigs estimation  
 Quality coverage: 9x in Q20 bases; sum-of-contigs estimation

----- NOTE: Estimated insert size may differ from sequence length  
 (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html))  
 NOTE: This sequence may represent more than one clone.  
 NOTE: This is a 'working draft' sequence. It currently  
 consists of 11 contigs. The true order of the pieces  
 is not known and their order in this sequence record is  
 arbitrary. Gaps between the contigs are represented as  
 runs of N, but the exact sizes of the gaps are unknown.  
 This record will be updated with the finished sequence  
 as soon as it is available and the accession number will  
 be preserved.

1 412811: contig of 412811 bp in length  
 \* 412812 412911: gap of unknown length  
 \* 412912 413928: contig of 1017 bp in length  
 \* 413929 414028: gap of unknown length  
 \* 414029 415313: contig of 1285 bp in length  
 \* 415314 415413: gap of unknown length

FEATURES  
 source  
 1. 430182  
 /organism="Rattus norvegicus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10116"  
 /clone="CH230-216J16"  
 misc\_feature  
 1. 1626  
 /notes="wgs end extension  
 clone\_end:Sp6"  
 1764..2821  
 /note="wgs end extension  
 clone\_end:Sp6"  
 misc\_feature  
 4770..6889  
 /notes="wgs end extension  
 clone\_end:Sp6"  
 7124..8011  
 /note="clone boundary  
 clone\_end:Sp6"  
 misc\_feature  
 end sequence:RWBLX56TV  
 240378..241275  
 /notes="clone boundary  
 clone\_end:T7"  
 misc\_feature  
 end sequence:RWBLX56TV  
 245462..246549  
 /notes="wgs end extension  
 clone\_end:T7"  
 misc\_feature  
 411785..412811  
 /notes="wgs end extension  
 clone\_end:T7"  
 gap  
 412812..412911  
 /estimated\_length=unknown  
 413929..414028  
 /estimated\_length=unknown  
 415314..415413  
 /estimated\_length=unknown  
 417241..417340  
 /estimated\_length=unknown  
 418442..418541  
 /estimated\_length=unknown  
 419682..419781  
 /estimated\_length=unknown  
 421093..421192  
 /estimated\_length=unknown  
 422231..422330  
 /estimated\_length=unknown  
 423752..423851  
 /estimated\_length=unknown  
 425982..426081  
 /estimated\_length=unknown

ORIGIN

Query Match 38.1%; Score 98.4; DB 14; Length 110000;  
 Best Local Similarity 87.1%; Pred. No. 8.1e-13;  
 Matches 108; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 1 CACCGGAGTGATGCGAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60

Db	33657	CAGCGAGGCGATGGGAAGCATGACATTCGGGATCTCGGAATTCACAGTCCAGCTCATCGGTACCGCT	33716
QY	61	GGCTACCGATGCGAGATGCGAGCATCAGAGGGGACCCCTGCGCAACGTCGGAATTCACCTCAG	120
Db	33717	GGCTACCGATGCGCGATGGCCACCATCAGAGGGGATCTCGCCACCTTGGAGTTACCCAG	33776
QY	121	GTAC 124	
Db	33777	GTAC 33780	
RESULT 39			
AC103040/c			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			

```

/note="wgs_end_extension
clone_end:T7"
6768..10860
/misc_feature
/note="wgs_end_extension
clone_end:T7"
10673..11460
/misc_feature
/note="clone_boundary
clone_end:T7"
site:ECORI
end sequence:BZ091454"
159678..159821
/misc_feature
/note="clone_boundary
clone_end:Sp5"
site:ECORI
end sequence:BZ091456"
238896..240200
/misc_feature
/note="wgs_end_extension
clone_end:Sp6"

ORIGIN
Query Match      38.1%; Score 98.4; DB 14; Length 240200;
Best Local Similarity 87.1%; Pred. No. 7.1e-13;
Matches 108; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGCAAGCAGCACTCCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 60
Db 86348 CAGCGGAGCGATGGAGAGCATGCTCCGGATCTGGAAATCTCCAGCTCATCCGCTATGCT 86289

Qy 61 GGCTACCATGATGCCAGATGCGAGCATCAGAGGGGACCTGCCAACGTGGAAATTCATCTCAG 120
Db 86288 GGCTACCATGATGCCAGATGCGAGCATCAGAGGGGATCTGCCACCTTGGAGTTCCACCAG 86229

Qy 121 GTAC 124
Db 86228 GTAC 86225

RESULT 40
AC106421
LOCUS
DEFINITION Rattus norvegicus clone CH230-126J7, *** SEQUENCING IN PROGRESS
***, 23 unordered pieces.
AC106421
VERSION AC106421.5 GI:30581088
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Rattus.
1 (bases 1 to 314746)
Muzny,D,Marie., Metzker,M,Lees., Abramson,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Blawalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falle,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Haves,A., Henderson,N., Hernandez,J.,
Hernandez,R., Hines,S., Iladun,S.L., Hodgson,A., Hogues,M.,
Hollins,B., Howells,S., Iladun,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,

```

```

Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorensuhera,L., Loulseghe,H., Lozado,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Mawhney,S., McLeod,M.P., McNeill,T.Z., Meenan,E.,
Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwaokemelehen,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L., L.,
Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Savary,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smaja,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Steinle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
Valas,R., Vera,V., Villaseana,D., Waldron,D., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wleczkyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 314746)
Worley,K.C.
Direct Submission
Submitted (12-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 314746)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (13-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On May 13, 2003 this sequence version replaced gi:24819147.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GKWN
Center clone name: CH230-126J7
----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 286975 bases at least Q40
Consensus quality: 291712 bases at least Q30
Consensus quality: 295672 bases at least Q20
Estimated insert size: 299042; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
* NOTE: This sequence may represent more than one clone.

```





**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 14:11:49 ; Search time 473 Seconds

(without alignments)  
3635.287 Million cell updates/sec

Title: US-10-713-137-1

Perfect score: 258

Sequence: 1 caggcgagtgatggcaagca.....ttgttccccagctgtgcac 258

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq 21:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2002bs:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*
- 14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	257.6	99.8	258	14	ADZ75764 Human ind
2	120.4	46.7	1152	4	Aah78096 Nucleotid
3	120.4	46.7	3462	4	Aah78095 Nucleotid
4	120.4	46.7	3462	14	ADV42931 Human psy
5	120.4	46.7	3855	8	ABX76286 Lung canc
6	120.4	46.7	3855	9	ADA09713 Human nit
7	120.4	46.7	3855	13	ACF87485 Human SIR
8	120.4	46.7	3928	13	ACN42845 Human dia
9	120.4	46.7	3946	4	Aac67035 Human ind
10	120.4	46.7	4062	2	Aax08434 Inducible
11	120.4	46.7	4062	10	ACA56880 Human sig
12	120.4	46.7	4062	12	ADI56676 Human pol
13	120.4	46.7	4062	12	ADJ74786 Marker ge
14	120.4	46.7	4062	12	ADJ74903 Marker ge
15	120.4	46.7	4070	2	Aat98199 Human ind
16	120.4	46.7	4133	13	ADQ38958 Human SNP
17	120.4	46.7	4145	2	Aaq66914 Sequence
18	120.4	46.7	4145	2	Aat10115 Nitric ox
19	120.4	46.7	4145	3	Aaa34818 Human ade

20	120.4	46.7	4145	3	AAF20940	Aaf20940 Human ind
21	120.4	46.7	4145	4	AAH47966	Aah47966 Mouse ind
22	120.4	46.7	4145	4	AAH47959	Aah47959 Human ind
23	120.4	46.7	4145	10	ABZ96634	Abz96634 Human ind
24	120.4	46.7	4145	11	ABD19732	Abd19732 Human ind
25	120.4	46.7	4164	2	AAQ77700	Aaq77700 Nitric-ox
26	120.4	46.7	4164	11	ADI32081	Adi32081 Human CDN
27	120.4	46.7	4164	13	ADS84148	Ads84148 Human lym
28	120.4	46.7	4221	13	ADQ38959	Adq38959 Human SNP
29	120.4	46.7	4221	14	ABE69128	Ab669128 Human mod
30	120.4	46.7	4277	13	ACN42844	Acn42844 Human dia
31	120.4	46.7	4278	13	ACN42843	Acn42843 Human dia
32	120.4	46.7	8222	3	AAF21450	Aaf21450 Human ind
33	120.4	46.7	8222	10	ABZ97144	Abz97144 Human nuc
34	120.4	46.7	8222	11	ABD19730	Abd19730 Human nuc
35	120.4	46.7	9513	3	AAA34820	Aaa34820 Human ade
36	120.4	46.7	9513	3	AAF20942	Aaf20942 Human low
37	120.4	46.7	9513	10	ABZ96636	Abz96636 Human nuc
38	120.4	46.7	9513	11	ABD20500	Abd20500 Human pul
39	120.4	46.7	35384	3	AAF21436	Aaf21436 Human enz
40	120.4	46.7	35459	10	ABZ97130	Abz97130 Human nuc
41	120.4	46.7	35459	11	ABD17969	Abd17969 Human enz
42	118.8	46.0	4150	4	AAC67036	Aac67036 Human ind
43	118.8	46.0	4150	13	ADS88001	Ads88001 Tumour tr
44	94.8	36.7	1033	2	AAQ79418	Aaq79418 Rat pancr
45	94.8	36.7	3530	2	AAQ79423	Aaq79423 Rat induc

ALIGNMENTS

RESULT 1

ADZ75764

ID ADZ75764 standard; DNA; 258 BP.

XX AC ADZ75764;

XX DT 28-JUL-2005 (first entry)

XX DE Human inducible nitric oxide synthase gene exon 7 SEQ ID NO:1.

XX ds; gene; high altitude pulmonary edema; pulmonary edema;  
XX respiratory-gen.; respiratory disease; SNP detection; allelic variation;  
XX exon.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX FT Variation 142  
XX FT /\*tag= a  
XX FT /standard\_name= "single nucleotide polymorphism"  
XX PN US2005106573-A1.  
XX PD 19-MAY-2005.  
XX PF 13-NOV-2003; 2003US-00713137.  
XX PR 13-NOV-2003; 2003US-00713137.  
XX PA (COUN-) COUNCIL SCI & IND RES INDIA.  
XX PI Pasha AQM, Ahsan A;  
XX DR WPI; 2005-384299/39.  
XX PT Detecting predisposition to high altitude pulmonary edema (HAPE) by  
XX amplifying intron 7 of human inducible nitric oxide synthase gene, and  
XX predicting and analyzing differences in the distribution of allelic  
XX variants.  
XX PS Claim 1; SEQ ID NO 1; 13pp; English.  
XX

CC The invention relates to a novel method for detecting predisposition to  
CC high altitude pulmonary edema (HAPE). The method comprises amplifying  
CC intron 7 of the human inducible nitric oxide synthase (iNOS) gene  
CC (ADZ75764) by designing and synthesizing forward and reverse  
CC oligonucleotide primers (ADZ75765+ADZ75766), and predicting and  
CC statistically analyzing differences in the distribution of the allelic  
CC variants in the populations, where GG genotype at 19480 position are at  
CC low risk of HAPE, and AA genotype at 19480 position are at high risk of  
CC HAPE. The present sequence represents exon 7 of the human iNOS gene.  
XX  
SQ Sequence 258 BP; 52 A; 80 C; 84 G; 41 T; 0 U; 1 Other;

Query Match 99.8%; Score 257.6; DB 14; Length 258;  
Best Local Similarity 100.0%; Pred. No. 1.3e-63;  
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CAGCGGAGTGATGCAAGCAGCAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
DB 1 CAGCGGAGTGATGCAAGCAGCAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
QY 61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120  
DB 61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120  
QY 121 GTACCCGGCCCGAGCTCAGCCRCGGCCATTTGGGGGGGGAGCCCGTGGTGAGCGAGTG 180  
DB 121 GTACCCGGCCCGAGCTCAGCCRCGGCCATTTGGGGGGGGAGCCCGTGGTGAGCGAGTG 180  
QY 181 ACAGAGTGGAGCCCGAGAGGAGACACGACGCCCGGGCTTACAGACTCACAGGGCCCGTCTT 240  
DB 181 ACAGAGTGGAGCCCGAGAGGAGACACGACGCCCGGGCTTACAGACTCACAGGGCCCGTCTT 240  
QY 241 GTTCCCGCAGCTGTGCATC 258  
DB 241 GTTCCCGCAGCTGTGCATC 258

RESULT 2  
AAH78096  
ID AAH78096 standard; DNA; 1152 BP.  
XX  
AC AAH78096;  
XX  
DT 26-NOV-2001 (first entry)  
XX  
DE Nucleotide sequence of a human inducible nitrogen oxide synthase.  
XX  
KW Inducible nitrogen oxide synthase; iNOS; organ rejection;  
KW cerebral infarction; vascular ischemia; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200166791-A1.  
XX  
PD 13-SEP-2001.  
XX  
PF 09-MAR-2001; 2001WO-JP001865.  
XX  
PR 10-MAR-2000; 2000JP-00072480.  
XX  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
XX  
PI Ishii Y, Ueda Y, Iwami M, Arakawa H, Notsu Y;  
XX  
WPI; 2001-570775/64.  
DR P-PSDB; AAG67464.  
XX  
PT Screening for compounds that inhibit in vitro inducible nitrogen oxide  
PT synthase useful for treating organ rejection, cerebral infarction and  
PT ischemia.  
XX  
PS Claim 11; Page 62; 73pp; Japanese.  
XX

CC The specification describes a method of screening for compounds that  
CC inhibit in vitro inducible nitrogen oxide synthase (iNOS) activity. The  
CC method comprises contacting the iNOS monomer with a candidate compound,  
CC and selecting those compounds that bind to it. As dimerisation of iNOS, is  
CC the final step of the acquisition of the iNOS enzymatic activity, iNOS  
CC inhibitor compounds can be quickly and efficiently screened. The  
CC inhibitors are useful for treatment and prevention of organ rejection,  
CC cerebral infarction and vascular ischemia. The present sequence encodes a  
CC human iNOS  
XX  
SQ Sequence 1152 BP; 275 A; 326 C; 322 G; 229 T; 0 U; 0 Other;

Query Match 46.7%; Score 120.4; DB 4; Length 1152;  
Best Local Similarity 99.2%; Pred. No. 2.6e-24;  
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CAGCGGAGTGATGGCAAGCAGCAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
DB 379 CAGCGGAGTGATGGCAAGCAGCAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 438  
QY 61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120  
DB 439 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 498  
QY 121 GT 122  
DB 499 CT 500

RESULT 3  
AAH78095  
ID AAH78095 standard; DNA; 3462 BP.  
XX  
AC AAH78095;  
XX  
DT 26-NOV-2001 (first entry)  
XX  
DE Nucleotide sequence of a human polypeptide.  
XX  
KW Inducible nitrogen oxide synthase; iNOS; organ rejection;  
KW cerebral infarction; vascular ischemia; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..3462  
FT /\*tag= a  
XX  
PN WO200166791-A1.  
XX  
PD 13-SEP-2001.  
XX  
PF 09-MAR-2001; 2001WO-JP001865.  
XX  
PR 10-MAR-2000; 2000JP-00072480.  
XX  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
XX  
PI Ishii Y, Ueda Y, Iwami M, Arakawa H, Notsu Y;  
XX  
WPI; 2001-570775/64.  
DR P-PSDB; AAG67463.

Screening for compounds that inhibit in vitro inducible nitrogen oxide  
PT synthase useful for treating organ rejection, cerebral infarction and  
PT ischemia.  
XX  
PS Disclosure; Page 50-53; 73pp; Japanese.  
XX  
XX The specification describes a method of screening for compounds that  
CC inhibit in vitro inducible nitrogen oxide synthase (iNOS) activity. The  
CC method comprises contacting the iNOS monomer with a candidate compound,  
CC and selecting those compounds that bind to it. As dimerisation of iNOS is

CC the final step of the acquisition of the iNOS enzymatic activity, iNOS  
 CC inhibitor compounds can be quickly and efficiently screened. The  
 CC inhibitors are useful for treatment and prevention of organ rejection,  
 CC cerebral infarction and vascular ischemia. The present sequence was used  
 CC in the course of the invention  
 XX  
 SQ Sequence 3462 BP; 801 A; 1027 C; 962 G; 672 T; 0 U; 0 Other;

Query Match 46.7%; Score 120.4; DB 4; Length 3462;  
 Best Local Similarity 99.2%; Pred. No. 3.3e-24;  
 Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGTCACTATCGCTATGCT 60  
 DB 745 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGTCACTATCGCTATGCT 804  
 QY 61 GGCTACAGATGCCAGATGCCAGATCAGAGGGGACCCTGCCAACCTGGAATTCATCTCAG 120  
 DB 805 GGCTACAGATGCCAGATGCCAGATCAGAGGGGACCCTGCCAACCTGGAATTCATCTCAG 864  
 QY 121 GT 122  
 DB 865 CT 866

RESULT 4  
 ID ADV42931 standard; cDNA; 3462 BP.  
 XX  
 AC ADV42931;  
 XX  
 DT 10-MAR-2005 (first entry)  
 XX  
 DE Human psychoneuroendocrine-immune expressed sequence tag SEQ ID NO 559.  
 XX  
 KW microarray; psychoneuroendocrine-immune; chronic fatigue;  
 KW non-insulin dependent diabetes; allergy; immune disorder; inflammation;  
 KW cancer; neoplasm; infection; expressed sequence tag; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004108899-A2.  
 XX  
 PD 16-DEC-2004.  
 XX  
 PF 04-JUN-2004; 2004WO-US017686.  
 XX  
 PR 04-JUN-2003; 2003US-0475915P.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Nicholson A, Vernon SD;  
 XX  
 DR WPI; 2005-031682/03.  
 XX  
 PT New microarray comprising probes for genes involved in  
 PT psychoneuroendocrine-immune (PNI) activity, useful in diagnosing a  
 PT condition associated with PNI activity, e.g., inflammatory or infectious  
 PT diseases.  
 XX  
 PS Claim 1; SEQ ID NO 559; 254pp; English.  
 XX  
 CC The invention relates to a new microarray which comprises probes for  
 CC genes involved in psychoneuroendocrine-immune (PNI) activity. The  
 CC microarray is useful in diagnosing a condition associated with PNI  
 CC activity, such as CFS, type-2 diabetes, allergic condition, inflammation,  
 CC cancer and infection. The present sequence represents a  
 CC psychoneuroendocrine-immune gene expressed sequence tag. Note the  
 CC specification mentions SEQ ID NO of up to 3314 but only sequences up to  
 CC SEQ ID NO 1829 are provided.  
 XX  
 SQ Sequence 3462 BP; 801 A; 1027 C; 962 G; 672 T; 0 U; 0 Other;

Query Match 46.7%; Score 120.4; DB 14; Length 3462;  
 Best Local Similarity 99.2%; Pred. No. 3.3e-24;  
 Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGTCACTATCGCTATGCT 60  
 DB 745 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGTCACTATCGCTATGCT 804  
 QY 61 GGCTACAGATGCCAGATGCCAGATCAGAGGGGACCCTGCCAACCTGGAATTCATCTCAG 120  
 DB 805 GGCTACAGATGCCAGATGCCAGATCAGAGGGGACCCTGCCAACCTGGAATTCATCTCAG 864  
 QY 121 GT 122  
 DB 865 CT 866

RESULT 5  
 ID ABX76286 standard; DNA; 3855 BP.  
 XX  
 AC ABX76286;  
 XX  
 DT 02-APR-2003 (first entry)  
 XX  
 DE Lung cancer-associated polynucleotide #150.  
 XX  
 KW Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;  
 KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;  
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;  
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;  
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200286443-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 18-APR-2002; 2002WO-US012476.  
 XX  
 PR 18-APR-2001; 2001US-0284770P.  
 PR 10-MAY-2001; 2001US-0290492P.  
 PR 09-NOV-2001; 2001US-0339245P.  
 PR 13-NOV-2001; 2001US-0350666P.  
 PR 29-NOV-2001; 2001US-0334370P.  
 PR 12-APR-2002; 2002US-0372246P.  
 XX  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 XX  
 PI Aziz N, Murray R;  
 XX  
 DR WPI; 2003-093161/08.  
 DR P-PSDB; ABU56557.  
 XX  
 PT Detecting a lung cancer-associated transcript in a cell from a patient  
 PT for treating lung cancer, by contacting a biological sample from the  
 PT patient with a polynucleotide that exhibits increased or decreased  
 PT expression in lung cancer.  
 XX  
 PS Claim 22; Page 301-302; 453pp; English.  
 XX  
 CC The invention relates to a method for detecting a lung cancer-associated  
 CC transcript in a cell from a patient, comprising contacting a biological  
 CC sample from the patient with a polynucleotide that selectively hybridizes  
 CC to a sequence that is at least 80 % identical to a gene that exhibits  
 CC increased or decreased expression in lung cancer samples. Lung cancer-  
 CC associated polynucleotides and polypeptides are used for identifying a  
 CC compound that modulates a lung cancer-associated polypeptide, for  
 CC inhibiting proliferation of a lung cancer-associated cell to treat lung  
 CC cancer in a patient and for treating a mammal having lung cancer by  
 CC administering a modulatory compound identified. The methods are useful  
 CC for treating lung cancer, such as small cell lung cancer, non-small cell

CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,  
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,  
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and  
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful  
CC for diagnostic purposes and as targets for screening for therapeutic  
CC compounds that modulate lung cancer, such as antibodies. Sequences  
CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the  
CC invention  
XX  
SQ Sequence 3855 BP; 894 A; 1136 C; 1067 G; 758 T; 0 U; 0 Other;  
Query Match 46.7%; Score 120.4; DB 8; Length 3855;  
Best Local Similarity 99.2%; Pred. No. 3.4e-24;  
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
DB 939 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 998  
QY 61 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 120  
DB 999 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 1058  
QY 121 GT 122  
DB 1059 CT 1060  
RESULT 6  
ADA09713  
ID ADA09713 standard; mRNA; 3855 BP.  
XX  
AC ADA09713;  
XX  
DT 06-NOV-2003 (first entry)  
XX  
DE Human nitric oxide synthase 2a (NOS2A) mRNA.  
XX  
KW Screening assay; nutraceutical testing; mRNA detection;  
KW INVADER detection assay; human; nitric oxide synthase 2A; NOS2A; ss.  
XX  
OS Homo sapiens.  
XX  
FN US2003092039-A1.  
XX  
PD 15-MAY-2003.  
XX  
PF 01-AUG-2002; 2002US-00210682.  
XX  
PR 01-AUG-2001; 2001US-0309279P.  
XX  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
XX  
PI Olson-Munoz MC, Donald G;  
XX  
DR WPI; 2003-567788/53.  
XX  
PT Testing nutraceutical by providing cells, nutraceutical, and INVADER  
PT assay detection reagents, exposing cells to nutraceutical, lysing cells;  
PT and contacting cell lysate with INVADER assay detection reagents.  
XX  
PS Disclosure; Fig 2; 25pp; English.  
XX  
CC The present invention relates to screening assays for testing  
CC nutraceuticals. The invention provides methods for detecting RNA in cells  
CC exposed to various types, concentrations, and combinations of  
CC nutraceuticals using the INVADER detection assay. The INVADER detection  
CC assay detects and quantifies test gene mRNA. The INVADER assay detection  
CC reagents comprise a probe and an INVADER oligonucleotide. The invention  
CC provides a high throughput, sensitive, quantitative, and cost-effective  
CC method of testing nutraceuticals. The present sequence represents human  
CC nitric oxide synthase 2A (NOS2A) mRNA.  
XX

SQ Sequence 3855 BP; 894 A; 1136 C; 1067 G; 0 T; 758 U; 0 Other;  
Query Match 46.7%; Score 120.4; DB 9; Length 3855;  
Best Local Similarity 80.3%; Pred. No. 3.4e-24;  
Matches 98; Conservative 23; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
DB 939 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 998  
QY 61 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 120  
DB 999 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 1058  
QY 121 GT 122  
DB 1059 CU 1060  
RESULT 7  
ACF87485  
ID ACF87485 standard; DNA; 3855 BP.  
XX  
AC ACF87485;  
XX  
DT 02-JUN-2005 (first entry)  
XX  
DE Human SIRS/sepsis diagnostic marker DNA fragment 6345.  
XX  
DE Systemic inflammatory response syndrome; SIRS; antibacterial;  
KW immunosuppressive; antiinflammatory; diagnosis; sepsis; ds.  
XX  
OS Homo sapiens.  
XX  
PN WC2004087949-A2.  
XX  
PD 14-OCT-2004.  
XX  
PF 31-MAR-2004; 2004WO-BP003419.  
XX  
PR 02-APR-2003; 2003DE-01015031.  
PR 08-AUG-2003; 2003DE-01036511.  
PR 02-SEP-2003; 2003DE-01040395.  
XX  
PA (SIRS-) SIRS LAB GMBH.  
XX  
PI Russwurm S, Reinhart K, Saluz H, Straube E, Zipfel PF, Daigner H;  
XX  
DR WPI; 2004-748070/73.  
XX  
PT In vitro detection of systemic inflammatory response syndrome and related  
PT conditions, for e.g. monitoring progression, comprises detecting abnormal  
PT expression of disease-related genes.  
XX  
PS Disclosure; Page; 75pp; German.  
XX  
CC The invention relates to a novel method for in vitro detection of  
CC systemic inflammatory response syndrome (SIRS). The method comprises  
CC detecting abnormal expression of disease-related genes, or their  
CC associated peptides. The method of the invention demonstrates  
CC antibacterial, immunosuppressive and antiinflammatory applications and  
CC may be used for early differential diagnosis, monitoring progression,  
CC assessing risk, assessing the likely response to treatment and for post  
CC mortem diagnosis of systemic inflammatory response syndrome, sepsis and  
CC sepsis-like conditions. The recombinant or synthetic nucleic acid  
CC sequences of the invention, or derived proteins or peptides, may be  
CC useful as calibrants in assays for the specified diseases, for evaluating  
CC activity or toxicity in screening for active agents and/or for  
CC preparation of agents for treatment or prevention of the specified  
CC diseases. The current sequence is that of a human SIRS/sepsis diagnostic  
CC marker DNA fragment of the invention. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at ftp.wipo.int/pub/published

CC pct. sequences. Furthermore, a number of arbitrary SEQ ID NO.s are  
 CC disclosed within the specification, however, these have not been taken  
 CC into account during indexing due to inconsistencies in application and  
 CC format

XX  
 SQ Sequence 3855 BP; 897 A; 1134 C; 1065 G; 759 T; 0 U; 0 Other;

Query Match 46.7%; Score 120.4; DB 13; Length 3855;  
 Best Local Similarity 99.2%; Pred. No. 3.4e-24; Mismatches 0; Indels 0; Gaps 0;  
 Matches 121; Conservative 0

QY 1 CAGCGAGTGATGGCAAGCAGCAGCTTCGGGGTGTGGAATGCTCAGTCTATCGCTATGCT 60  
 |||||  
 Db 939 CAGCGAGTGATGGCAAGCAGCAGCTTCGGGGTGTGGAATGCTCAGTCTATCGCTATGCT 998

QY 61 GGCTACCATGATGGCAGATGGCAGATCAGAGGGACCTGCGCAAGTGAATTCATCTAG 120  
 |||||  
 Db 999 GGCTACCATGATGGCAGATGGCAGATCAGAGGGACCTGCGCAAGTGAATTCATCTAG 1058

QY 121 GT 122  
 |||||  
 Db 1059 CT 1060

RESULT 8  
 ACN42845  
 ID ACN42845 standard; cDNA; 3928 BP.  
 XX  
 AC ACN42845;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX  
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1720.  
 XX  
 KW ss; gene; gene therapy; human diagnostic and therapeutic polynucleotide;  
 KW dithp.  
 KW  
 OS Homo sapiens.  
 XX  
 XX WO2004023973-A2.  
 XX  
 XX 25-MAR-2004.  
 XX  
 XX 12-SEP-2003; 2003WO-US028227.  
 XX  
 XX 12-SEP-2002; 2002US-0410259P.  
 PR  
 PR 12-SEP-2002; 2002US-0410260P.  
 XX  
 XX (INCY-) INCYTE CORP.  
 XX  
 XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;  
 PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Bider LV;  
 PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;  
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;  
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;  
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtan BS;  
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;  
 PI Patary S, Shi X, Suarez CJ;  
 XX  
 XX WPI; 2004-329368/30.  
 DR  
 DR P-PSDB; ABM84193.  
 XX  
 XX New diagnostic and therapeutic polynucleotides and polypeptides, useful  
 PT in diagnosing a condition, disease or disorder associated with human  
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
 PT in gene mapping.  
 XX  
 XX Claim 1; Page; 190pp; English.  
 PS  
 XX The invention relates to novel diagnostic and therapeutic polynucleotides  
 CC selected from one of the 2722 sequences defined in the specification. A  
 CC polynucleotide of the invention may have a use in gene therapy. The human  
 CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be

CC used to diagnose a particular condition, disease or disorder associated  
 CC with human molecules, e.g. cell proliferative disorders,  
 CC autoimmune/inflammatory disorders, developmental disorder, endocrine  
 CC disorder, neurological disorders, gastrointestinal disorders, or  
 CC infections caused by virus, bacteria, fungi or parasite. The dithp  
 CC molecules may also be used in genetic mapping, in identifying individuals  
 CC from minute biological samples, in detecting single nucleotide  
 CC polymorphisms, as molecular weight markers, and for somatic or germline  
 CC gene therapy. The present sequence represents a dithp polynucleotide of  
 CC the invention. Note: The sequence data for this patent is not represented  
 CC in the printed specification, but was obtained in electronic format  
 CC directly from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)  
 XX  
 SQ Sequence 3928 BP; 928 A; 1151 C; 1086 G; 763 T; 0 U; 0 Other;

Query Match 46.7%; Score 120.4; DB 13; Length 3928;  
 Best Local Similarity 99.2%; Pred. No. 3.4e-24; Mismatches 0; Indels 0; Gaps 0;  
 Matches 121; Conservative 0

QY 1 CAGCGAGTGATGGCAAGCAGCAGCTTCGGGGTGTGGAATGCTCAGTCTATCGCTATGCT 60  
 |||||  
 Db 998 CAGCGAGTGATGGCAAGCAGCAGCTTCGGGGTGTGGAATGCTCAGTCTATCGCTATGCT 1057

QY 61 GGCTACCATGATGGCAGATGGCAGATCAGAGGGACCTGCGCAAGTGAATTCATCTAG 120  
 |||||  
 Db 1058 GGCTACCATGATGGCAGATGGCAGATCAGAGGGACCTGCGCAAGTGAATTCATCTAG 1117

QY 121 GT 122  
 |||||  
 Db 1118 CT 1119

RESULT 9  
 AAC67035  
 ID AAC67035 standard; DNA; 3946 BP.  
 XX  
 AC AAC67035;  
 XX  
 XX 03-APR-2001 (first entry)  
 XX  
 XX Human inducible nitric oxide synthase coding sequence #1.  
 DE  
 XX Human; influenza virus; antisense; inducible nitric oxide synthase; iNOS;  
 KW ds.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200078946-A2.  
 PN  
 XX 28-DEC-2000.  
 PD  
 XX 19-JUN-2000; 2000WO-US016810.  
 PF  
 XX 17-JUN-1999; 99US-0139479P.  
 PR  
 XX (EVIR-) EASTERN VIRGINIA MEDICAL SCHOOL.  
 PA  
 XX Keller ET, Gravenstein S, Hall DM;  
 PI WPI; 2001-102720/11.  
 DR  
 XX  
 XX Treating viral influenza with antisense oligonucleotides that hybridize  
 PT with inducible nitric oxide synthase mRNA and inhibit synthesis of the  
 PT enzyme, reducing the production of nitric oxide in lungs.  
 XX  
 XX Disclosure; Fig 1; 21pp; English.  
 PS  
 XX The present invention provides a novel method of treating influenza virus  
 CC infection by administering an antisense oligonucleotide directed at the  
 CC human inducible nitric oxide synthase (iNOS) mRNA. This is useful in  
 CC preventing the symptoms of influenza infection  
 XX  
 XX Sequence 3946 BP; 918 A; 1149 C; 1073 G; 806 T; 0 U; 0 Other;

Query Match 46.7%; Score 120.4; DB 4; Length 3946;  
 Best Local Similarity 99.2%; Pred. No. 3.4e-24;  
 Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGCAAGCAGCACTTCCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 60  
 DB 745 CAGCGGAGTGATGCAAGCAGCACTTCCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 804

QY 61 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCTGCCAAGCTGGGAATTCACCTCAG 120  
 DB 805 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCTGCCAAGCTGGGAATTCACCTCAG 864

QY 121 GT 122  
 DB 865 CT 866

RESULT 10  
 AAX08434  
 ID AAX08434 standard; DNA; 4062 BP.  
 XX AC AAX08434;  
 XX DT 28-JUN-1999 (first entry)  
 XX DE Inducible nitric oxide synthase gene.  
 XX KW Manganese containing superoxide dismutase; MnSOD; IDDM;  
 XX KW diabetes mellitus; treatment; therapy; nitric oxide; NO; beta cell;  
 XX KW fatty acids; lipotoxic; cytotoxic; cytokine; osteoporosis;  
 XX KW inflammatory disease; autoimmune disease; neurodegenerative disease; ss.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 XX CDS 106..3567  
 XX FT /\*tag= a  
 XX FT /product= "Nitric oxide synthase"  
 XX FT  
 XX PN WO9906059-A2.  
 XX PD 11-FEB-1999.  
 XX PF 30-JUL-1998; 98WO-US015781.  
 XX PR 30-JUL-1997; 97US-0055092P.  
 XX PR 03-MAR-1998; 98US-0076676P.  
 XX PR (TEXA ) UNIV TEXAS SYSTEM.  
 XX PA (BETA-) BETAGENE INC.  
 XX PI Hohmeier H, Thigpen A, Clark SA, Newgard CB, Unger RH;  
 XX PI Shimabukuro M, Koyama K, Ohneda M, Lee Y;  
 XX WPI; 1999-153448/13.  
 XX DR P-PSDB; AAW96322.  
 XX PT Protection of mammalian cells against immunotoxicity or lipotoxicity -  
 XX PT used for treating, e.g. diabetes, obesity, wasting syndromes,  
 XX PT osteoporosis, inflammatory diseases, autoimmune diseases or  
 XX PT neurodegenerative diseases.  
 XX PS Disclosure; Page 244-247; 253pp; English.  
 XX CC Inhibition of cytokine mediated immunotoxicity of cells can be achieved  
 XX CC by blocking free radical production or the accumulation of free radicals  
 XX CC in that cell. Treatment of insulin dependent diabetes mellitus (IDDM) can  
 XX CC be achieved by blocking nitric oxide (NO) production in a pancreatic  
 XX CC beta cell and by providing a composition comprising an agent that reduces  
 XX CC levels of fatty acids in the cells and protects beta-cells of the subject  
 XX CC against lipid-mediated cell death. Cells can also be protected against  
 XX CC nitric oxide mediated cytotoxicity by introducing into the cell an

CC antioxising agent. The methods can be used for protecting cells against  
 CC immunotoxicity mediated by, e.g. IL-1 beta, IL-1 alpha, gamma IFN, TNF  
 CC alpha, TNF beta, IL-8, IL-2, IL-6, IL-3, IL-5, IL-7, IL-9, IL-14,  
 CC IL-17, granulocyte-macrophage colony stimulating factor or monocyte  
 CC chemottractant protein-1. The methods can be used for the treatment of  
 CC e.g. insulin-dependent diabetes mellitus (IDDM), NIDDM, obesity, wasting  
 CC syndromes, short stature, osteoporosis, inflammatory diseases, autoimmune  
 CC diseases, or neurodegenerative diseases  
 XX SQ Sequence 4062 BP; 966 A; 1178 C; 1099 G; 819 T; 0 U; 0 Other;  
 Query Match 46.7%; Score 120.4; DB 2; Length 4062;  
 Best Local Similarity 99.2%; Pred. No. 3.4e-24;  
 Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGCAAGCAGCACTTCCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 60  
 DB 850 CAGCGGAGTGATGCAAGCAGCACTTCCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 909

QY 61 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCTGCCAAGCTGGGAATTCACCTCAG 120  
 DB 910 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCTGCCAAGCTGGGAATTCACCTCAG 969

QY 121 GT 122  
 DB 970 CT 971

RESULT 11  
 ACAS6880  
 ID ACAS6880 standard; cDNA; 4062 BP.  
 XX AC ACAS6880;  
 XX DT 06-JUN-2003 (first entry)  
 XX DE Human signalling pathway polynucleotide probe SEQ ID NO 1478.  
 XX KW Human; probe; ss; array element; Parkinson's disease;  
 XX KW signalling pathway population; cancer; adenocarcinoma; leukaemia;  
 XX KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.  
 XX OS Homo sapiens.  
 XX PN US6500938-B1.  
 XX PD 31-DEC-2002.  
 XX PF 30-JAN-1998; 98US-00016434.  
 XX PR 30-JAN-1998; 98US-00016434.  
 XX PA (INCY-) INCYTE GENOMICS INC.  
 XX PI Au-Young J, Seilhamer JJ;  
 XX WPI; 2003-352189/33.  
 XX PT Combination of polynucleotide probes, useful as array elements in a  
 XX PT microarray for monitoring the expression of a number of target  
 XX PT polynucleotides.  
 XX PS Claim 1; SEQ ID NO 1478; 65pp; English.  
 XX CC The invention relates to a combination which, comprises a number of  
 XX CC polynucleotide probes comprising a sequence selected from one of the 1490  
 XX CC sequences mentioned in the specification. The combination is useful as an  
 XX CC array element in a microarray for monitoring the expression of a number  
 XX CC of target polynucleotides. The microarray is particularly useful in the  
 XX CC diagnosis and treatment of cancer and immunopathology and neuropathology.  
 XX CC The microarray is useful in diagnostics and treatment regimens, drug  
 XX CC discovery and development, toxicological and carcinogenicity studies,  
 XX CC forensics and pharmacogenomics. The microarray is also useful for



CC monitoring progression of diseases and for developing sophisticated  
CC profiles for the effects of currently available therapeutic drugs. The  
CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs  
CC and genomic fragments and in research and diagnostic applications. The  
CC array can detect changes in expression in a large number of genes coding  
CC for different signaling pathway populations which can be used to diagnose  
CC various diseases including cancer e.g. adenocarcinoma and leukaemia,  
CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease  
CC and Parkinson's disease. The present sequence represents a polynucleotide  
CC probe of the invention. Note: the sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?DocID=06500938B1  
XX  
SQ Sequence 4062 BP; 966 A; 1178 C; 1099 G; 819 T; 0 U; 0 Other;  
  
Query Match 46.7%; Score 120.4; DB 10; Length 4062;  
Best Local Similarity 99.2%; Pred. No. 3.4e-24;  
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 CAGCGAGTGATGGCAAGCAGACTTCGGGTGTGGAATGCTCAGCTCATCGCTATGCT 60  
DB 850 CAGCGAGTGATGGCAAGCAGACTTCGGGTGTGGAATGCTCAGCTCATCGCTATGCT 909  
  
QY 61 GGCTACCATGATCCAGATGCGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120  
DB 910 GGCTACCATGATCCAGATGCGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 969  
  
QY 121 GT 122  
DB 970 CT 971  
  
RESULT 12  
ADI56676  
ID ADI56676 standard; DNA; 4062 BP.  
AC ADI56676;  
XX  
DT 22-APR-2004 (first entry)  
DE Human polynucleotide probe #1478.  
XX  
KW Human; probe; ss; receptor-like polypeptide; transducing polypeptide;  
KW effector-like polypeptide; cancer; immunopathology; neuropathology;  
KW drug development; toxicology; carcinogenicity;  
KW signalling pathway polypeptide; adrenal gland; bladder; bone;  
KW bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS;  
KW diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology;  
KW dementia; amnesia; epilepsy; Alzheimer's disease; depression.  
XX  
OS Homo sapiens.  
XX  
XX US2004010136-A1.  
XX  
PD 15-JAN-2004.  
XX  
PF 26-NOV-2002; 2002US-00305720.  
XX  
PR 30-JAN-1998; 98US-00016434.  
XX  
PA (INCY-) INCYTE GENOMICS INC.  
XX  
PI Au-Young J, Seilhamer JJ;  
XX  
XX WPI; 2004-090520/09.  
XX  
XX New composition comprising polynucleotide probes, useful as array  
PT elements in a microarray for monitoring the expression of target  
PT polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic  
PT fragments.  
XX  
PS Claim 6; SEQ ID NO 1478; 73pp; English.

XX The invention relates to a composition of polynucleotide probes  
CC comprising first polynucleotide probes comprising at least a portion of a  
CC gene encoding a receptor-like polypeptide, second polynucleotide probes  
CC comprising at least a portion of a gene encoding a transducing  
CC polypeptide and third polynucleotide probes comprising at least a portion  
CC of a gene encoding an effector-like polypeptide. The probes of the  
CC composition are useful as array elements in a microarray for monitoring  
CC the expression of target polynucleotides. The microarray is useful in the  
CC diagnosis and treatment of cancer, an immunopathology or a  
CC neuropathology. It can also be used for drug discovery and development.  
CC toxicological and carcinogenicity studies, forensics or pharmacogenomics.  
CC Microarrays can also be used for monitoring the progression of diseases  
CC that may be associated with the altered expression of signalling pathway  
CC polypeptides. The composition can also be used to purify a subpopulation  
CC of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile  
CC is also useful for the diagnosis and treatment of cancer e.g. cancers of  
CC the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,  
CC an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or  
CC ulcerative colitis, or a neuropathology, e.g. dementia, amnesia,  
CC epilepsy, Alzheimer's disease or depression. This sequence represents a  
CC human polynucleotide probe of the invention. Note: The sequence data for  
CC this patent did not form part of the printed specification but was  
CC obtained in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 4062 BP; 966 A; 1178 C; 1099 G; 819 T; 0 U; 0 Other;  
  
Query Match 46.7%; Score 120.4; DB 12; Length 4062;  
Best Local Similarity 99.2%; Pred. No. 3.4e-24;  
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 CAGCGAGTGATGGCAAGCAGACTTCGGGTGTGGAATGCTCAGCTCATCGCTATGCT 60  
DB 850 CAGCGAGTGATGGCAAGCAGACTTCGGGTGTGGAATGCTCAGCTCATCGCTATGCT 909  
  
QY 61 GGCTACCATGATCCAGATGCGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120  
DB 910 GGCTACCATGATCCAGATGCGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 969  
  
QY 121 GT 122  
DB 970 CT 971  
  
RESULT 13  
ADJ74786  
ID ADJ74786 standard; DNA; 4062 BP.  
XX  
AC ADJ74786;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Marker gene SEQ ID NO:38.  
XX  
KW bronchial asthma; chronic obstructive pulmonary disease;  
KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;  
KW gene therapy; marker gene; gene; ds.  
XX  
OS Homo sapiens.  
XX  
XX EP1394274-A2.  
XX  
PD 03-MAR-2004.  
XX  
PF 04-AUG-2003; 2003EP-00254857.  
XX  
PR 06-AUG-2002; 2002JP-00229312.  
PR 20-MAR-2003; 2003JP-00077212.  
XX  
PA (GENO-) GENOX RES INC.  
XX  
PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;

XX WPI; 2004-193155/19.

XX Testing for bronchial asthma or chronic obstructive pulmonary disease by

XX comparing the expression level of a marker gene in a biological sample

XX from a subject with the expression level of the gene in a sample from a

XX healthy subject.

XX Claim 1; SEQ ID NO 38; 241pp; English.

XX The present invention describes a method of testing for bronchial asthma

XX or chronic obstructive pulmonary disease. The method comprises

XX determining the expression level of a marker gene in a biological sample

XX from a subject, comparing the expression level determined with the

XX expression level of the marker gene in a biological sample from a healthy

XX subject, and judging whether the subject has bronchial asthma or chronic

XX obstructive pulmonary disease. The marker gene comprises: (a) a group of

XX genes (S1) whose expression levels increase when respiratory epithelial

XX cells are stimulated with interleukin-13; or (b) a group of genes (S2)

XX whose expression levels decrease when respiratory epithelial cells are

XX stimulated with interleukin-13. Also described: (1) a reagent (I) for

XX testing for bronchial asthma or chronic obstructive pulmonary disease;

XX (2) a kit for screening for a candidate compound for a therapeutic agent

XX to treat bronchial asthma or chronic obstructive pulmonary disease; (3)

XX an animal model for bronchial asthma or chronic obstructive pulmonary

XX disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a

XX method for producing an animal model for bronchial asthma or chronic

XX obstructive pulmonary disease; (6) a therapeutic agent for bronchial

XX asthma or chronic obstructive pulmonary disease, comprising the compound,

XX a marker gene or an antisense nucleic acid corresponding to a portion of

XX the marker gene, a ribozyme, a polynucleotide that suppresses the

XX expression of the gene through an RNAi effect or an antibody recognising

XX a protein encoded by a marker gene; and (7) a DNA chip for testing for

XX bronchial asthma or a chronic obstructive pulmonary disease, on which a

XX probe has been immobilised to assay a marker gene. (I) has respiratory

XX and antiasthmatic activities, and can be used in gene therapy. The method

XX is useful for testing for or screening for a therapeutic agent for

XX bronchial asthma or chronic obstructive pulmonary disease. The present

XX sequence is used in the exemplification of the present invention.

SQ Sequence 4062 BP; 966 A; 1178 C; 1099 G; 819 T; 0 U; 0 Other;

Query Match 46.7%; Score 120.4; DB 12; Length 4062;

Best Local Similarity 99.2%; Pred. No. 3.4e-24;

Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 60

DB 850 CAGCGGAGTGATGGCAAGCAGCACTTCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 909

QY 61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTTGGAATTCACCTCAG 120

DB 910 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTTGGAATTCACCTCAG 969

QY 121 GT 122

DB 970 CT 971

RESULT 14

ADJ74903

ID ADJ74903 standard; DNA; 4062 BP.

XX

AC ADJ74903;

XX

DT 20-MAY-2004 (first entry)

XX

XX Marker gene SEQ ID NO:155.

XX

XX bronchial asthma; chronic obstructive pulmonary disease;

XX respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;

XX gene therapy; marker gene; gene; ds.

XX

OS Homo sapiens.

XX

PN EP1394274-A2.

XX

PD 03-MAR-2004.

XX

XX

PF 04-AUG-2003; 2003EP-00254857.

XX

PR 06-AUG-2002; 2002JP-00229312.

PR 20-MAR-2003; 2003JP-00077212.

XX

XX (GENO-) GENOX RES INC.

XX

XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;

XX WPI; 2004-193155/19.

XX Testing for bronchial asthma or chronic obstructive pulmonary disease by

XX comparing the expression level of a marker gene in a biological sample

XX from a subject with the expression level of the gene in a sample from a

XX healthy subject.

XX Claim 1; SEQ ID NO 155; 241pp; English.

XX The present invention describes a method of testing for bronchial asthma

XX or chronic obstructive pulmonary disease. The method comprises

XX determining the expression level of a marker gene in a biological sample

XX from a subject, comparing the expression level determined with the

XX expression level of the marker gene in a biological sample from a healthy

XX subject, and judging whether the subject has bronchial asthma or chronic

XX obstructive pulmonary disease. The marker gene comprises: (a) a group of

XX genes (S1) whose expression levels increase when respiratory epithelial

XX cells are stimulated with interleukin-13; or (b) a group of genes (S2)

XX whose expression levels decrease when respiratory epithelial cells are

XX stimulated with interleukin-13. Also described: (1) a reagent (I) for

XX testing for bronchial asthma or chronic obstructive pulmonary disease;

XX (2) a kit for screening for a candidate compound for a therapeutic agent

XX to treat bronchial asthma or chronic obstructive pulmonary disease; (3)

XX an animal model for bronchial asthma or chronic obstructive pulmonary

XX disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a

XX method for producing an animal model for bronchial asthma or chronic

XX obstructive pulmonary disease; (6) a therapeutic agent for bronchial

XX asthma or chronic obstructive pulmonary disease, comprising the compound,

XX a marker gene or an antisense nucleic acid corresponding to a portion of

XX the marker gene, a ribozyme, a polynucleotide that suppresses the

XX expression of the gene through an RNAi effect or an antibody recognising

XX a protein encoded by a marker gene; and (7) a DNA chip for testing for

XX bronchial asthma or a chronic obstructive pulmonary disease, on which a

XX probe has been immobilised to assay a marker gene. (I) has respiratory

XX and antiasthmatic activities, and can be used in gene therapy. The method

XX is useful for testing for or screening for a therapeutic agent for

XX bronchial asthma or chronic obstructive pulmonary disease. The present

XX sequence is used in the exemplification of the present invention.

SQ Sequence 4062 BP; 966 A; 1178 C; 1099 G; 819 T; 0 U; 0 Other;

Query Match 46.7%; Score 120.4; DB 12; Length 4062;

Best Local Similarity 99.2%; Pred. No. 3.4e-24;

Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 60

DB 850 CAGCGGAGTGATGGCAAGCAGCACTTCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 909

QY 61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTTGGAATTCACCTCAG 120

DB 910 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTTGGAATTCACCTCAG 969

QY 121 GT 122

DB 970 CT 971

RESULT 15  
AAT98199  
ID AAT98199 standard; cDNA; 4070 BP.  
XX AC AAT98199;  
XX DT 11-MAY-1998 (first entry)  
XX DE Human inducible nitric oxide synthetase cDNA.  
XX KW Nitric oxide synthetase; NOS; iNOS; HPI NOS; human; erectile dysfunction;  
XX KW impotence; gene therapy; corpora cavernosa; relaxant; ss.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX FT CDS 197..3658  
XX FT /\*tag= a  
XX PN WO9742965-A1.  
XX PD 20-NOV-1997.  
XX PF 09-MAY-1997; 97WO-US007643.  
XX PR 10-MAY-1996; 96US-0017373P.  
XX PA (GONZ/) GONZALEZ-CADAVID N F.  
XX RA (RAJF/) RAJFER J.  
XX PI Gonzalez-Cadavid NF, Rajfer J;  
XX WPI; 1998-008577/01.  
XX P-PSDB; AAW36113.  
XX PT Treatment of erectile dysfunction - by introducing an agent into penile  
XX PT tissue, particularly for inducing cavernosal smooth muscle relaxation or  
XX PT increasing NOS levels.  
XX PS Claim 14; Page 35-38; 53pp; English.  
XX CC This cDNA sequence includes a coding region for human penis inducible  
XX CC nitric oxide synthetase (HPI NOS) (see AAW36113). It was isolated by  
XX CC reverse transcription of mRNA from human penile smooth muscle cells with  
XX CC iNOS antisense primers, combined with PCR amplification of the resulting  
XX CC cDNA fragments. The invention is directed to a method of treating  
XX CC erectile dysfunction in a patient by providing an agent capable of  
XX CC treating erectile dysfunction, and introducing an effective amount of the  
XX CC agent into the penile tissue of the patient. Preferably, the agent  
XX CC induces cavernosal smooth muscle relaxation, and/or produces an increase  
XX CC in the level of NOS in tissue. Preferably, the NOS is iNOS, and the agent  
XX CC is introduced into the corpora cavernosa of the penis. The agent is  
XX CC preferably an NOS inducer, an NOS protein such as HPI NOS, a cDNA encoding  
XX CC an NOS such as HPI NOS, or cDNA-transformed penile cells, especially  
XX CC corpora cavernosa cells  
XX SQ Sequence 4070 BP; 947 A; 1197 C; 1112 G; 814 T; 0 U; 0 Other;  
Query Match 46.7%; Score 120.4; DB 2; Length 4070;  
Best Local Similarity 99.2%; Pred. No. 3.4e-24;  
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CAGCGGAGTGATGGCAAGCAGCACTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
DB 941 CAGCGGAGTGATGGCAAGCAGCACTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1000  
QY 61 GGCTACAGATGCCAGATGGCAGATCAGAGGGGACCCCTGCCACGTGGGAATTCACCTCAG 120  
DB 1001 GGCTACAGATGCCAGATGGCAGATCAGAGGGGACCCCTGCCACGTGGGAATTCACCTCAG 1060  
QY 121 GT 122  
DB 1061 CT 1062

RESULT 16  
ADQ38958  
ID ADQ38958 standard; DNA; 4133 BP.  
XX AC ADQ38958;  
XX DT 18-NOV-2004 (first entry)  
XX DE Human SNP containing myocardial infarction-associated gene, SEQ ID 621.  
XX KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;  
XX KW cardiant; gene therapy; human; gene; ds.  
XX OS Homo sapiens.  
XX PN WO2004058052-A2.  
XX PD 15-JUL-2004.  
XX PF 22-DEC-2003; 2003WO-US040978.  
XX PR 20-DEC-2002; 2002US-0434778P.  
XX PR 10-MAR-2003; 2003US-0453135P.  
XX PR 30-APR-2003; 2003US-0466412P.  
XX PR 23-SEP-2003; 2003US-0504955P.  
XX PA (APPL-) APPLERA CORP.  
XX PI Cargill M, Devlin JJ, Iakubova O;  
XX WPI; 2004-533949/51.  
XX P-PSDB; ADQ39786.  
XX PT Identifying an individual who has an altered risk for developing  
XX PT myocardial infarction by detecting a single nucleotide polymorphism in  
XX PT the individual's nucleic acids.  
XX PS Claim 7; SEQ ID NO 621; 145pp; English.  
XX CC The invention relates to a novel method for identifying an individual who  
XX CC has an altered risk for developing myocardial infarction. The method  
XX CC comprises detecting a single nucleotide polymorphism (SNP) in any one of  
XX CC the nucleotide sequences given in the specification in the individual's  
XX CC nucleic acids, where the presence of the SNP is correlated with an  
XX CC altered risk for myocardial infarction in the individual. The invention  
XX CC further comprises: an isolated nucleic acid molecule comprising at least  
XX CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in  
XX CC the specification or its complement and encoding any one of the amino  
XX CC acid sequences given in the specification; an isolated polypeptide  
XX CC comprising an amino acid sequence given in the specification; an antibody  
XX CC that specifically binds to the polypeptide or its antigen-binding  
XX CC fragment; an amplified polynucleotide containing an SNP given in the  
XX CC specification and which is between about 16 and 1000 nucleotides in  
XX CC length; a kit for detecting an SNP in a nucleic acid, comprising the  
XX CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a  
XX CC nucleic acid molecule; a method of detecting a variant polypeptide; and a  
XX CC method for identifying an agent useful in treating or preventing  
XX CC myocardial infarction. The novel detection method has cardiant activity.  
XX CC The nucleic acids of the invention may be used in gene therapy. The  
XX CC method is useful in identifying an individual who has an increased or  
XX CC decreased risk for developing myocardial infarction and for preparing a  
XX CC composition for treating or preventing myocardial infarction. This  
XX CC polynucleotide sequence represents a human myocardial infarction-  
XX CC associated gene containing one or more SNPs of the invention. Note: This  
XX CC sequence was not shown in the specification. The sequence has come from  
XX CC an electronic sequence listing downloaded from the WIPO website.  
XX SQ Sequence 4133 BP; 960 A; 1198 C; 1118 G; 840 T; 0 U; 17 Other;  
Query Match 46.7%; Score 120.4; DB 13; Length 4133;  
Best Local Similarity 99.2%; Pred. No. 3.4e-24;

Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
 Db 939 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 998  
 Qy 61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCTGCCAACGTGGAAATTCACCTCAG 120  
 Db 999 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCTGCCAACGTGGAAATTCACCTCAG 1058  
 Qy 121 GT 122  
 Db 1059 CT 1060

RESULT 17  
 ID AAQ66914 standard; cDNA; 4145 BP.  
 AC AAQ66914;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 28-DEC-1994 (first entry)  
 XX  
 DE Sequence of the cDNA clone for human hepatocyte inducible nitric oxide  
 DE synthase.  
 XX  
 KW Nitric oxide synthase; hepatocyte; hypotensive shock; therapy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 207..3668  
 FT /\*tag= a  
 XX  
 PN WO9412645-A2.  
 XX  
 PD 09-JUN-1994.  
 XX  
 PF 23-NOV-1993; 93WO-US011401.  
 XX  
 PR 25-NOV-1992; 92US-00981344.  
 XX  
 PA (UYPI-) UNIV PITTSBURGH.  
 XX  
 PI Billiar TR, Nussler AK, Geller DA, Simmons RL;  
 XX  
 DR WPI; 1994-200273/24.  
 DR P-PSDB; AAR55764.  
 XX  
 PT cDNA clone encoding human inducible nitric oxide synthase - used to  
 PT prevent the hypotensive shock seen with sepsis.  
 PS  
 PS Claim 23; Fig 1; 53pp; English.  
 XX  
 CC AAQ66914 is from human hepatocyte inducible nitric oxide synthase cDNA  
 CC clone PHINOS from lambda Zap II cDNA library. The original source was  
 CC induced human hepatocyte RNA. HINOS cDNA plasmid is pref. transformed in  
 CC E. coli SOLR (ATCC 69126). The inventors claim a clone with the cDNA  
 CC sequence in AAQ66914 and a cDNA clone which encodes AAR55764. The cloning  
 CC and expression of a human tissue nitric oxide synthase cDNA provides a  
 CC source of the enzyme for therapeutic purposes, for example to prevent the  
 CC hypotensive shock seen with sepsis. (Updated on 25-MAR-2003 to correct FN  
 CC field.)  
 XX  
 SQ Sequence 4145 BP; 968 A; 1203 C; 1126 G; 848 T; 0 U; 0 Other;

Query Match 46.7%; Score 120.4; DB 2; Length 4145;  
 Best Local Similarity 99.2%; Pred. No. 3.4e-24;  
 Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
 Db 951 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1010  
 Qy 61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCTGCCAACGTGGAAATTCACCTCAG 120  
 Db 1011 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCTGCCAACGTGGAAATTCACCTCAG 1070

Db 951 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1010  
 Qy 61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCTGCCAACGTGGAAATTCACCTCAG 120  
 Db 1011 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCTGCCAACGTGGAAATTCACCTCAG 1070  
 Qy 121 GT 122  
 Db 1071 CT 1072

RESULT 18  
 AAT10115  
 ID AAT10115 standard; cDNA; 4145 BP.  
 XX  
 AC AAT10115;  
 XX  
 DT 13-MAY-1996 (first entry)  
 DT  
 XX  
 DE Nitric oxide synthase cDNA clone PHINOS.  
 XX  
 KW Inducible nitric oxide synthase; iNOS; hepatocyte; gene therapy;  
 KW vascular occlusive disease; cancer; infection; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 207..3668  
 FT /\*tag= a  
 XX  
 PN WO9600006-A1.  
 XX  
 PD 04-JAN-1996.  
 XX  
 PF 20-JUN-1995; 95WO-US007849.  
 XX  
 PR 24-JUN-1994; 94US-00265046.  
 XX  
 PA (UYPI-) UNIV PITTSBURGH.  
 XX  
 PI Billiar TR, Tzeng E, Nussler AK, Geller DA, Simmons RL;  
 XX  
 DR WPI; 1996-068641/07.  
 DR P-PSDB; AAR88464.  
 XX  
 PT Inducible nitric oxide synthase gene - useful in gene therapy to treat,  
 PT e.g. vascular occlusive disease and cancer.  
 PS  
 PS Claim 72; Page 53-58; 91pp; English.  
 XX  
 CC A cDNA clone (AAT10115), designated PHINOS, codes for the human  
 CC hepatocyte inducible nitric oxide synthase (iNOS = AAR88464). It was  
 CC obt'd. by isolating mRNA from hepatocytes induced in vitro for iNOS  
 CC biosynthesis, preparing a cDNA library in a phage lambda Zap II vector,  
 CC and screening with a cross-species iNOS probe. The cDNA can be used to  
 CC prepare iNOS for therapeutic use. Alternatively, it is used in gene  
 CC therapy strategies for treatment of vascular occlusive disease associated  
 CC with atherosclerosis, vascular bypass and diabetes mellitus, tumor cell  
 CC growth, and microbial infections  
 XX  
 SQ Sequence 4145 BP; 968 A; 1205 C; 1124 G; 848 T; 0 U; 0 Other;

Query Match 46.7%; Score 120.4; DB 2; Length 4145;  
 Best Local Similarity 99.2%; Pred. No. 3.4e-24;  
 Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
 Db 951 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1010  
 Qy 61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCTGCCAACGTGGAAATTCACCTCAG 120  
 Db 1011 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCTGCCAACGTGGAAATTCACCTCAG 1070

QY 121 GT 122  
Db 1071 CT 1072

RESULT 19  
AAA34818  
ID AAA34818 standard; DNA; 4145 BP.  
XX  
AC AAA34818;  
XX  
XX  
DT 28-JUL-2000 (first entry)  
XX  
DE Human adenosine receptor related polynucleotide SEQ ID NO:2507.  
XX  
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KW phosphorothioate; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiallergic; antiasthmatic; cytosstatic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200009525-A2.  
XX  
PD 24-FEB-2000.  
XX  
XX 03-AUG-1999; 99WO-US017712.  
XX  
PR 03-AUG-1998; 98US-0095212P.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
PI Nyce JW;  
XX  
DR WPI; 2000-205971/18.  
XX  
XX  
PT New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers.  
XX  
PS Disclosure; Page 664-665; 1343pp; English.  
XX  
XX The present invention describes a new composition comprising an antisense  
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
CC nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiasthmatic, cytosstatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
CC impaired respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
CC carcinomas, and cancers which may metastasize to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of the  
CC ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. AAA32313 to AAA3512 represent the  
CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
CC AAA33992) are specifically claimed ONs from the present invention. N.B.  
CC Sequences given in the disclosure of the present invention do not match  
CC up with their corresponding SEQ ID NO: sequences given in the sequence  
CC listing

XX SQ Sequence 4145 BP; 968 A; 1203 C; 1126 G; 848 T; 0 U; 0 Other;  
Query Match 46.7%; Score 120.4; DB 3; Length 4145;  
Best Local Similarity 99.2%; Pred. No. 3.4e-24;  
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CAGCGAGTGATGGCAAGCAGACGATTCGGGGTGTGGAAATGCTCAGCTCATCGCTATGCT 60  
Db 951 CAGCGAGTGATGGCAAGCAGACGATTCGGGGTGTGGAAATGCTCAGCTCATCGCTATGCT 1010  
QY 61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCTGCCAACGTTGAATTCATCTCAG 120  
Db 1011 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCTGCCAACGTTGAATTCATCTCAG 1070  
QY 121 GT 122  
Db 1071 CT 1072

RESULT 20  
AAF20940  
ID AAF20940 standard; DNA; 4145 BP.  
XX  
AC AAF20940;  
XX  
XX 14-MAR-2001 (first entry)  
XX  
DE Human inducible nitric oxide synthase polynucleotide fragment #2507.  
XX  
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
KW human; airway disorder; bronchoconstriction; lung inflammation;  
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytosstatic;  
KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
KW cancer; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200062736-A2.  
XX  
XX 26-OCT-2000.  
XX  
XX 24-MAR-2000; 2000WO-US008020.  
XX  
XX 06-APR-1999; 99US-0127958P.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX (NYCE/) NYCE J W.  
XX  
PI Nyce JW;  
XX  
XX WPI; 2000-679539/66.  
XX  
XX Low adenosine (A) content antisense oligonucleotides which do not trigger  
PT adenosine receptors during metabolism, useful e.g. for treating cancers  
PT and respiratory obstructions.  
XX  
PS Disclosure; Page 254-255; 1592pp; English.  
XX  
XX The present invention describes low adenosine (A) content antisense  
CC oligonucleotides and compositions (I) comprising them. In the antisense  
CC oligonucleotides the A is replaced by a 'universal' or alternative base.  
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
CC immunosuppressive, antiasthmatic, hypotensive and cytosstatic activities.  
CC The antisense oligonucleotides and (I) can be used to down-regulate the  
CC expression and/or activity of target polypeptides associated with  
CC lung/respiratory disorders and malignancies, such as stimulating and  
CC activating peptide factors and transmitters, transcription factors,

CC immunoglobulins and antibodies, antibody receptors, cytokines and  
 CC chemokines, endogenously produced specific and non-specific enzymes,  
 CC binding proteins, adhesion molecules and their receptors, cytokine and  
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
 CC nervous system (CNS) and peripheral nervous and non-nervous system  
 CC receptors, CNS and peripheral nervous and non-nervous system peptide  
 CC transmitters, defensins, growth factors, vasoactive peptides and  
 CC receptors, binding proteins and malignancy associated proteins. The  
 CC antisense oligonucleotides may be used in this way to treat disorders  
 CC including respiratory obstruction (especially pulmonary obstruction  
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or  
 CC surfactant hypoproduction which are associated with a disease or  
 CC condition selected from pulmonary vasoconstriction, inflammation,  
 CC allergies, asthma, impeded respiration, respiratory distress syndrome  
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
 CC hyperinflation, emphysema, chronic obstructive pulmonary disease (COPD),  
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
 CC and/or cancer. AAF10434 to AAF21543 represent human polynucleotide  
 CC fragments and antisense oligonucleotides used in the exemplification of  
 CC the present invention  
 XX  
 SQ Sequence 4145 BP; 968 A; 1203 C; 1126 G; 848 T; 0 U; 0 Other;  
 Query Match 46.7%; Score 120.4; DB 3; Length 4145;  
 Best Local Similarity 99.2%; Pred. No. 3.4e-24;  
 Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CAGCGGAGTGATGGCAGCAGCAGCTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
 DB 951 CAGCGGAGTGATGGCAGCAGCAGCTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1010  
 QY 61 GGCTACCAGATGCCAGATGGCAGCAGCAGCAGGAGCCCTGCCACGTTGGAATTCACCTCAG 120  
 DB 1011 GGCTACCAGATGCCAGATGGCAGCAGCAGGAGGAGCCCTGCCACGTTGGAATTCACCTCAG 1070  
 QY 121 GT 122  
 DB 1071 CT 1072  
 RESULT 21  
 AAH47966  
 ID AAH47966 standard; cDNA; 4145 BP.  
 XX  
 AC AAH47966;  
 XX  
 DT 02-OCT-2001 (first entry)  
 XX  
 DE Mouse inducible nitric oxide synthase encoding cDNA 1.  
 XX  
 KW Antisense oligonucleotide; inducible nitric oxide synthase;  
 KW modulate expression; immunomodulator; antidiabetic; cardiovascular;  
 KW cardiant; neuroprotective; vasotropic; ischaemia; reperfusion injury;  
 KW 2'-O-methoxyethyl; phosphorothioate; mouse; ss.  
 XX  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 CDS 207..3668  
 FT /\*tag= a  
 FT /product= "inducible nitric oxide synthase"  
 XX  
 PN WO200152902-A1.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PF 15-JAN-2001; 2001WO-US001381.  
 XX  
 PR 24-JAN-2000; 2000US-00490208.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Bennett CF, Dean NM, Cowseert LM;

XX WPI; 2001-465340/50.  
 DR P-PSDB; AAG64498.  
 XX  
 PT New antisense oligonucleotides for modulating the expression of inducible  
 PT nitric oxide synthase in cells or tissues, particularly useful for  
 PT treating e.g. immunological, cardiovascular or neurological disorders, or  
 PT ischaemia.  
 XX  
 PS Example 13; Page 98-103; 144pp; English.  
 XX  
 CC The invention relates to antisense compounds, especially  
 CC oligonucleotides, which are targeted to a nucleic acid encoding inducible  
 CC nitric oxide synthase and which specifically hybridise to and modulate  
 CC expression of inducible nitric oxide synthase. The antisense compounds  
 CC have immunomodulator, antidiabetic, cardiovascular, cardiant,  
 CC neuroprotective, disorder and vasotropic activity. The antisense  
 CC oligonucleotides are useful for inhibiting the expression of inducible  
 CC nitric oxide synthase in cells or tissues. In particular, the antisense  
 CC oligonucleotides are useful for treating diseases or disorders associated  
 CC with inducible nitric oxide synthase, e.g. diabetes, immunological  
 CC disorder, cardiovascular disorder, neurological disorder or  
 CC ischaemia/reperfusion injury. The antisense oligonucleotides are also  
 CC useful for research and diagnostics. The present sequence is that of  
 CC mouse inducible nitric oxide synthase (Genbank accession number M92649)  
 XX  
 SQ Sequence 4145 BP; 968 A; 1203 C; 1126 G; 848 T; 0 U; 0 Other;  
 Query Match 46.7%; Score 120.4; DB 4; Length 4145;  
 Best Local Similarity 99.2%; Pred. No. 3.4e-24;  
 Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CAGCGGAGTGATGGCAGCAGCAGCTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
 DB 951 CAGCGGAGTGATGGCAGCAGCAGCTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1010  
 QY 61 GGCTACCAGATGCCAGATGGCAGCAGCAGGAGCCCTGCCACGTTGGAATTCACCTCAG 120  
 DB 1011 GGCTACCAGATGCCAGATGGCAGCAGCAGGAGGAGCCCTGCCACGTTGGAATTCACCTCAG 1070  
 QY 121 GT 122  
 DB 1071 CT 1072  
 RESULT 22  
 AAH47959  
 ID AAH47959 standard; cDNA; 4145 BP.  
 XX  
 AC AAH47959;  
 XX  
 DT 02-OCT-2001 (first entry)  
 XX  
 DE Human inducible nitric oxide synthase encoding cDNA 1.  
 XX  
 KW Antisense oligonucleotide; inducible nitric oxide synthase;  
 KW modulate expression; immunomodulator; antidiabetic; cardiovascular;  
 KW cardiant; neuroprotective; vasotropic; ischaemia; reperfusion injury;  
 KW 2'-O-methoxyethyl; phosphorothioate; human; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 CDS 207..3668  
 FT /\*tag= a  
 FT /product= "inducible nitric oxide synthase"  
 XX  
 PN WO200152902-A1.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PF 15-JAN-2001; 2001WO-US001381.  
 XX

```
PR 24-JAN-2000; 2000US-00490208.
XX (ISIS-) ISIS PHARM INC.
XX Bennett CP, Dean NM, Cowsert LM;
XX WPI; 2001-465340/50.
DR P-PSDB; AAG64497.
XX
XX New antisense oligonucleotides for modulating the expression of inducible
PT nitric oxide synthase in cells or tissues, particularly useful for
PT treating e.g. immunological, cardiovascular or neurological disorders, or
PT ischemia.
XX
XX Example 13; Page 92-97; 144pp; English.
XX
XX The invention relates to antisense compounds, especially
CC oligonucleotides, which are targeted to a nucleic acid encoding inducible
CC nitric oxide synthase and which specifically hybridize to and modulate
CC expression of inducible nitric oxide synthase. The antisense compounds
CC have immunomodulator, antidiabetic, cardiovascular, cardiac,
CC neuroprotective, disorder and vasotropic activity. The antisense
CC oligonucleotides are useful for inhibiting the expression of inducible
CC nitric oxide synthase in cells or tissues. In particular, the antisense
CC oligonucleotides are useful for treating diseases or disorders associated
CC with inducible nitric oxide synthase, e.g. diabetes, immunological
CC disorder, cardiovascular disorder, neurological disorder or
CC ischaemia/reperfusion injury. The antisense oligonucleotides are also
CC useful for research and diagnostics. The present sequence is that of
CC human inducible nitric oxide synthase (GenBank accession number L09210)
XX
SQ Sequence 4145 BP; 968 A; 1203 C; 1126 G; 848 T; 0 U; 0 Other;

Query Match 46.7%; Score 120.4; DB 4; Length 4145;
Best Local Similarity 99.2%; Pred.No. 3.4e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
DB |||||
551 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1010

QY 61 GGCTACCATGCCAGATGCCAGATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 120
DB |||||
1011 GGCTACCATGCCAGATGCCAGATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 1070

QY 121 GT 122
DB 1071 CT 1072

RESULT 23
ABZ96634
ID ABZ96634 standard; DNA; 4145 BP.
XX
AC ABZ96634;
XX
XX 17-OCT-2003 (first entry)
XX
XX Human inducible nitric oxide synthase nucleic acid.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antisthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
```

---

```
PF 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Disclosure; SEQ ID NO 11876; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antinflammatory steroid and ubiquinone. A composition of the invention
CC has antinflammatory, antiallergic, antisthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 4145 BP; 968 A; 1203 C; 1126 G; 848 T; 0 U; 0 Other;

Query Match 46.7%; Score 120.4; DB 10; Length 4145;
Best Local Similarity 99.2%; Pred.No. 3.4e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
DB |||||
951 CAGCGGAGTGATGGCAAGCAGCACTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1010

QY 61 GGCTACCATGCCAGATGCCAGATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 120
DB |||||
1011 GGCTACCATGCCAGATGCCAGATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 1070

QY 121 GT 122
DB 1071 CT 1072

RESULT 24
ABD19732
ID ABD19732 standard; DNA; 4145 BP.
XX
XX ABD19732;
XX
XX 29-JUL-2004 (first entry)
XX
XX Human inducible nitric oxide synthase DNA fragment #3.
XX
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;
XX surfactant depletion; antiallergic; antiinflammatory; antisthmatic;
XX analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
```





```
RESULT 26
AD132081
ID ADI32081 standard; cDNA; 4164 BP.
XX
AC ADI32081;
XX
XX
DT 17-JUN-2004 (first entry)
XX
DE Human cDNA #1407.
XX
XX Human; gene; ss; immunological response; immunopathological condition;
XX Crohn's disease; asthma; ulcerative colitis; hyperesinophilia;
KW irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
KW acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;
XX osteopathic; antiarthritic; antirheumatic; cytostatic.
XX
OS Homo sapiens.
XX
XX US6607879-B1.
XX
XX 19-AUG-2003.
XX
XX 09-FEB-1998; 98US-00023655.
XX
XX 09-FEB-1998; 98US-00023655.
XX
XX (INCY-) INCYTE CORP.
XX
XX Cocks BG, Stuart SG, Seilhamer JU;
XX
XX WPI; 2003-895307/82.
XX
XX A composition comprising a plurality of cDNAs, useful for detecting
XX altered expression of genes in an immunological response or for
XX diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
XX or osteoarthritis.
XX
XX Claim 1; SEQ ID NO 1407; 50pp; English.
XX
XX The invention relates to a composition comprising a plurality of cDNAs
XX for detecting the altered expression of genes in an immunological
XX response. The invention also relates to a method of diagnosing or
XX monitoring the treatment of an immunopathological condition in a sample,
XX comprising obtaining nucleic acids from a sample, contacting the nucleic
XX acids of the sample with an array comprising the plurality of cDNAs under
XX conditions to form one or more hybridisation complexes, detecting the
XX hybridisation complexes and comparing the levels of the detected
XX hybridisation complexes with the level of hybridisation complexes
XX detected in a non-diseased sample, where an altered level of the detected
XX hybridisation complexes correlates with the presence of an
XX immunopathological condition. Also disclosed are an expression profile
XX comprising a microarray and a plurality of detectable complexes and a
XX method for identifying a plurality of polynucleotide probes. The cDNAs
XX are useful as hybridisable array elements in a microarray for monitoring
XX the expression of target polynucleotides. The microarray can be used in
XX the diagnosis of an immunopathology, such as Crohn's disease, asthma,
XX ulcerative colitis, hyperesinophilia, irritable bowel syndrome,
XX osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
XX identifying agents for the treatment of the diseases. The microarray may
XX also be used in drug discovery and development, toxicological and
XX carcinogenicity studies, forensics or pharmacogenomics. The composition
XX may also be used in purification of a subpopulation of mRNAs, cDNAs or
XX genomic fragments. This sequence represents a human cDNA of the
XX invention. Note: The sequence data for this patent did not form part of
XX the printed specification but was obtained in electronic format directly
XX from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX Sequence 4164 BP; 974 A; 1210 C; 1127 G; 853 T; 0 U; 0 Other;
SQ
Query Match 46.7%; Score 120.4; DB 11; Length 4164;
Best Local Similarity 99.2%; Pred. No. 3.4e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAGCGAGTGATGGCAAGCAGACGACTTCGGGTGTGGAAATGCTCAGCTCATCGCTATGCT 60
DB 970 CAGCGAGTGATGGCAAGCAGACGACTTCGGGTGTGGAAATGCTCAGCTCATCGCTATGCT 1029
QY 61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCTGCCAACGTTCACTCAG 120
DB 1030 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCTGCCAACGTTCACTCAG 1089
QY 121 GT 122
DB 1090 CT 1091
RESULT 27
AD84148
ID ADS84148 standard; cDNA; 4164 BP.
XX
AC ADS84148;
XX
XX 11-AUG-2005 (first entry)
XX
XX Human lymph node cDNA #1407.
XX
XX ss; gene; human; immunological response; blood cell; cancer;
XX immunopathological; AIDS; allergy; anaemia; asthma; atherosclerosis;
XX bronchitis; ulcerative colitis; diabetes; multiple sclerosis;
XX osteoporosis; pancreatitis; infection; arthritis; lymph node.
XX
XX Homo sapiens.
XX
XX US2004077003-A1.
XX
XX 22-APR-2004.
XX
XX 14-AUG-2003; 2003US-00641643.
XX
XX 09-FEB-1998; 98US-00023655.
XX
XX (INCY-) INCYTE CORP.
XX
XX Cocks BG, Stuart SG, Seilhamer JJ;
XX
XX WPI; 2004-387937/36.
XX
XX New compositions having a number of first, second and third
XX polynucleotide probes, useful in research and diagnostic applications in
XX cancer and immunological conditions e.g. AIDS, diabetes, osteoporosis and
XX infections.
XX
XX Claim 15; SEQ ID NO 1407; 16pp; English.
XX
XX The invention relates to polynucleotides which are used as probes to
XX detect genes differentially expressed in an immunological response,
XX abundantly expressed in an immunological response and/or coding for a
XX polypeptide known to regulate blood cell biology. The polynucleotides are
XX useful in research and diagnostic applications particularly in cancer and
XX immunopathological conditions, such as AIDS, allergies, anaemia, asthma,
XX atherosclerosis, bronchitis, ulcerative colitis, diabetes, multiple
XX sclerosis, osteoporosis, pancreatitis, infections and arthritis. The
XX present sequence represents a human lymph node cDNA used to detect blood
XX cell and immunological response gene expression. Note: The present
XX sequence does not appear in the printed specification but was obtained in
XX electronic format from the USPTO web site
XX (seqdata.uspto.gov/sequence.html?DocID=20040077003).
XX
XX Sequence 4164 BP; 974 A; 1210 C; 1127 G; 853 T; 0 U; 0 Other;
SQ
Query Match 46.7%; Score 120.4; DB 13; Length 4164;
Best Local Similarity 99.2%; Pred. No. 3.4e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```



CC agent, the system provides a reference activity and detecting a test  
CC agent-biased activity of the assay system, where a difference between the  
CC test agent-biased activity and the reference activity identifies the test  
CC agent as a candidate IGR pathway modulating agent. The invention also  
CC relates to methods for modulating an IGR pathway of a cell or in a  
CC mammalian cell and a method for diagnosing a disease in a patient. The  
CC methods are useful for diagnosing or treating cancer or for identifying  
CC modulators of an IGR pathway, which may be utilized as therapeutic  
CC targets for disorders associated with defective IGR function, such as  
CC cancer. This sequence represents a human modulator of IGR pathway  
CC polynucleotide of the invention.

XX Sequence 4221 BP; 1001 A; 1221 C; 1138 G; 861 T; 0 U; 0 Other;

Query Match 46.7%; Score 120.4; DB 14; Length 4221;

Best Local Similarity 99.2%; Pred. No. 3.4e-24;

Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAAATGCTCAGCTCATCGCTATGCT 60

DB 1009 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAAATGCTCAGCTCATCGCTATGCT 1068

QY 61 GCCTACCAAGATCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTCAG 120

DB 1069 GCCTACCAAGATCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTCAG 1128

QY 121 GT 122

DB 1129 CT 1130

RESULT 30

ACN42844

ID ACN42844 standard; cDNA; 4277 BP.

XX AC

XX ACN42844;

DT 18-NOV-2004 (first entry)

XX Human diagnostic and therapeutic polynucleotide SEQ ID NO:1719.

XX ss; gene; gene therapy; human diagnostic and therapeutic polynucleotide;

KW dithp.

XX Homo sapiens.

XX WO2004023973-A2.

XX 25-MAR-2004.

PF 12-SEP-2003; 2003WO-US028227.

PR 12-SEP-2002; 2002US-0410259P.

PR 12-SEP-2002; 2002US-0410260P.

XX (INCY-) INCYTE CORP.

XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;

PI Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Eider LV;

PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;

PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;

PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;

PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;

PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

PI Patury S, Shi X, Suarez CJ;

XX WPI; 2004-329368/30.

DR P-PSDB; ABM84192.

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful  
PT in diagnosing a condition, disease or disorder associated with human  
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
PT in gene mapping.

XX Claim 1; Page: 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides  
CC selected from one of the 2722 sequences defined in the specification. A  
CC polynucleotide of the invention may have a use in gene therapy. The human  
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be  
CC used to diagnose a particular condition, disease or disorder associated  
CC with human molecules, e.g. cell proliferative disorders,  
CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
CC disorder, neurological disorders, gastrointestinal disorders, or  
CC infections caused by virus, bacteria, fungi or parasite. The dithp  
CC molecules may also be used in genetic mapping, in identifying individuals  
CC from minute biological samples, in detecting single nucleotide  
CC polymorphisms, as molecular weight markers, and for somatic or germline  
CC gene therapy. The present sequence represents a dithp polynucleotide of  
CC the invention. Note: The sequence data for this patent is not represented  
CC in the printed specification, but was obtained in electronic format  
CC directly from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)  
XX  
SQ Sequence 4277 BP; 973 A; 1253 C; 1237 G; 814 T; 0 U; 0 Other;

Query Match 46.7%; Score 120.4; DB 13; Length 4277;

Best Local Similarity 99.2%; Pred. No. 3.4e-24;

Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAAATGCTCAGCTCATCGCTATGCT 60

DB 1348 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAAATGCTCAGCTCATCGCTATGCT 1407

QY 61 GCCTACCAAGATCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTCAG 120

DB 1408 GCCTACCAAGATCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTCAG 1467

QY 121 GT 122

DB 1468 CT 1469

RESULT 31

ACN42843

ID ACN42843 standard; cDNA; 4278 BP.

XX AC

XX ACN42843;

DT 18-NOV-2004 (first entry)

XX Human diagnostic and therapeutic polynucleotide SEQ ID NO:1718.

XX ss; gene; gene therapy; human diagnostic and therapeutic polynucleotide;

KW dithp.

XX Homo sapiens.

XX WO2004023973-A2.

XX 25-MAR-2004.

PF 12-SEP-2003; 2003WO-US028227.

PR 12-SEP-2002; 2002US-0410259P.

PR 12-SEP-2002; 2002US-0410260P.

XX (INCY-) INCYTE CORP.

XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;

PI Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Eider LV;

PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;

PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;

PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;

PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;

PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

PI Patury S, Shi X, Suarez CJ;

XX WPI; 2004-329368/30.  
 DR P-FSDB; ABM84191.  
 XX  
 PT New diagnostic and therapeutic polynucleotides and polypeptides, useful  
 PT in diagnosing a condition, disease or disorder associated with human  
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
 PT in gene mapping.  
 XX  
 XX Claim 1; Page; 190pp; English.  
 PS  
 XX The invention relates to novel diagnostic and therapeutic polynucleotides  
 CC selected from one of the 2722 sequences defined in the specification. A  
 CC polynucleotide of the invention may have a use in gene therapy. The human  
 CC polynucleotide and therapeutic polynucleotides (dithp) or polypeptides may be  
 CC used to diagnose a particular condition, disease or disorder associated  
 CC with human molecules, e.g. cell proliferative disorders,  
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
 CC disorder, neurological disorders, gastrointestinal disorders, or  
 CC infections caused by virus, bacteria, fungi or parasite. The dithp  
 CC molecules may also be used in genetic mapping, in identifying individuals  
 CC from minute biological samples, in detecting single nucleotide  
 CC polymorphisms, as molecular weight markers, and for somatic or germline  
 CC gene therapy. The present sequence represents a dithp polynucleotide of  
 CC the invention. Note: The sequence data for this patent is not represented  
 CC in the printed specification, but was obtained in electronic format  
 CC directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm  
 XX  
 SQ Sequence 4278 BP; 972 A; 1253 C; 1238 G; 815 T; 0 U; 0 Other;  
 Query Match 46.7%; Score 120.4; DB 13; Length 4278;  
 Best Local Similarity 99.2%; Pred. No. 3.4e-24;  
 Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CAGCGGAGTGATGCGAAGCAGCACTTCGGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 60  
 DB 1348 CAGCGGAGTGATGCGAAGCAGCACTTCGGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 1407  
 QY 61 GGCTACCAAGTGCAGATGGCAGATCAGAGGGGACCTGCCAACGTTGGAATTCATCTCAG 120  
 DB 1408 GGCTACCAAGTGCAGATGGCAGATCAGAGGGGACCTGCCAACGTTGGAATTCATCTCAG 1467  
 QY 121 GT 122  
 DB 1468 CT 1469  
 RESULT 32  
 AAF21450  
 ID AAF21450 standard; DNA; 8222 BP.  
 XX  
 AC AAF21450;  
 XX  
 DT 14-MAR-2001 (first entry)  
 XX  
 DE Human inducible nitric oxide synthase polynucleotide fragment #3017.  
 XX  
 KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
 KW human; airway disorder; bronchoconstriction; lung inflammation;  
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
 KW cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200062736-A2.  
 XX  
 XX 26-OCT-2000.  
 PD

XX 24-MAR-2000; 2000WO-US008020.  
 PF XX  
 PR 06-APR-1999; 99US-0127958P.  
 XX  
 PA (UYEC-) UNIV EAST CAROLINA.  
 PA (NYCE/) NYCE J W.  
 XX  
 PI Nyce JW;  
 XX  
 DR WPI; 2000-679539/66.  
 XX  
 PT Low adenosine (A) content antisense oligonucleotides which do not trigger  
 PT adenosine receptors during metabolism, useful e.g. for treating cancers  
 PT and respiratory obstructions.  
 XX  
 PS Disclosure; Page 252-254; 1592pp; English.  
 XX  
 CC The present invention describes low adenosine (A) content antisense  
 CC oligonucleotides and compositions (I) comprising them. In the antisense  
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.  
 CC The antisense oligonucleotides and (I) can be used to down-regulate the  
 CC expression and or activity of target polypeptides associated with the  
 CC lung/respiratory disorders and malignancies, such as stimulating and  
 CC activating peptide factors and transmitters, transcription factors,  
 CC immunoglobulins and antibodies, antibody receptors, cytokines and  
 CC chemokines, endogenously produced specific and non-specific enzymes,  
 CC binding proteins, adhesion molecules and their receptors, cytokine and  
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
 CC nervous system (CNS) and peripheral nervous and non-nervous system  
 CC receptors, CNS and peripheral nervous and non-nervous system peptide  
 CC transmitters, defensins, growth factors, vasoactive peptides and  
 CC receptors, binding proteins and malignancy associated proteins. The  
 CC antisense oligonucleotides may be used in this way to treat disorders  
 CC including respiratory obstruction (especially pulmonary obstruction  
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or  
 CC surfactant hypoproduction which are associated with a disease or  
 CC condition selected from pulmonary vasoconstriction, inflammation,  
 CC allergies, asthma, impeded respiration, respiratory distress syndrome  
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
 CC fragments and antisense oligonucleotides used in the exemplification of  
 CC the present invention  
 XX  
 SQ Sequence 8222 BP; 1731 A; 2574 C; 2360 G; 1557 T; 0 U; 0 Other;  
 Query Match 46.7%; Score 120.4; DB 3; Length 8222;  
 Best Local Similarity 99.2%; Pred. No. 4e-24;  
 Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CAGCGGAGTGATGCGAAGCAGCACTTCGGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 60  
 DB 951 CAGCGGAGTGATGCGAAGCAGCACTTCGGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 1010  
 QY 61 GGCTACCAAGTGCAGATGGCAGATCAGAGGGGACCTGCCAACGTTGGAATTCATCTCAG 120  
 DB 1011 GGCTACCAAGTGCAGATGGCAGATCAGAGGGGACCTGCCAACGTTGGAATTCATCTCAG 1070  
 QY 121 GT 122  
 DB 1071 CT 1072  
 RESULT 33  
 ABZ97144  
 ID ABZ97144 standard; DNA; 8222 BP.  
 XX  
 XX ABZ97144;  
 AC  
 XX

DT 17-OCT-2003 (first entry)  
XX Human nucleic acid sequence.  
DE  
XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytotatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
XX Homo sapiens.  
XX WO200285308-A2.  
XX 31-OCT-2002.  
XX 23-APR-2002; 2002WO-US013135.  
XX 24-APR-2001; 2001US-0286137P.  
XX (EPIG-) EPIGENESIS PHARM INC.  
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX WPI; 2003-229219/22.  
XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
XX Disclosure; SEQ ID NO 12386; 872pp; English.  
PS  
XX The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytotatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 8222 BP; 1731 A; 2574 C; 2360 G; 1557 T; 0 U; 0 Other;  
SQ  
Query Match 46.7%; Score 120.4; DB 10; Length 8222;  
Best Local Similarity 99.2%; Pred. No. 4e-24;  
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CAGCGGAGTGATGGCAAGCAGCACTCCGGGTGTGGAAATGCTCAGTCTATCCGCTATGCT 60  
DB 951 CAGCGGAGTGATGGCAAGCAGCACTCCGGGTGTGGAAATGCTCAGTCTATCCGCTATGCT 1010  
QY 61 GGTACACAGATGCCAGATGGCAGATCAGAGGGGACCTGCGACAGTGGGAATTCACCTCAG 120  
DB 1011 GGTACACAGATGCCAGATGGCAGATCAGAGGGGACCTGCGACAGTGGGAATTCACCTCAG 1070  
QY 121 GT 122  
DB 1071 CT 1072

RESULT 34  
ABD19730  
ID ABD19730 standard; DNA; 8222 BP.  
XX  
AC ABD19730;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Human inducible nitric oxide synthase DNA fragment 1897.  
XX  
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;  
KW analgesic; hypotensive; immunosuppressive; cytotatic; cystic fibrosis;  
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
KW pulmonary transplantation rejection; ds.  
XX  
XX Homo sapiens.  
XX WO200285309-A2.  
XX 31-OCT-2002.  
XX 23-APR-2002; 2002WO-US013143.  
XX 24-APR-2001; 2001US-0286036P.  
XX (EPIG-) EPIGENESIS PHARM INC.  
XX  
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX WPI; 2003-093058/08.  
XX Pharmaceutical composition for treating asthma, has antisense  
PT oligonucleotide containing less percentage of adenosine, targeted to  
PT nucleic acids associated with lung airway or lung dysfunction, and  
PT bronchodilating agent.  
XX  
XX Claim 15; SEQ ID NO 12386; 763pp; English.  
PS  
XX This invention describes a novel composition (a) a first active agent,  
CC comprising oligonucleotides, effective for alleviating.  
CC bronchoconstriction, respiratory tract inflammation, allergies and  
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
CC surfactant depletion or hyposecretion, when administered to a mammal. The  
CC oligonucleotides are derived from a gene encoding or regulating  
CC expression of a target polypeptide associated with lung airway or lung  
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
CC The invention also describes a kit, that comprises: (a) a delivery  
CC device, in separate containers, (b) the oligonucleotides, (c)  
CC instructions for adding a carrier and for use of the kit. The composition  
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,  
CC analgesic, hypotensive, immunosuppressive and cytotatic activity, is a  
CC beta-adrenergic agonist. The composition is useful for preventing or  
CC treating a respiratory, lung or malignant disease. The administered  
CC composition comprises oligo and is administered to reduce the production  
CC or availability, or to increase the degradation of the target mRNA or to  
CC reduce the amount of target polypeptide present in the lungs. The  
CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
CC inflammation, allergies and/or surfactant hypoproduction are associated  
CC with a disease or condition such as pulmonary vasoconstriction,  
CC inflammation, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary  
CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
CC The reduced adenosine content of the anti-sense oligos corresponding to  
CC thymidines present in the target RNA serves to prevent the breakdown of  
CC the oligonucleotides into products that free adenosine into the system

CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it

SQ Sequence 8222 BP; 1731 A; 2574 C; 2360 G; 1557 T; 0 U; 0 Other;

Query Match 46.7%; Score 120.4; DB 11; Length 8222;  
 Best Local Similarity 99.2%; Pred. No. 4e-24;  
 Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGCGAAGCAGCAGCTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
 |||||  
 Db 951 CAGCGGAGTGATGCGAAGCAGCAGCTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1010  
 |||||  
 Qy 61 GGCTACCAAGTCCAGATGCGCAGCATCAGAGGGGACCTGCCACGCGGAATTCACCTCAG 120  
 |||||  
 Db 1011 GGCTACCAAGTCCAGATGCGCAGCATCAGAGGGGACCTGCCACGCGGAATTCACCTCAG 1070  
 |||||

Qy 121 GT 122

Db 1071 CT 1072

# RESULT 35

AAA34820  
 ID AAA34820 standard; DNA; 9513 BP.

AC AAA34820;

XX 28-JUL-2000 (first entry)

DE Human adenosine receptor related polynucleotide SEQ ID NO:2509.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;  
 KW phosphorothioate; impaired respiration; inflammation; allergy;  
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX Homo sapiens.

OS WO200009525-A2.

PN 24-FEB-2000.

PD 03-AUG-1999; 99WO-US017712.

XX 03-AUG-1998; 98US-0095212P.

PR (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW;

PI WPI; 2000-205971/18.

DR New antisense oligonucleotides useful for treating e.g. pulmonary  
 XX vasoconstriction, inflammation, allergies, asthma, hypertension,  
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
 PT cancers.

XX Disclosure; Page 666-669; 1343pp; English.

XX The present invention describes a new composition comprising an antisense  
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
 CC nucleic acids involved in bronchoconstriction, allergies, and/or  
 CC inflammation. The ON can have antiinflammatory, antiallergic,  
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
 CC useful for the treatment of diseases associated with inflammation,  
 CC impaired airways, including lung disease and diseases whose secondary  
 CC effects afflict the lungs of a subject. They can be used for treating  
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,

CC impeded respiration, respiratory distress syndrome, pain, cystic  
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
 CC carcinomas, and cancers which may metastasise to the lungs, including  
 CC breast and prostate cancer. The reduction of the adenosine content of the  
 CC ONs reduces side effects. The A-containing ONs break down with the  
 CC release of deoxyadenosine which activates adenosine receptors causing  
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the  
 CC nucleotide sequences given in the sequence listing from the present  
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.  
 CC Sequences given in the disclosure of the present invention do not match  
 CC up with their corresponding SEQ ID NO: sequences given in the sequence  
 CC listing

SQ Sequence 9513 BP; 2107 A; 2869 C; 2671 G; 1866 T; 0 U; 0 Other;

Query Match 46.7%; Score 120.4; DB 3; Length 9513;  
 Best Local Similarity 99.2%; Pred. No. 4.1e-24;  
 Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGCGAAGCAGCAGCTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
 |||||

Db 2242 CAGCGGAGTGATGCGAAGCAGCAGCTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 2301  
 |||||

Qy 61 GGCTACCAAGTCCAGATGCGCAGCATCAGAGGGGACCTGCCACGCGGAATTCACCTCAG 120  
 |||||

Db 2302 GGCTACCAAGTCCAGATGCGCAGCATCAGAGGGGACCTGCCACGCGGAATTCACCTCAG 2361  
 |||||

Qy 121 GT 122

Db 2362 CT 2363

# RESULT 36

AAF20942

ID AAF20942 standard; DNA; 9513 BP.

XX AAF20942;

XX 14-MAR-2001 (first entry)

DE Human low adenosine antisense oligonucleotide #2509.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
 KW human; airway disorder; bronchoconstriction; lung inflammation;  
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
 KW cancer; ss.

XX Homo sapiens.

OS WO2000062736-A2.

PN 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US008020.

PR 06-APR-1999; 99US-0127958P.

XX (UYEC-) UNIV EAST CAROLINA.

XX (NYCE/) NYCE J W.

XX Nyce JW;

DR WPI; 2000-679539/66.

XX Low adenosine (A) content antisense oligonucleotides which do not trigger  
 PT adenosine receptors during metabolism, useful e.g. for treating cancers  
 PT and respiratory obstructions.

XX Disclosure; Page 737-739; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense  
 CC oligonucleotides and compositions (I) comprising them. In the antisense  
 CC oligonucleotides the A is replaced by a 'universal' or alternative base.  
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
 CC immunosuppressive, antiallergic, hypotensive and cytostatic activities.  
 CC The antisense oligonucleotides and (I) can be used to down-regulate the  
 CC expression and/or activity of target polypeptides associated with  
 CC lung/respiratory disorders and malignancies, such as stimulating and  
 CC activating peptide factors and transmitters, transcription factors,  
 CC immunoglobulins and antibodies, antibody receptors, cytokines and  
 CC chemokines, endogenously produced specific and non-specific enzymes,  
 CC binding proteins, adhesion molecules and their receptors, cytokine and  
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
 CC nervous system (CNS) and peripheral nervous and non-nervous system  
 CC receptors, CNS and peripheral nervous and non-nervous system peptide  
 CC transmitters, defensins, growth factors, vasoactive peptides and  
 CC receptors, binding proteins and malignancy associated proteins. The  
 CC antisense oligonucleotides may be used in this way to treat disorders  
 CC including respiratory obstruction (especially pulmonary obstruction  
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or  
 CC surfactant hypoproduction which are associated with a disease or  
 CC condition selected from pulmonary vasoconstriction, inflammation,  
 CC allergies, asthma, impeded respiration, respiratory distress syndrome  
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
 CC fragments and antisense oligonucleotides used in the exemplification of  
 CC the present invention

XX Sequence 9513 BP; 2107 A; 2868 C; 2672 G; 1866 T; 0 U; 0 Other;

Query Match 46.7%; Score 120.4; DB 3; Length 9513;  
 Best Local Similarity 99.2%; Pred. No. 4.1e-24;  
 Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGTGTGGAATGCTCAGCTCATCGCTATGCT 60  
 |||||  
 Db 2242 CAGCGGAGTGATGGCAAGCAGCACTTCGGGTGTGGAATGCTCAGCTCATCGCTATGCT 2301

QY 61 GGCTACCATGCGCAGATGCGCAGCATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 120  
 |||||  
 Db 2302 GGCTACCATGCGCAGATGCGCAGCATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 2361

QY 121 GT 122  
 Db 2362 CT 2363

RESULT 37  
 ID ABZ96636

XX ABZ96636 standard; DNA; 9513 BP.

XX AC ABZ96636;

XX 17-OCT-2003 (first entry)

XX Human nucleic acid sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiallergic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

OS:

XX Homo sapiens.

PN WO200295308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

XX Disclosure; SEQ ID NO 11878; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antialsthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 9513 BP; 2107 A; 2869 C; 2671 G; 1866 T; 0 U; 0 Other;

Query Match 46.7%; Score 120.4; DB 10; Length 9513;  
 Best Local Similarity 99.2%; Pred. No. 4.1e-24;  
 Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGTGTGGAATGCTCAGCTCATCGCTATGCT 60  
 |||||  
 Db 2242 CAGCGGAGTGATGGCAAGCAGCACTTCGGGTGTGGAATGCTCAGCTCATCGCTATGCT 2301

QY 61 GGCTACCATGCGCAGATGCGCAGCATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 120  
 |||||  
 Db 2302 GGCTACCATGCGCAGATGCGCAGCATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 2361

QY 121 GT 122  
 Db 2362 CT 2363

RESULT 38  
 ID ABD20500

XX ABD20500 standard; DNA; 9513 BP.

XX AC ABD20500;

XX 29-JUL-2004 (first entry)

XX Human pulmonary and inflammatory target DNA #111.

XX	Human, antiseize; bronchoconstriction; allergy; hyposecretion; pain; respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; antiallergic; antiinflammatory; antiasthmatic; analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; respiratory distress syndrome; allergic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; pulmonary transplantation rejection; ds.	2242	CAGCGAGTGATGGCAAGCAGCACTCCGGGTGTGGAAATGCTCAGCTCATCGGTATGCT	23
XX	Homo sapiens.	OS		
XX		XX		
PN	WO200285309-A2.	PN		
XX		XX		
PD	31-OCT-2002.	PD		
XX		XX		
PF	23-APR-2002; 2002WO-US013143.	PF		
XX		XX		
XX	24-APR-2001; 2001US-0286036P.	XX		
PR	(SPIG-) EPIGENESIS PHARM INC.	PR		
XX		XX		
PA	Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D; Miller S, Tang L, Shahbuddin S; WPI; 2003-093058/08.	PA		
XX		XX		
PI	Pharmaceutical composition for treating asthma, has antiseize oligonucleotide containing less percentage of adenosine, targeted to nucleic acids associated with lung allergy or lung dysfunction, and bronchodilating agent.	PI		
XX		XX		
PT	Claim 15; SEQ ID NO 11893; 763pp; English.	PT		
XX		XX		
PS	This invention describes a novel composition (a) a first active agent, comprising oligonucleotides, effective for alleviating bronchoconstriction, respiratory tract inflammation, allergies and reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors, surfactant depletion or hyposecretion, when administered to a mammal. The oligonucleotides are derived from a gene encoding or regulating expression of a target polypeptide associated with lung allergy or lung dysfunction or cancer and can be anti-sense to the corresponding mRNA. The invention also describes a kit, that comprises: (a) a delivery device, in separate containers, (b) the oligonucleotides, (c) instructions for adding a carrier and for use of the kit. The composition of the invention has antiallergic, antiinflammatory, antiasthmatic, analgesic, hypotensive, immunosuppressive and cytostatic activity, is a beta-adrenergic agonist. The composition is useful for preventing or treating a respiratory, lung or malignant disease. The administered composition comprises oligo and is administered to reduce the production or availability, or to increase the degradation of the target mRNA or to reduce the amount of target polypeptide present in the lungs. The pulmonary obstruction, and/or bronchoconstriction and/or lung inflammation, allergies and/or surfactant hypoproduction are associated with a disease or condition such as pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary transplantation rejection, pulmonary infections, bronchitis or cancer. The reduced adenosine content of the anti-sense oligos corresponding to the thymidines present in the target RNA serves to prevent the breakdown of the oligonucleotides into products that free adenosine into the system e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to prevent any unwanted effects due to it	PS		
XX		XX		
SQ	Sequence 9513 BP; 2107 A; 2869 C; 2671 G; 1866 T; 0 U; 0 Other;	SQ		
XX		XX		
Query Match	46.7%; Score 120.4; DB 11; Length 9513;			
Best Local Similarity	99.2%; Pred. No. 4.1e-24;			
Matches 121; Conservative	0; Mismatches 1; Indels 0; Gaps 0;			
Qy	1 CAGCGAGTGATGGCAAGCAGCACTCCGGGTGTGGAAATGCTCAGCTCATCGGTATGCT	60		



CC including respiratory obstruction (especially pulmonary obstruction  
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or  
CC surfactant hypoproduction which are associated with a disease or  
CC condition selected from pulmonary vasoconstriction, inflammation,  
CC allergies, asthma, impeded respiration, respiratory distress syndrome  
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
CC fragments and antisense oligonucleotides used in the exemplification of  
CC the present invention  
XX  
SQ Sequence 35384 BP; 7013 A; 10128 C; 10025 G; 7883 T; 0 U; 335 Other;  
  
Query Match 46.7%; Score 120.4; DB 3; Length 35384;  
Best Local Similarity 99.2%; Pred. No. 5.5e-24;  
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 CAGCGGAGTGATGGCAAGCAGCAGCTTCGGGGTGTGGAATGCTCAGTCAATCGCTATGCT 60  
DB 28113 CAGCGGAGTGATGGCAAGCAGCAGCTTCGGGGTGTGGAATGCTCAGTCAATCGCTATGCT 28172  
|||||  
QY 61 GGCTACCAAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGTGAATTCATCTCAG 120  
DB 28173 GGCTACCAAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGTGAATTCATCTCAG 28232  
|||||  
QY 121 GT 122  
DB 28233 CT 28234  
|||||  
RESULT 40  
ABZ97130  
ID ABZ97130 standard; DNA; 35459 BP.  
XX  
AC ABZ97130;  
DT 17-OCT-2003 (first entry)  
XX  
DE Human nucleic acid sequence.  
XX  
KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiqunone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
FN WO200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WO-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
XX (EPIG-) EPIGENESIS PHARM INC.  
XX  
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
XX WPI; 2003-229219/22.  
XX  
XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiqunone.  
XX  
XX Disclosure; SEQ ID NO 12372; 872pp; English.  
XX  
XX The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiqunone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiqunone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 35459 BP; 7025 A; 10160 C; 10041 G; 7897 T; 0 U; 336 Other;  
  
Query Match 46.7%; Score 120.4; DB 10; Length 35459;  
Best Local Similarity 99.2%; Pred. No. 5.5e-24;  
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 CAGCGGAGTGATGGCAAGCAGCAGCTTCGGGGTGTGGAATGCTCAGTCAATCGCTATGCT 60  
DB 28188 CAGCGGAGTGATGGCAAGCAGCAGCTTCGGGGTGTGGAATGCTCAGTCAATCGCTATGCT 28247  
|||||  
QY 61 GGCTACCAAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGTGAATTCATCTCAG 120  
DB 28248 GGCTACCAAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAAGTGAATTCATCTCAG 28307  
|||||  
QY 121 GT 122  
DB 28308 CT 28309  
|||||  
  
Search completed: December 13, 2005, 16:32:42  
Job time : 476 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 15:55:10 ; Search time 3759 Seconds  
(without alignments)  
3211.244 Million cell updates/sec

Title: US-10-713-137-1  
Perfect score: 258  
Sequence: 1 cagcgagtgatggcgaagca.....ttgtcccccagctgtgcatc 258

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST.\*  
1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_est3.\*  
4: gb\_est4.\*  
5: gb\_est5.\*  
6: gb\_est6.\*  
7: gb\_est7.\*  
8: gb\_est8.\*  
9: gb\_gse1.\*  
10: gb\_gse2.\*  
11: gb\_gse3.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120.4	46.7	2994	11 DQ047444	DQ047444 Homo sapi
2	120.4	46.7	2994	11 DQ047445	DQ047445 Pan trogl
C 3	108.2	41.9	453	9 AQ214630	AQ214630 HS 3117 A
4	104.4	40.5	553	1 AW654110	AW654110 103369 MA
C 5	98.2	38.1	523	9 AQ800595	AQ800595 HS 5314 B
C 6	93.6	36.3	518	9 AQ720606	AQ720606 HS_5542_B
7	90.2	35.0	842	9 CC520102	CC520102 CH240_367
8	78.2	30.3	3437	10 AY419784	AY419784 Homo sapi
9	77.2	29.9	486	10 CG668876	CG668876 OST465233
10	77.2	29.9	526	10 CG506126	CG506126 OST55467
11	77.2	29.9	3420	10 AY419786	AY419786 Mus muscu
12	77.2	29.9	5622	4 BC083183	BC083183 Mus muscu
13	77.2	29.9	5626	4 BC066101	BC066101 Mus muscu
14	76.8	29.8	3430	10 AY419785	AY419785 Pan trogl
15	74.6	28.9	540	10 CG650955	CG650955 OST410927
16	74	28.7	820	6 CF251860	CF251860 hdm005_c0
17	74	28.7	892	5 BU125423	BU125423 603151629
18	72.8	28.2	581	11 FR0038163	AL125664 Fugu rubr
19	70	27.1	621	9 A2231351	A2231351 RPCI-23-8
C 20	69.8	27.1	581	11 FR00318175	AL125676 Fugu rubr
C 21	67.4	26.1	470	9 AQ095690	AQ095690 HS 3017 A
22	64.4	25.0	520	5 BQ551961	BQ551961 H4012EII-

23	64.4	25.0	711	3	BM950581	BM950581 UI-M-EH0P
24	64.4	25.0	843	7	CN527461	CN527461 UI-M-HQ0-
25	64.4	25.0	4120	4	AK077896	AK077896 Mus muscu
26	64	24.8	660	6	CF744130	CF744130 UI-M-GV0-
27	61.2	23.7	544	8	CX385385	CX385385 JGI_XZT65
28	61.2	23.7	721	3	BP178167	BP178167 BP178167
29	54.8	21.2	286	9	AZ044226	AZ044226 RPCI-23-3
30	54.8	21.2	3612	11	DQ045247	DQ045247 Homo sapi
31	49.4	19.1	625	3	BJ088070	BJ088070 BJ088070
32	48.6	18.8	619	11	FR0038157	AL125658 Fugu rubr
33	46.8	18.1	3449	11	DQ045248	DQ045248 Pan trogl
34	45.2	17.5	506	7	CK016997	CK016997 AGENCOURT
35	43.2	16.7	688	5	BU425320	BU425320 603961089
36	42.4	16.4	1171	8	DR123141	DR123141 49091370
C 37	40.2	15.6	567	8	DN757217	DN757217 GL-CF-140
C 38	39.8	15.4	797	1	AJ394075	AJ394075 AJ394075
39	39.6	15.3	771	7	CN459880	CN459880 UI-M-HB0-
40	39.4	15.3	721	3	BJ733387	BJ733387 BJ733387
C 41	39.2	15.2	925	10	CNS0091P	AL053013 Drosophill
C 42	38.8	15.0	657	6	CA090625	CA090625 SCSGAN210
C 43	38.8	15.0	692	7	CO570671	CO570671 AGENCOURT
44	38.6	15.0	301	4	AK185276	AK185276 Mus muscu
C 45	38.6	15.0	311	5	BX919466	BX919466 BX919466

ALIGNMENTS

RESULT 1  
DQ047444  
LOCUS  
DEFINITION Homo sapiens NOS2A gene, VIRTUAL TRANSCRIPT, partial sequence, GSS 02-JUN-2005  
ACCESSION DQ047444  
VERSION DQ047444.1 GI:66900643  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2994)  
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees  
JOURNAL (er) PLOS Biol. 3 (6), E170 (2005)  
PUBMED 15869325  
REFERENCE 2 (bases 1 to 2994)  
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.  
FEATURES  
source  
1. .2994  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="17"  
<1. .>2994  
/gene="NOS2A"  
/locus\_tag="HC15370"  
gene  
ORIGIN  
Query Match 46.7%; Score 120.4; DB 11; Length 2994;  
Best Local Similarity 99.2%; Pred. No. 6.7e-21;  
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY      1  CAGCGGAGTGATGGCAAGCAGACTTCGGGGTGTGGATGCTCAGCTCATCCGCTATGCT 60
Db      745  CAGCGGAGTGATGGCAAGCAGACTTCGGGGTGTGGATGCTCAGCTCATCCGCTATGCT 804

QY      61  GGCTACCAAGTCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTTGGAATTCACCTCAG 120
Db      805  GGCTACCAAGTCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTTGGAATTCACCTCAG 864

QY      121  GT 122
Db      865  CT 866

RESULT 2
DQ047445
LOCUS      2994 bp      DNA      linear      GSS 02-JUN-2005
DEFINITION Pan troglodytes NOS2A gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION  DQ047445
VERSION    DQ047445.1 GI:66900644
KEYWORDS   GSS.
SOURCE     Pan troglodytes (chimpanzee)
ORGANISM   Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiinae; Pan.
REFERENCE  1 (bases 1 to 2994)
AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civallo,D.,
            White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
TITLE     A scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
JOURNAL   (et) PLOS Biol. 3 (6), E170 (2005)
PUBMED   15869325
REFERENCE  2 (bases 1 to 2994)
AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civallo,D.,
            White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
TITLE     Direct Submission
JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
            them based on alignment. Translation starts at the beginning of
            alignment.
FEATURES   Location/Qualifiers
            source          1..2994
                        /organism="Pan troglodytes"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:9598"
            gene            <1..>2994
                        /gene="NOS2A"
                        /locus_tag="HC15370"
ORIGIN
Query Match      46.7%; Score 120.4; DB 11; Length 2994;
Best Local Similarity 99.2%; Pred. No. 6.7e-21;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  CAGCGGAGTGATGGCAAGCAGACTTCGGGGTGTGGATGCTCAGCTCATCCGCTATGCT 60
Db      745  CAGCGGAGTGATGGCAAGCAGACTTCGGGGTGTGGATGCTCAGCTCATCCGCTATGCT 804

QY      61  GGCTACCAAGTCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTTGGAATTCACCTCAG 120
Db      805  GGCTACCAAGTCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTTGGAATTCACCTCAG 864

QY      121  GT 122
Db      865  CT 866

RESULT 3

```

```

AQ214630/c
LOCUS      453 bp      DNA      linear      GSS 18-SEP-1998
DEFINITION HS_3117_A1_F08_T7 CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=3117 Col=15 Row=K, genomic survey
            sequence.
ACCESSION  AQ214630
VERSION    AQ214630.1 GI:3625831
KEYWORDS   GSS.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiinae; Homo.
REFERENCE  1 (bases 1 to 453)
AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., and
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D., and
            Hood,L.
TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
PUBMED   1049764
COMMENT    Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Sequence Tagged Connector
            Plate: 3117 row: K column: 15
            Class: BAC ends
            High quality sequence stop: 453.
FEATURES   Location/Qualifiers
            source          1..453
                        /organism="Homo sapiens"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:9606"
                        /clone="Plate=3117 Col=15 Row=K"
                        /sex="male"
                        /clone_lib="CIT Approved Human Genomic Sperm Library D"
                        /note="Organ: sperm; Vector: pBelBAC11; BAC Clones in
                        E-Coli DH10B"
ORIGIN
Query Match      41.9%; Score 108.2; DB 9; Length 453;
Best Local Similarity 94.0%; Pred. No. 8.2e-16;
Matches 110; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1  CAGCGGAGTGATGGCAAGCAGACTTCGGGGTGTGGATGCTCAGCTCATCCGCTATGCT 60
Db      140  CAGCGGAGTGATGGCAAGCAGACTTCGGGGTGTGGATGCTCAGCTCATCCGCTATGCT 81

QY      61  GGCTACCAAGTCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTTGGAATTCACCT 117
Db      80  GGCTACCAAGTCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGAGGTNTTCAAT 24

RESULT 4
AQ654110
LOCUS      553 bp      mRNA      linear      EST 25-APR-2001
DEFINITION 103369 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  AQ654110
VERSION    AQ654110.1 GI:7419936
KEYWORDS   EST.
SOURCE     Bos taurus (cow)
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE  1 (bases 1 to 553)
AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
            Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,

```

Chitko-McKown, C.G., Perteau, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., and Keele, J.W.  
 Sequence evaluation of four pooled-tissue normalized bovine CDNA libraries and construction of a gene index for cattle  
 Genome Res. 11 (4), 626-630 (2001)  
 11282978

Contact: Smith TPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390

Email: smith@email.marc.usda.gov  
 Single pass sequencing. Bases called and alt trimmed with phred  
 v0.980904.e. Vector identified by cross\_match with the -minscore 18  
 and -mismatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCCAGTCACGACG

Plate: 95 row: 1 column: 4

Seq primer: ATTAGTGACACTATAG.

Location/Qualifiers

1. .553

/organism="Bos taurus"

/mol\_type="mRNA"

/db\_xref="taxon:9913"

/tissue\_type="pooled"

/lab\_host="DH10B"

/clone\_lib="MARC lBOV"

/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;  
 Library made from pooled tissue from lymph node, ovary,  
 fat, hypothalamus, and pituitary."

#### FEATURES

source

#### ORIGIN

Query Match 40.5%; Score 104.4; DB 1; Length 553;  
 Best Local Similarity 91.0%; Pred. No. 8.5e-17;  
 Matches 111; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CAGCGAGTGATGCGACGACGACTTCGGGTGTGGATGCTCAGCTCCTCCGCTATGCT 60  
 Db 69 CAGCGAGCGATGGGAGCATGACTTCGGGTCTGGAAACGCCAGCTCATCCGCTATGCC 128

Qy 61 GGCTACCATGCGCAGATGCGAGCATCAGAGGGGACCTGCCACGTGGGAATTCACCTCAG 120  
 Db 129 GGCTACCATGCGCAGATGCGAGCATCAGAGGGGACCTGCCACGTGGGAGTTACACAG 188

Qy 121 GT 122  
 Db 189 CT 190

RESULT 5  
 AQ800595/c  
 LOCUS  
 DEFINITION  
 HS\_5314\_B2 D01 T7A RPCI-11 Human Male BAC Library Homo sapiens  
 genomic\_clone Plates=890 Col=2 Row=H, genomic survey sequence.

ACCESSION  
 AQ800595

VERSION  
 AQ800595.1 GI:5717850

KEYWORDS  
 GSS.

SOURCE  
 Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.

1 (bases 1 to 523)

REFERENCE  
 AUTHORS  
 Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,  
 Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and  
 Hood, L.

TITLE  
 Sequence-tagged connectors: A sequence approach to mapping and  
 scanning the human genome

JOURNAL  
 PUBMED  
 10449764

COMMENT  
 Contact: Mahairas GG, Wallace JC, Hood L  
 High Throughput Sequencing Center

University of Washington  
 401 Queen Anne Avenue North, Seattle, WA 98109, USA  
 Tel: (206) 616-3618  
 Fax: (206) 616-3887  
 Email: jwallace@u.washington.edu  
 Clones are derived from the human BAC library RPCI-11. For BAC  
 library availability, please contact Pieter de Jong  
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from  
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering\_bac.htm)  
 or from Resear h Genetics (info@resgen.com). BAC end Web Server:  
 http://www.htsc.washington.edu  
 Plate: 890 row: H column: 2  
 Seq primer: T7  
 Class: BAC ends  
 High quality sequence stop: 523.

#### FEATURES

source

1. .523

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

/clone="Plate=890 Col=2 Row=H"

/sex="male"

/clone\_lib="RPCI-11 Human Male BAC Library"

/note="Vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI;  
 Male blood DNA was isolated from one randomly chosen donor  
 and partially digested with a combination of EcoRI and  
 EcoRI Methylase. Size selected DNA was cloned into the  
 pBACE3.6 vector at EcoRI sites"

#### ORIGIN

Query Match 38.1%; Score 98.2; DB 9; Length 523;  
 Best Local Similarity 96.2%; Pred. No. 3.6e-15;  
 Matches 100; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGCGAGTGATGCGACGACGACTTCGGGTGTGGATGCTCAGCTCCTCCGCTATGCT 60  
 Db 139 CAGCGAGTGATGCGACGACGACTTCGGGTGTGGATGCTCAGCTCCTCCGCTATGCT 80

Qy 61 GGCTACCATGCGCAGATGCGAGCATCAGAGGGGACCTGCCAA 104  
 Db 79 GGCTACCATGCGCAGATGCGAGCATCAGAGGGGACCTGCCAA 36

#### RESULT 6

AQ720606/c

LOCUS

DEFINITION

HS\_5542\_B1\_H02\_T7A RPCI-11 Human Male BAC Library Homo sapiens  
 genomic\_clone Plates=1118 Col=3 Row=P, genomic survey sequence.

ACCESSION

AQ720606

VERSION

AQ720606.1 GI:5480275

KEYWORDS

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.

1 (bases 1 to 518)

REFERENCE

AUTHORS

Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and  
 Hood, L.

TITLE

Sequence-tagged connectors: A sequence approach to mapping and  
 scanning the human genome

JOURNAL

PUBMED

10449764

COMMENT

Contact: Mahairas GG, Wallace JC, Hood L  
 High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC  
 library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering.bac.htm>) or from Resear h Genetics ([info@resgen.com](mailto:info@resgen.com)). BAC end Web Server: <http://www.htsc.washington.edu>

Plate: 1118 row: P column: 3

Seq primer: T7

Class: BAC ends

High quality sequence stop: 518.

Location/Qualifiers

1. .518

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

/clones="Plates:1118 Col=3 Row=P"

/sex="male"

/clone\_lib="RPC1-11 Human Male BAC Library"

/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

## ORIGIN

Query Match 36.3%; Score 93.6; DB 9; Length 518;  
Best Local Similarity 95.0%; Pred. No. 5.8e-14;  
Matches 96; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAGCGAGTGTGGCAACACGACTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60

Db 134 CAGCGAGTGTGGCAACACGACTTCGGATGTGGAATGCTCAGCTCATCCGCTATGCT 75

Qy 61 GGCTACAGATGCCAGATGGCAGCATCAGAGGGGACCTGTC 101

Db 74 GGCTACAGATGCCAGATGGCAGCATCAGAGGGGACCTGTC 34

## RESULT 7

CC520102  
LOCUS CH240\_367118.T7 CHORI-240 Bos taurus genomic clone CH240\_367118,  
DEFINITION genomic survey sequence.

ACCESSION CC520102

VERSION CC520102.1 GI:31838390

KEYWORDS GSS.

SOURCE Bos taurus (cow)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Bovinae; Bos.

## REFERENCE

AUTHORS

Holt, R., Stott, J., Yang, G., Barber, S., Smal, D., Prabhu, A.-L.,  
Tsai, M., Cloutier, A., Lee, D., Gira, N., Olson, T., Mayo, M.,  
Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R.,  
Matheson, C., Wye, N., Masson, A., Brown-John, M., Jones, S.,  
Schein, J., Marra, M., de Jong, P., McWilliam, S., Barris, W.,  
Dairymple, B. P. and Fellam, R.

Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398  
Unpublished (2003)

Other GSSs: CH240\_367118.TARBAC13P2

Contact: Rob Holt

Sequencing

The British Columbia Cancer Agency Genome Science Centre

600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6

Tel: 604-877-6085

Fax: 604-877-6276

Email: [rholt@bcgsc.ca](mailto:rholt@bcgsc.ca)

Clones are derived from the bovine BAC library CHORI-240

(<http://www.chori.org/bacpac/bovine240.htm>). For BAC library  
availability, please contact Pieter de Jong ([pdejong@mail.cho.org](mailto:pdejong@mail.cho.org)).  
Clones may be purchased from BACPAC Resources

(<http://www.chori.org/bacpac/ordering/information.htm>). This work  
was undertaken as part of the International Bovine BAC Mapping  
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the

British Columbia Genome Sciences Centre, Canada.

Plate: 367 row: I column: 18

Seq primer: T7

Class: BAC ends.

## FEATURES

source

1. .842

/organism="Bos taurus"

/mol\_type="genomic DNA"

/strain="breed: Hereford"

/db\_xref="taxon:9913"

/clones="CH240\_367118"

/sex="Male"

/cell\_type="Blood"

/clone\_lib="CHORI-240"

/note="vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull Li Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 35.0%; Score 90.2; DB 9; Length 842;

Best Local Similarity 76.9%; Pred. No. 4.9e-13;

Matches 110; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 1 CAGCGAGTGTATGCAAGCAGCAGCTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60

Db 471 CAGAGGACCCAGCCAGCAGCAGCTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 530

Qy 61 GGCTACAGATGCCAGATGGCAGCATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 120

Db 531 GGCTACAGCAGCCGACGCTCCATCTCTGGGGAGCCAGCAACGTGGAGTTCACGGAG 590

Qy 121 GTACCCGGCCAGCCTCAGCCRC 143

Db 591 GTAGCGCCCCCGCCCTCCCTCC 613

## RESULT 8

AY419784

LOCUS

DEFINITION Homo sapiens NOS1 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.

ACCESSION AY419784

VERSION AY419784.1 GI:39775741

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.

## REFERENCE

AUTHORS

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,  
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios

Science 302 (5652), 1960-1963 (2003)

JOURNAL

PUBMED 14671302

## REFERENCE

2 (bases 1 to 3437)

AUTHORS

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,  
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.

Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

This sequence as made by sequencing genomic exons and ordering them  
based on alignment.

## FEATURES

source

1. .3437

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

[illegible]

LOCUS AY419786 3420 bp DNA linear GSS 17-DEC-2003  
DEFINITION Mus musculus NOS1 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION AY419786  
VERSION AY419786.1 GI:39775743  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidae; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 3420)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 3420)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (15-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence as made by sequencing genomic exons and ordering them  
based on alignment.  
FEATURES  
source Location/Qualifiers  
1..3420  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
<1..>3420  
/gene="NOS1"  
/locus\_tag="HCM7006"  
gene  
ORIGIN  
Query Match 29.9%; Score 77.2; DB 10; Length 3420;  
Best Local Similarity 77.0%; Pred. No. 1.6e-09;  
Matches 94; Conservative 0; Mismatches 28; Indels 0; Gaps 0;  
Qy 1 CAGCGGAGTGTGCGACGACGACTTCGGGTGTGGAACTGCTAGCTATCCGCTATGCT 60  
Dy 553 CAAAGGACTGTAGTGCAGCATGACTTCGAGTGTGGAACTGCGAGCTCATCCGCTATGCC 612  
Qy 61 GGCTACCAAGTCCAGATGCCAGATCAGAGGGGACCTGCCACGTTGGAATTCACATCAG 120  
Dy 613 GGCTACCAAGCAGCAGATGGCTTACTCTGGCGATCCAGTATGTGGAGTTCACAGAG 672  
Qy 121 GT 122  
Dy 673 AT 674  
RESULT 12  
BC083183  
LOCUS BC083183 5622 bp mRNA linear HTC 30-MAR-2005  
DEFINITION Mus musculus nitric oxide synthase 1, neuronal, mRNA (CDNA clone  
IMAGE:30533636), containing frame-shift errors.  
ACCESSION BC083183  
VERSION BC083183.1 GI:52789385  
KEYWORDS HTC.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidae; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 5622)  
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,  
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,

Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,  
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Haieh,F.,  
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,  
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.I.,  
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,  
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,  
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,  
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,  
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,  
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,  
Fahey,J., Helton,E., Kettman,M., Madan,A., Young,A.C., Shovchenko,Y.,  
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,  
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,  
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalius,D.E.,  
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.  
Mammalian Gene Collection Program Team  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
PUBMED 12477932  
REFERENCE 2 (bases 1 to 5622)  
AUTHORS NIH MGC Project  
TITLE Direct Submission  
JOURNAL Submitted (24-SEP-2004) National Institutes of Health, Mammalian  
Gene Collection (MGC), Bethesda, MD 20892-2590, USA  
COMMENT NIH-MGC Project URL: http://mgc.nci.nih.gov  
Contact: MGC help desk  
Email: ggapbs-f@mail.nih.gov  
Tissue Procurement: Dr. James Lin, University of Iowa  
cDNA Library Preparation: M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: http://www.nisc.nih.gov/  
Contact: nisc\_mgc@hgrl.nih.gov  
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,  
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,  
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,  
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,  
Maduro,Q.L., Masiello,C., Maekeri,B., Mastrian,S.D., McCloskey,J.C.,  
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,  
Teursegoun,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,  
Young,A., Zhang,L.-H. and Green,E.D.  
Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Series: IRAC Plate: 176 Row: 0 Column: 2  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 6724320  
This clone has the following problem: frame shifted.  
FEATURES  
source Location/Qualifiers  
1..5622  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:30533636"  
/tissue\_type="Brain"  
/clone\_lib="NIH\_EMAP\_G10"  
/lab\_host="DH10B"  
/note="Vector: pYX-ASC"  
ORIGIN  
Query Match 29.9%; Score 77.2; DB 4; Length 5622;  
Best Local Similarity 77.0%; Pred. No. 1.7e-09;  
Matches 94; Conservative 0; Mismatches 28; Indels 0; Gaps 0;  
Qy 1 CAGCGGAGTGTGCGACGACGACTTCGGGTGTGGAACTGCTCAGCTCATCCGCTATGCT 60  
Dy 1860 CAAAGGACTGTGCGAAGCATGACTTCGAGTGTGGAACTCGCAGCTCATCCGCTATGCC 1919



QY 61 GGCTACAGATCCAGATCGAGCATCAGAGGGACCCCTGCCAACCTGGAAATTCACCTCAG 120  
 Db 1920 GGTCAAGAGCCAGATGGCTCTACCTTGGGGATCCAGCTATATGTGGAGTTCACAGAG 1979

QY 121 GT 122  
 Db 1980 AT 1981

RESULT 13  
 BC066101  
 LOCUS  
 DEFINITION Mus musculus nitric oxide synthase 1, neuronal, mRNA (cDNA clone IMAGE:30533636), containing frame-shift errors.  
 ACCESSION BC066101  
 VERSION BC066101.1 GI:41946848  
 KEYWORDS  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE  
 AUTHORS Strausberg R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalusz, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
 TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 PUBMED 12477932  
 REFERENCE 2 (bases 1 to 5626)  
 AUTHORS Strausberg, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (02-FEB-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK  
 COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: Dr. James Lin, University of Iowa  
 cDNA Library Preparation: M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
 DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr. Thomas L. Casavant.  
 Web site: <http://genome.uiowa.edu>  
 Contact: [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu); [tom-casavant@uiowa.edu](mailto:tom-casavant@uiowa.edu)  
 Bonaldo, M.F., Akabogu, I., Bair, T., Bair, J., Crouch, K., Davis, A., Fiehler, K., Keppel, C., Kucaba, T., Lebeck, M., Melo, A., Schaefer, K., Scheetz, T., Smith, C., Snir, E., Tack, D., Trout, K., Walters, J., Casavant, T., Soares, M.B.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: Plate: Row: Column: 0  
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6724320

This clone has the following problem: frame shifted.

## FEATURES

Location/Qualifiers  
 source

1..5626  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:30533636"  
 /tissue\_type="Brain"  
 /clone\_lib="NIH BMAP\_G10"  
 /lab\_host="DH10B"  
 /note="Vector: pYX-ASC"

## ORIGIN

Query Match 29.9%; Score 77.2; DB 4; Length 5626;  
 Best Local Similarity 77.0%; Pred. No. 1.7e-09;  
 Matches 94; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 CAGCGAGTGTGGCAAGCAGCTTCGGGTGTGGATGCTCAGCTCATCGCTATGCT 60  
 |||||  
 Db 1860 CAAAGGACTGTATGGCAAGCATGACTTCGAGTGTGGAACTCGCAGCTCATCGCTATGCC 1919  
 |||||

QY 61 GGCTACCATCCAGATCCAGATGGCAGCATCAGAGGGACCCCTGCCAACCTGGAAATTCACCTCAG 120  
 |||||  
 Db 1920 GGTCAAGCAGCAGATGGCTCTACCTTGGCGATCCAGCTATATGTGGAGTTCACAGAG 1979  
 |||||

QY 121 GT 122  
 Db 1980 AT 1981

## RESULT 14

AV419785  
 LOCUS

DEFINITION Pan troglodytes NOS1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY419785

VERSION AY419785.1 GI:39775742

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Pan.

REFERENCE 1 (bases 1 to 3430)

AUTHORS Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous

gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 3430)

AUTHORS Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

COMMENT This sequence as made by sequencing genomic exons and ordering them

based on alignment.

FEATURES

source

Location/Qualifiers

1..3430

/organism="Pan troglodytes"

/mol\_type="genomic DNA"

/db\_xref="taxon:9598"

<1\_>3430

/gene="NOS1"

/locus\_tag="HCM7006"

ORIGIN

Query Match 29.8%; Score 76.8; DB 10; Length 3430;  
 Best Local Similarity 77.5%; Pred. No. 2e-09; Mismatches 0; Indels 0; Gaps 0;  
 Matches 93; Conservative 0

QY 1 CAGCGAGTGTGGCAAGCAGACTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
 |||||  
 Db 546 CAGAGCAGACGGCGAAGCAGACTTCGGAGTCTGGAATCCAGCTCATCCGCTACGCT 605  
 |||||  
 QY 61 GCCTACCAAGTCCAGATGGCAGATCAGAGGGGACCTGCCAAGCTGGAATTCACCTCAG 120  
 |||||  
 Db 606 GGCTACAAGCAGCCGACGGCTCCACCTCGGGGACCCAGGCCAATGTGCAGTTCACAGAG 665  
 |||||

## RESULT 15

CG650955  
 LOCUS OST410927 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST410927,  
 mRNA sequence.

ACCESSION CG650955

VERSION CG650955.1 GI:37474804

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS Zambrowicz B.P., Abuin A., Ramirez-Solis R., Richter L.J.,  
 Figgott J., BeltrandelRio H., Buxton E.C., Edwards J., Finch R.A.,  
 Fridde C.J., Gupta A., Hansen G., Hu Y., Huang W., Jaing C.,  
 Key B.W. Jr., Kipp P., Kohlhauff B., Ma Z.-Q., Markesich D.,  
 Payne R., Potter D.G., Qian N., Shaw J., Schrick J., Shi Z.-Z.,  
 Sparks M.J., Van Sligtenhorst I., Vogel P., Walke W., Xu N.,  
 Zhu Q., Person C. and Sands A.T.

TITLE Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap  
 screen to identify potential targets for therapeutic intervention

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

## PUBMED

14610273

COMMENT Contact: Zambrowicz BP

OmniBank

Lexicon Genetics Incorporated

4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: material@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as  
 described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

Class: Gene Trap.

Location/Qualifiers

1..540  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="129Sv/Ev"  
 /db\_xref="taxon:10090"  
 /clone="OST410927"  
 /cell\_type="embryonic stem cell"  
 /clone\_lib="Mus musculus 129Sv/Ev"

## ORIGIN

Query Match 28.9%; Score 74.6; DB 10; Length 540;  
 Best Local Similarity 75.4%; Pred. No. 5.8e-09;  
 Matches 92; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1 CAGCGAGTGTGGCAAGCAGACTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
 |||||  
 Db 27 CAAAGACTGTATGGCAAGCATGACTTCGGAGTGTGGAATCGTGTGGAATTCATCCGCTATGCC 86  
 |||||

QY 61 GCCTACCAAGTCCAGATGGCAGATCAGAGGGGACCTGCCAAGCTGGAATTCACCTCAG 120  
 |||||  
 Db 87 GGCTACAAGCAGCCGACGGTCTTACCTTGGCGATCCAGCTAATGTGGAGTTCACAGAG 146  
 |||||

QY 121 GT 122

Db 147 AT 148

## RESULT 16

CF251860

LOCUS

DEFINITION hdm005\_c06 LPS-activated macrophage cell line Gallus gallus cDNA,  
 mRNA sequence.

ACCESSION CF251860

VERSION CF251860.1 GI:33485115

KEYWORDS EST.

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 820)

AUTHORS Wittzell H., Bed'Hom B., Morin V., Young J.R., Whittaker C.J.,

Chausee A.M. and Zoorob R.

TITLE A collection of chicken ESTs from activated immune cells

JOURNAL Unpublished (2003)

COMMENT Contact: Zoorob R

UPR 1983

CNRS

7 rue Guy Moquet, BP 8, 94801 Villejuif cedex, France

Tel: 33 1 49 58 35 00

Fax: 33 1 49 58 33 81

Email: zoorob@vjf.cnrs.fr.

## FEATURES

source Location/Qualifiers  
 1..820  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9031"  
 /cell\_line="HD11"  
 /clone\_lib="LPS-activated macrophage cell line"  
 /note="Vector: pTriplex2"

## ORIGIN

Query Match 28.7%; Score 74; DB 6; Length 820;  
 Best Local Similarity 75.4%; Pred. No. 9e-09;  
 Matches 92; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1 CAGCGAGTGTGGCAAGCAGACTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
 |||||  
 Db 356 CAGAGGACTCATGGAAACATGATTCGCGTGTGGAAACAGCCAGCTCATCCGATATGCT 415  
 |||||

QY 61 GGCTACCAAGTCCAGATGGCAGATGCGAGGGGACCTGCCAAGCTGGAATTCACCTCAG 120  
 |||||  
 Db 416 GGATATCAATGCCAGATGGGTCTGTCTATAGGAGACCTGCAAGTGTGGAGTTCACAAAG 475  
 |||||

QY 121 GT 122

Db 476 TT 477

## RESULT 17

BU125423

LOCUS

DEFINITION BU151629F1 CSEQCUL19 Gallus gallus cDNA clone CHEST15918 5', mRNA  
 sequence.

ACCESSION BU125423

VERSION BU125423.1 GI:25336332

KEYWORDS EST.

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 892)

AUTHORS Boardman P.E., Sanz-Ezquerro J., Overton I.M., Burt D.W., Bosch E.,

Fong W.T., Tickle C., Brown W.R.A., Wilson S.A. and Hubbard S.J.

TITLE A Comprehensive Collection of Chicken cDNAs

JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)

PUBMED 12445392

COMMENT Contact: Simon Hubbard

Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612089930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

## FEATURES

```
1 .892  
/organism="Gallus gallus"  
/mol_type="mRNA"  
/strain="Compton line 151"  
/db_xref="taxon:9031"  
/clone="CHEST1518"  
/sex="Female"  
/dev_stage="adult"  
/lab_host="HL10B"  
/clone_lib="CSSEQHL19"  
/note="Organ: liver; Vector:  
EcoRI; Site: 2; NotI; Modifi-  
[Stratagene] vector to acc-  
T-trimmed protocol (Constr-  
cloned cDNA libraries from  
cloned DNA sequencing by Glen-  
6,387,624). Cut pBluescript  
Ligate in double stranded  
BamHI sites [5'ggccgcctcgac-  
cgaattccttccttctggttgaggcgc
```

```
[ ] aaatttttttttttgggagatcggggggggggggggggaacgcgca
      RIGIN

Query Match          28.7%; Score 74; DB 5; Length 892;
Best Local Similarity 75.4%;
    Pres.No. 9.1e-09;
Matches 92: Conservative 0; Mismatches 30; Indels 0; Gaps 0;
```

Qy	1	CAGCGAGTGATGGCAGCA	CGACTTCGGGTGTGGAA	TGCTCAGCTCATCCGCTAT	GTCT	50
Db	667	CAGAGGACTGATGGGAA	ACATGATTTCCGTGTTT	GGAA	CAGCCAGCTCATCCGAT	GTCT
Qy	61	GGCTACCA	GATGCCAGATCGG	CAGCAT	CAGAGGGACCTG	CCACGTTGGAATTCAC
Db	727	GGATATCA	AAATCCAGATGGTCT	CTCATAGGAGAC	CCTGCAAGTGTGGAGTT	TCCACAAAG

Qy 121 GT 122  
|  
Db 787 TT 788

RESULT 18				
FR0038163				
LOCUS	FR0038163	581 bp	DNA	linear
DEFINITION	Fugu rubripes GSS sequence, clone 064O07cF12, genomic survey sequence.			

ACCESSION VERSION	KEYWORDS	SOURCE	ORGANISM
ALU125664.1	GI:6107279	GSS; genome survey sequence.	
ALU125664.1	Takifugu rubripes (Fugu rubripes)		
	Takifugu rubripes		
	Takifugu rubripes		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;		
	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;		
	Tetraodontidae; Tetraodontidae; Takifugu.		

REFERENCE	
AUTHORS	Elgar,G., Clark,M.S., Meek,S., Smith,S., Warner,S., Edwards,Y.J., Bouchireb,N., Cottage,A., Yeo,G.S., Umrانيا,Y., Williams,G. and Brenner,S.
TITLE	Generation and analysis of 25 Mb of genomic DNA from the pufferfish Fugu rubripes by sequence scanning
JOURNAL	Genome Res. 9 (10), 960-971 (1999)
PUBMED	10523524
REFERENCE	2 (bases 1 to 581)
AUTHORS	Elgar,G., Clark,M.S., Smith,S., Meek,S., Warner,S., Edwards,Y.J.K., Umrانيا,Y., Williams,G. and Brenner,S.
TITLE	Direct Submission

## JOURNAL

Submitted (11-OCT-1999) MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridge, CB10 1SB, UK Email:

COMMENT  
vector: pBluescript II KS  
v type: phagemid  
PRIMER: KS

DESCR:  
One pass dye-terminator sequencing of cosmid cloned genomic sequence.

**FEATURES**  
**SOURCE**

```
Location/Qualifiers
1. .581
/organism="Takifugu rubripes"
/mol_type="genomic DNA"
/db_xref=taxon:31033
/_clone="064007CF12"
/_clone_lib="cosmid 064007"
```

## ORIGIN

Query Match	28.2%;	Score 72.8;	DB 11;	Length 581;
Best Local Similarity	74.2%;	Prod. NO. 1.8e-08;		
Matches 92;	Conservative	0;	Mismatches 32;	Indels 0; Gaps 0
1	CAGCGGAGTGATGGCAAGCAGACTTCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT	60		
217	CGAGAGCAGATGGGCAACATGACTTTTCAGTGTGGAAACAGTCAGCTGATTCGTTATGCT	276		
61	GGCTACCCAGATGCCAGATGGCAGCATCAGAGGGGACCTGCCAAGTCGGAATTCACCTCAG	120		
277	GGGTACAACAGCCTGATGCTCACATCCTGGGGGACCCCTGCTAATGTTGAATTTACTCAG	336		
121	GTAC	124		
337	GTGC	340		

## RESULT 19

AZ231351	AZ231351	621 bp	DNA	linear	GSS 14-JUN-2000
LOCUS	RPC1-23-82G23.TJ	RPC1-23	Mus musculus	genomic clone	RPC1-23-82G23,
DEFINITION	genomic survey sequence.				
ACCESSION	AZ231351				
VERSION	AZ231351.1	GI:8539397			
KEYWORDS	GSS				

**KEYWORDS**  
**SOURCE**

ORGANISM	Mus musculus
REFERENCE	1 (bases 1 to 621)

## REFERENCE

AUTHORS	Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
TITLE	Mouse BAC End Sequences from Library RPCI-23
JOURNAL	Unpublished (1999)
COMMENT	Other GSSs: RPCI-23-82G23.TV

## CONCLUSIONS

Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: [shbao@igir.org](mailto:shbao@igir.org)

Email: szhaoc@tiger.org

Clones are derived from the mouse BAC library rPC1-23. For BAC library availability, please contact ptieter de Jong (ptieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.html) or from Resea ch Genetics (info@resgen.com). BAC end page: [http://www.tigr.org/tdb/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html) plate: 82 row: G column: 23

Seq primer: SP6

Class: BAC ends.

Location/Qualifiers

1. .621

```
/organism="Mus musculus"
/mol_type="genomic DNA"
/strains="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-82G23"
/sex="Female"
/lab_host="DH10B"
/clone_lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:
EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney_and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
```

## ORIGIN

```
Query Match      27.1%; Score 70; DB 9; Length 621;
Best Local Similarity 77.4%; Pred. No. 9.7e-08;
Matches 96; Conservative 1; Mismatches 26; Indels 1; Gaps 1;

Qy 41 CTCAGCTCATCGCTATCGTGGTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCGTG 100
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 CACAGCTCATCGGTACCGTGGTACCAGATGCCAGATGGCAGCATCAGAGGGGATCGTG 60

Qy 101 CCAAGCTGGAATTCACTCAGGTACCGCGCCAGCCTCAGCCRCGCGCATTTGGCGGGG 160
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 CCACCTTGAGGTTCACCAGGTA-CTGACTCAGCCTCTCCTAGATCCCTGTGGGCAGGGG 119

Qy 161 AGCC 164
    |||
Db 120 ACCC 123
```

RESULT 20  
FR0038175/c

```
LOCUS      581 bp DNA linear GSS 25-FEB-2004
DEFINITION Fugu rubripes GSS sequence, clone 064007ce10, genomic survey
sequence.
ACCESSION AL125676
VERSION AL125676.1 GI:6107291
KEYWORDS GSS; genome survey sequence.
SOURCE Takifugu rubripes (Fugu rubripes)
ORGANISM Takifugu rubripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontoidea; Tetraodontidae; Takifugu.
```

```
REFERENCE 1
AUTHORS Elgar,G., Clark,M.S., Meek,S., Smith,S., Warner,S., Edwards,Y.J.,
Bouchireb,N., Cottage,A., Yeo,G.S., Umrans,Y., Williams,G. and
Brenner,S.
```

```
TITLE Generation and analysis of 25 Mb of genomic DNA from the pufferfish
Fugu rubripes by sequence scanning
JOURNAL Genome Res. 9 (10), 960-971 (1999)
```

```
REFERENCE 2 (bases 1 to 581)
AUTHORS Elgar,G., Clark,M.S., Smith,S., Meek,S., Warner,S., Edwards,Y.J.K.,
Umrans,Y., Williams,G. and Brenner,S.
```

```
TITLE Direct Submission
JOURNAL Submitted (11-OCT-1999) MRC Human Genome Mapping Project Resource
Centre, Hinxton, Cambridge, CB10 1SB. UK Email:
```

```
COMMENT biohelp@hgm.mrc.ac.uk
Vector: pBluescript II KS
V_type: phagemid
PRIMER: KS
DESCR: One pass dye-terminator sequencing of cosmid cloned genomic
sequence.
```

FEATURES  
source

```
Location/Qualifiers
1..581
/organism="Takifugu rubripes"
/mol_type="genomic DNA"
```

```
/db_xref="taxon:31033"
/clone="064007ce10"
/clone_lib="cosmid 064007"
```

## ORIGIN

```
Query Match      27.1%; Score 69.8; DB 11; Length 581;
Best Local Similarity 71.8%; Pred. No. 1.1e-07;
Matches 89; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGCATGCACAGCAGCAGCTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 380 CCGAGGACAGATGCCAAACATGACTTTTCGATGTGGAAACAGTCAGCTGATTCGTTATGCT 321

Qy 61 GGCTATCAGATGCCAGATGCAGCATCAGAGGGGACCCCTGCCAACGTGGGAATTCACTCAG 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 320 GGGNACAAACAGCCTGATGTGCAGATCCTGCGGGACCCCTGCTATGTTGTAATTTTATGAG 261

Qy 121 GTAC 124
    |||
Db 260 GTGC 257
```

RESULT 21  
AQ095690/c

```
LOCUS      470 bp DNA linear GSS 27-AUG-1998
DEFINITION HS 3017 A1 F08 MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3017 Col=15 Row=K, genomic survey
sequence.
```

```
ACCESSION AQ095690
VERSION AQ095690.1 GI:3463425
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
```

```
REFERENCE 1 (bases 1 to 470)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., and
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
```

```
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
```

```
PUBMED 10449764
```

```
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
```

```
Fax: (206) 616-3887
```

```
Email: jwallace@u.washington.edu
```

```
Sequence Tagged Connector
```

```
Plate: 3017 row: K column: 15
```

```
Class: BAC ends
```

```
High quality sequence stop: 470.
```

```
FEATURES Location/Qualifiers
```

```
source
```

```
1..470
```

```
/organism="Homo sapiens"
```

```
/mol_type="genomic DNA"
```

```
/db_xref="taxon:9606"
```

```
/clone="plate=3017 Col=15 Row=K"
```

```
/sex="male"
```

```
/clone_lib="CIT Approved Human Genomic Sperm Library D"
```

```
/note="Organ: sperm; Vector: pBelBAC11; BAC Clones in
```

```
E-Coli DH10B"
```

## ORIGIN

```
Query Match      26.1%; Score 67.4; DB 9; Length 470;
Best Local Similarity 98.6%; Pred. No. 4.5e-07;
Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 CAGCGGAGTGCATGCACAGCAGCAGCTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```

Db      69  CAGCGGAGTGATGGCAAGCAGACTTCGGGGTGTGGAATGCTCAGCTCATCCGATATGCT 10
QY      61  GGCTACCAAG 69
        |||||
Db      9  GGCTACCAAG 1

RESULT 22
BQ551961
LOCUS   H4012E11-5 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone
DEFINITION
ACCESSION   BQ551961
VERSION     BQ551961.1
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE   1 (bases 1 to 520)
AUTHORS    VanBuren,V., Piao,Y., Dudekula,D.B., Qian,Y., Carter,M.G.,
TITLE      Martin,P.R., Stagg,C.A., Basseu,U., Aiba,K., Hamatani,T.,
JOURNAL    Kargul,G.J., Luo,A.G., Kelso,J., Hide,W. and KO,M.S.H.
PUBMED     Assembly, verification, and initial annotation of NIA 7.4K mouse
COMMENT     cDNA clone set
           Genome Res. 12 (12), 1999-2003 (2002)
           12466305
           Other ESTs: H4012E11-3
           Contact: Yong Qian
           Laboratory of Genetics
           National Institute on Aging/National Institutes of Health
           333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
           Email: cdna@lgaun.grc.nia.nih.gov
           This clone set has been freely distributed to the community. Please
           visit http://lgaun.grc.nia.nih.gov/cDNA/NIA_7_4k.html for details.
           Plate: H4012 row: E column: 11
           Seq primer: -21M13 Reverse
           High quality sequence stop: 520
           POLYA=No.

FEATURES             Location/Qualifiers
     source           1..520
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="niaEST:H4012E11-5"
                     /db_xref="taxon:10090"
                     /clone="H4012E11"
                     /sex="mixed"
                     /dev_stage="mixed"
                     /lab_host="DH10B"
                     /clone_lib="NIA Mouse 7.4K cDNA Clone Set"
                     /note="Vector: pSPORT1; Site.1: SalI; Site.2: NotI; This
clone is among a rearranged set of 7,407 clones from more
than 20 cDNA libraries."

ORIGIN
Query Match      25.0%; Score 64.4; DB 5; Length 520;
Best Local Similarity 70.5%; Pred. No. 2.8e-06;
Matches 86; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY      1  CAGCGGAGTGATGGCAAGCAGACTTCGGGGTGTGGAATGCTCAGCTCATCCGATATGCT 60
Db      8  CAGCGCTGCCCTCGCGGGAGACTTCGGGATCTGGAACAGCCAGCTGATACGCTATGCG 67
QY      61  GGCTACCAAGTGCAGATGGCAGATCAGAGGGGACCTGCCACGCTGGGAATTCACCTCAG 120
Db      68  GGCTATAGGACGACGAGATGGCTCCGTGCGAGGGGACCCGCCAACGCTGGAGATCACTGAG 127
QY      121  GT 122
Db      128  CT 129

Db      69  CAGCGGAGTGATGGCAAGCAGACTTCGGGGTGTGGAATGCTCAGCTCATCCGATATGCT 10
QY      61  GGCTACCAAG 69
        |||||
Db      9  GGCTACCAAG 1

RESULT 23
BQ950581
LOCUS   UI-M-EH0p-buu-d-15-0-UI.r1 NIH_BMAP_EH0p Mus musculus cDNA clone
DEFINITION
ACCESSION   BQ950581
VERSION     BQ950581.1
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE   1 (bases 1 to 711)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
           Email: cgapbs@mail.nih.gov
           Tissue Procurement: Dr. James Lin, University of Iowa
           cDNA library preparation: Dr. M. Bento Soares, University of Iowa
           cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
           DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
           Clone Distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           This clone was contributed by the Brain Molecular Anatomy Project
           (BMAP)
           Seq primer: pYX-5.

FEATURES             Location/Qualifiers
     source           1..711
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5687006"
                     /tissue_type="whole brain"
                     /dev_stage="embryo 18.5 dpc"
                     /lab_host="DH10B (T1 phage resistant)"
                     /clone_lib="NIH_BMAP_EH0p"
                     /note="Organ: Brain; Vector: pYX-Asc; Site.1: EcoR I;
Site.2: Not I; The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA
tail, is CAGCCAGCAGC. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP): 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Institute of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN
Query Match      25.0%; Score 64.4; DB 3; Length 711;
Best Local Similarity 70.5%; Pred. No. 2.9e-06;
Matches 86; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY      1  CAGCGGAGTGATGGCAAGCAGACTTCGGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db      32  CAGCGCTGCCCTCGCGGGAGACTTCGGGATCTGGAACAGCCAGCTGATACGCTATGCG 91
QY      61  GGCTACCAAGTGCAGATGGCAGATCAGAGGGGACCTGCCAACGCTGGGAATTCACCTCAG 120
Db      92  GGCTATAGGACGACGAGATGGCTCCGTGCGAGGGGACCCGCCAACGCTGGAGATCACTGAG 151
QY      121  GT 122
Db      152  CT 153

```



Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.  
URL:http://genome.gsc.riken.jp/  
URL:http://fantom.gsc.riken.jp/.

FEATURES  
source  
1..4120  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="FANTOM DB:6030422B05"  
/clone="6030422B05"  
/sex="male"  
/tissue\_type="testis"  
/clone\_lib="RIKEN full-length enriched mouse cDNA library"  
/dev\_stage="13 days embryo"  
22..3630  
/notes="unnamed protein product; nitric oxide synthase 3,  
endothelial cell (MGI:97362, GB|NM\_008713, evidence:  
BLASTN, 9%, match=3633)  
putative"  
/codon\_start=1  
/protein\_id="BAC37052.1"  
/db\_xref="GI:26346807"  
/translation="MGNLSVGOEPGPPCGGLGLGLGKGGPASPAPPSQAPAP  
PSPTRPADHSPPLTPPDGPRFRVKNMEVGSITDYLISAQQDGPCTSRCLGSL  
VPPKLSRFTQSPTEQLLQARDFIQYNSIRKSGQAHEQLVEAEVATG  
TYQLRESLFTGAKARNAPRCVRIQWKLQVDFARDCTAQMFTYCNHIVAT  
NRGLNSAIVTFVQPCRGDPRFVNSQLIRYAGYQQSGVRGDPANVEITLCIQH  
GWTGNGRFDVPLLLQAQDEPPELFTLPEMVLVLEPHEPTLEWAAELRWYALPA  
VSNMLIEIGLEFPAPPSQWYNSSEIGMRDLCDPHYNLTEDVAVCMDLDTTSSSL  
WKKAAVEINVAHLSLTAKVTIVDHHAAATASFMKLENEQKRGCCPADWNIYVPP  
ISGSLTPVHFQEMVNTFLSPAFRIQPDPMKSGAAGIIRKTKFEVANAIVKVSASL  
MGTVMKRVKATILYSEAGRAQSYAQLGRLFKAPDPRVLCMDYDVVLSHEALV  
LVTSTFGNDPPENGESFAAALMEMSGPYNSPRPEOHKSYKIRFNSVSCDPLVSS  
WRBKRKESNTDSAGALGTLRCVFGIGSRAPYHFCAPAFADVTRLEELGQRLSLQ  
QGBELCQBEAFRGAAQAAQACETFCVGEDAKAARDIFSFKRWKQKRVLSQTA  
ESQLPLGLTHVRHRRMFOATILSVENLQSKSTRATILVRLDTGGQGLYQPGDHI  
GVCPPNRPGLVEALLSRVEDPPEFTEPVAVELEKSGPPGPPGWRDRLPCTLRQ  
ALTYFDLITSPSPRLILSLTAESESEQLEALSQDPRRYEKKWFCSTPLLEVL  
EQPSVALPAPLITLPLLPQRYVSSAPSPGHEIHLTIAVLARTDGLGPHLY  
GVCSVMSQLKAGDPVFCFCIRGAPSPRLPDNPLCIVLPGPGIAPFGFMDRLHD  
IEIKGQAPMTLVFCGRCSQLDLHVRDEVLDAQRGVFGQVLTATSRDPGSKTYVQ  
DLRLTEAAEVRHVLCEQGHMFVCGDVTWATSVLQTVKRLATEGMEMLDEAGDVIG  
VLRDQQRHYEDIIFGLTLRTQEVTSRINTQSFSLQERQLRGAVPMSFDPGPPETPGS"

CDS  
1..4120  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="FANTOM DB:6030422B05"  
/clone="6030422B05"  
/sex="male"  
/tissue\_type="testis"  
/clone\_lib="RIKEN full-length enriched mouse cDNA library"  
/dev\_stage="13 days embryo"  
22..3630  
/notes="unnamed protein product; nitric oxide synthase 3,  
endothelial cell (MGI:97362, GB|NM\_008713, evidence:  
BLASTN, 9%, match=3633)  
putative"  
/codon\_start=1  
/protein\_id="BAC37052.1"  
/db\_xref="GI:26346807"  
/translation="MGNLSVGOEPGPPCGGLGLGLGKGGPASPAPPSQAPAP  
PSPTRPADHSPPLTPPDGPRFRVKNMEVGSITDYLISAQQDGPCTSRCLGSL  
VPPKLSRFTQSPTEQLLQARDFIQYNSIRKSGQAHEQLVEAEVATG  
TYQLRESLFTGAKARNAPRCVRIQWKLQVDFARDCTAQMFTYCNHIVAT  
NRGLNSAIVTFVQPCRGDPRFVNSQLIRYAGYQQSGVRGDPANVEITLCIQH  
GWTGNGRFDVPLLLQAQDEPPELFTLPEMVLVLEPHEPTLEWAAELRWYALPA  
VSNMLIEIGLEFPAPPSQWYNSSEIGMRDLCDPHYNLTEDVAVCMDLDTTSSSL  
WKKAAVEINVAHLSLTAKVTIVDHHAAATASFMKLENEQKRGCCPADWNIYVPP  
ISGSLTPVHFQEMVNTFLSPAFRIQPDPMKSGAAGIIRKTKFEVANAIVKVSASL  
MGTVMKRVKATILYSEAGRAQSYAQLGRLFKAPDPRVLCMDYDVVLSHEALV  
LVTSTFGNDPPENGESFAAALMEMSGPYNSPRPEOHKSYKIRFNSVSCDPLVSS  
WRBKRKESNTDSAGALGTLRCVFGIGSRAPYHFCAPAFADVTRLEELGQRLSLQ  
QGBELCQBEAFRGAAQAAQACETFCVGEDAKAARDIFSFKRWKQKRVLSQTA  
ESQLPLGLTHVRHRRMFOATILSVENLQSKSTRATILVRLDTGGQGLYQPGDHI  
GVCPPNRPGLVEALLSRVEDPPEFTEPVAVELEKSGPPGPPGWRDRLPCTLRQ  
ALTYFDLITSPSPRLILSLTAESESEQLEALSQDPRRYEKKWFCSTPLLEVL  
EQPSVALPAPLITLPLLPQRYVSSAPSPGHEIHLTIAVLARTDGLGPHLY  
GVCSVMSQLKAGDPVFCFCIRGAPSPRLPDNPLCIVLPGPGIAPFGFMDRLHD  
IEIKGQAPMTLVFCGRCSQLDLHVRDEVLDAQRGVFGQVLTATSRDPGSKTYVQ  
DLRLTEAAEVRHVLCEQGHMFVCGDVTWATSVLQTVKRLATEGMEMLDEAGDVIG  
VLRDQQRHYEDIIFGLTLRTQEVTSRINTQSFSLQERQLRGAVPMSFDPGPPETPGS"

ORIGIN  
Query Match 25.0%; Score 64.4; DB 4; Length 4120;  
Best Local Similarity 70.5%; Pred. No. 3.8e-06;  
Matches 86; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGCAAGACGACCTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
Db 715 CAGCGCTGCTCCCTGCGCGGGAGACTTCGGATCTGGAACAGCCAGCTGATACGCTATGCG 774  
QY 61 GGCTACCGAGTCCAGATGGCAGATCAGAGGGGACCCCTGCCACGTGGAAATTCACCTAG 120  
Db 775 GGCTATAGCAGCAGGATGGCTCGGTGCGAGGGGACCCCGCCACCTAGGATCACTGAG 834  
QY 121 GT 122  
Db 835 CT 836

RESULT 26  
CF744130  
LOCUS  
DEFINITION  
IMAGE:30620991 5', mRNA sequence.  
ACCESSION  
CF744130  
VERSION  
CF744130.1 GI:37640469

KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

EST.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
NIH-MGC http://mgc.mci.nih.gov/.  
1 (bases 1 to 660)  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: c9apbs@mail.nih.gov  
Tissue Procurement: Dr. James Lin, University of Iowa  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at  
http://genome.uiowa.edu/distribution/mousefl.html  
This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP)

Seq primer: pYX-5.  
Location/Qualifiers  
1..660  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:30620991"  
/tissue\_type="whole brain"  
/dev\_stage="1, 5, and 15 days newborn"  
/lab\_host="DH10B (T1 phage resistant)"  
/clone\_lib="NIH BMAP GVO"  
/note="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I;  
Site 2: Not I; The library was constructed according  
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. Denatured RNA was size fractionated on a 1% agarose  
gel. First strand cDNA synthesis was primed with oligo-dT  
primer containing a Not I site. Double strand cDNA was  
size selected according to mRNA size fraction, ligated with  
EcoR I adaptor, digested with NotI and then cloned  
directionally into pYX-Asc vector. The library tag  
sequence located between the Not I site and the polyA tail  
is CGAAGCTGAAT. This library was created for the University  
of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the  
Developing Mouse Nervous System', supported by National  
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,  
program coordinator."

ORIGIN  
Query Match 24.8%; Score 64; DB 6; Length 660;  
Best Local Similarity 76.0%; Pred. No. 3.7e-06;  
Matches 79; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 19 CAGCACTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGGCTACGAGTCCAGAT 78  
Db 1 CATGACTTCGAGTGTGGAACCTCGCAGCTCATCCGCTATGCTGGCTACGAGTCCAGAT 60  
QY 79 GGCAGCATCAGAGGGGACCTGCCAACGTGGAAATTCACCTCAGGT 122  
Db 61 GGCTCTACCTTGGCGGATCCAGCTAATGTGGAGTTTCAGAGAT 104

RESULT 27  
CX385985  
LOCUS  
DEFINITION  
IMAGE:7639850 5', mRNA sequence.  
ACCESSION  
CX385985.1 GI:57154542  
VERSION  
EST.  
KEYWORDS  
Xenopus tropicalis (western clawed frog)  
Xenopus tropicalis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;





Fax: 301 838 0208  
 Email: szhao@tigr.org  
 Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics (info@resgen.com). BAC end page: [http://www.tigr.org/tdb/bac/ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tdb/bac/ends/mouse/bac_end_intro.html)  
 Plate: 368 row: A column: 5  
 Seq primer: T7  
 Class: BAC ends.

#### FEATURES

source  
 1. .286  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="RPCI-23-368A5"  
 /sex="Female"  
 /lab\_host="DH10B"  
 /clone\_lib="RPCI-23"  
 /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRU Life Technologies)."

#### ORIGIN

Query Match 21.2%; Score 54.8; DB 9; Length 286;  
 Best Local Similarity 75.2%; Pred. No. 0.0006;  
 Matches 79; Conservative 1; Mismatches 24; Indels 1; Gaps 1;  
 QY 60 TGGCTACCATGCGAGCATGCGAGCATGCGAGGGACCTGCGCAACGTGAATTCACCTCA 119  
 Db 1 TGGCTACCATGCGAGCATGCGAGCATGCGAGGGAGTGTGCCACCTTGGAGTTCACCCA 60  
 QY 120 GGTACCGCGCCAGCTCAGCCGCCATTTGGGGGGGAGCC 164  
 Db 61 GGTA-CTGACTCAGCTCTCTAGATCCCTGTGTGGCGAGGGGAGCC 104

#### RESULT 30

DQ045247  
 LOCUS Homo sapiens NOS3 gene, VIRTUAL TRANSCRIPT, partial sequence,  
 DEFINITION genomic survey sequence.  
 DQ045247  
 ACCESSION DQ045247.1 GI:66896462  
 VERSION GSS.  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
 1 (bases 1 to 3612)  
 Hubisz,M.J., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,  
 White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
 A Scan for Positively Selected Genes in the Genomes of Humans and  
 Chimpanzees  
 (er) PLOS Biol. 3 (6), E170 (2005)  
 15869325  
 2 (bases 1 to 3612)  
 Hubisz,M.J., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,  
 White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
 Direct Submission  
 Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 This sequence was made by sequencing genomic exons and ordering  
 them based on alignment. Translation starts at the beginning of

#### alignment.

FEATURES  
 source  
 1. .3612  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /chromosome="7"  
 <1. .>3612  
 /gene="NOS3"  
 /locus\_tag="HC11004"

#### ORIGIN

Query Match 21.2%; Score 54.8; DB 11; Length 3612;  
 Best Local Similarity 65.6%; Pred. No. 0.0013;  
 Matches 80; Conservative 0; Mismatches 42; Indels 0; Gaps 0;  
 QY 1 CAGCGGAGTGATGGCAAGCACCACACTTCGGGGTGTGAATGCTCAGCTCATCGCTATGCT 60  
 Db 697 CAGCGCTGCCCTGGCGGAGGAGACTTCGGAATCTGAACAGCAGCTGTGGCTACGGC 756  
 QY 61 GGTACCATGATGCCAGATGGCAGCATCAGAGGGGACCTTGCACCACTGGAATTCACCTCAG 120  
 Db 757 GGTACCGCAGCAGGACGGCTCTGTGCGGGGGGACCCAGCCACGTGGAGATCACCGAG 816  
 QY 121 GT 122  
 Db 817 CT 818

#### RESULT 31

BJ088070 625 bp mRNA linear EST 29-SRP-2003  
 LOCUS BJ088070 NIBB Mochii normalized Xenopus tailbud library Xenopus  
 DEFINITION laevis cDNA clone XLO91118 3', mRNA sequence.  
 ACCESSION BJ088070  
 VERSION BJ088070.1 GI:17585186  
 KEYWORDS EST.  
 SOURCE Xenopus laevis (African clawed frog)  
 ORGANISM  
 Xenopus laevis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 Xenopodinae; Xenopus; Xenopus.  
 REFERENCE 1 (bases 1 to 625)  
 AUTHORS Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara,Y.  
 Expressed genes in X. laevis embryo  
 Unpublished (2001)  
 Contact: Tadasu Shin-i  
 Center For Genetic Resource Information  
 National Institute of Genetics  
 1111 Yata, Mishima, Shizuoka 411-8540, Japan  
 Tel: 81-559-81-6856  
 Fax: 81-559-81-6855  
 Email: tshini@genes.nig.ac.jp  
 The information of this clone is available through the following  
 URL.  
 http://xenopus.nibb.ac.jp

#### FEATURES

source  
 1. .625  
 /organism="Xenopus laevis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:8355"  
 /clone="XLO91118"  
 /tissue\_type="whole embryo"  
 /dev\_stage="stage 25"  
 /clone\_lib="NIBB Mochii normalized Xenopus tailbud  
 library"

#### ORIGIN

Query Match 19.1%; Score 49.4; DB 3; Length 625;  
 Best Local Similarity 68.7%; Pred. No. 0.026;  
 Matches 68; Conservative 0; Mismatches 31; Indels 0; Gaps 0;



Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Plate: LIA014805 row: 1 column: 11  
 High quality sequence stop: 626.  
 Location/Qualifiers

#### FEATURES.

1. .906  
 /organism="Danio rerio"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7955"  
 /clone="IMAGE:704445"  
 /tissue\_type="whole body"  
 /lab\_host="DH10B"  
 /clone\_lib="NIH ZGC 10"  
 /note="Vector: pExpress1; Site 1: NotI; Site 2: EcoRV;  
 Bulk tissue was collected from a whole adult individual from the Tubingen strain. 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was cloned into the Not I and EcoRV sites of pExpress-1. Library was size-selected for >1 kb fragments. A normalized version of this library is also available (NIH\_ZGC\_7). Library was constructed by Open Biosystems (Huntsville, AL)."

#### ORIGIN

Query Match 17.5%; Score 45.2; DB 7; Length 906;  
 Best Local Similarity 66.3%; Pred. No. 0.34; Indels 0; Gaps 0;  
 Matches 65; Conservative 0; Mismatches 33; Indels 0; Gaps 0;  
 QY 25 TTCCGGGTGTGAATGCTCAGCTCATCCGCTATGCTGGCTACCGATGCCAGATGCCAGC 84  
 |||||  
 Db 680 TTTCCCGTGTGGACGGTCAAGCTGATAAAGTATGCTGGCTATCAGATGGATGTTAGT 739  
 |||||  
 QY 85 ATCAGAGGGGACCCCTGCCAACGTGGAAATTCACTCAGGT 122  
 |||||  
 Db 740 GTGATCGCGGACCCCGCGGTGTAGACTTTACACAGGT 777  
 |||||

#### RESULT 35

BU425320 688 bp mRNA linear EST 29-NOV-2002  
 LOCUS 603961089F1 CSEQRBN09 Gallus gallus cDNA clone CHEST936a24 5', mRNA  
 DEFINITION

sequence.

ACCESSION BU425320

VERSION BU425320.1 GI:25917996

KEYWORDS EST.

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

REFERENCE 1 (bases 1 to 688)

AUTHORS Boardman,P.E., Sans-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,

Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.

TITLE A Comprehensive Collection of Chicken cDNAs

JOURNAL Curr Biol. 12 (22), 1965-1969 (2002)

PUBLISHED 1244392

COMMENT Contact: Simon Hubbard

Department of Biomolecular Sciences

University of Manchester Institute of Science and Technology

(UMIST)

PO Box 88, Manchester, M60 1QD, UK

Tel: 01612008930

Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.

Location/Qualifiers

1. .688

/organism="Gallus gallus"

/mol\_type="mRNA"

/strain="Layer and broiler"

/db\_xref="taxon:9031"

/clones="CHEST936a24"

/sex="Male and female"

#### FEATURES

source

/tissue\_type="Chondrocytes isolated from growth plate cartilage"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="CSEQRBN09"  
 /note="Vector: pBluescript II KS(+); Site 1: EcoRI;  
 Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

#### ORIGIN

Query Match 16.7%; Score 43.2; DB 5; Length 688;  
 Best Local Similarity 75.0%; Pred. No. 1.1; Indels 0; Gaps 0;  
 Matches 54; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
 QY 51 CCGCTATGCTGGCTACCGATGCCAGATGCCAGATGCCAGGGGACCTGCCAACGTGGA 110  
 |||||  
 Db 3 CCGATATGCTGGATATCAATGCCAGATGGGTCTGTCATAGGAGACCTGCCAAGTGTGGA 62  
 |||||  
 QY 111 ATTCACTCAGGT 122  
 |||||  
 Db 63 GTTCACAAAGTT 74  
 |||||

#### RESULT 36

DR123141 1171 bp mRNA linear EST 15-JUN-2005  
 LOCUS 49091370 Drosophila pseudoobscura embryonic cDNA library Drosophila  
 DEFINITION pseudoobscura cDNA clone K7 5', mRNA sequence.

ACCESSION DR123141

VERSION DR123141.1 GI:67839839

KEYWORDS EST.

SOURCE Drosophila pseudoobscura

ORGANISM Drosophila pseudoobscura

REFERENCE 1 (bases 1 to 1171)

AUTHORS Richards,S., Liu,Y., Bettencourt,B.R., Hradecky,P., Letovsky,S.,

Nielsen,R., Thornton,K., Hubisz,M.J., Chen,R., Meisel,R.P.,

Couronne,O., Hua,S., Smith,M.A., Zhang,P., Liu,J., Bussemaker,H.J.,

van Batenburg,M.F., Howells,S.L., Scherer,S.E., Sodergren,E.,

Matthews,B.B., Crosby,M.A., Schroeder,A.J., Ortiz-Barrientos,D.,

Rives,C.M., Metzker,M.L., Muzny,D.M., Scott,G., Steffen,D.,

Wheeler,D.A., Worley,K.C., Havlak,P., Durbin,K.J., Egan,A.,

Gill,R., Hume,J., Morgan,M.B., Miner,G., Hamilton,C., Huang,Y.,

Waldron,L., Verdusco,D., Clerc-Blankenburg,K.P., Dubchak,I.,

Noor,M.A., Anderson,W., White,K.P., Clark,A.G., Schaeffer,S.W.,

Geibart,W., Weinstein,G.M. and Gibbs,R.A.

Comparative genome sequencing of Drosophila pseudoobscura:

chromosomal, gene, and cis-element evolution

Genome Res. 15 (1), 1-18 (2005)

15632085

COMMENT Contact: Stephen Richards

Human Genome Sequencing Center

Baylor College of Medicine

One Baylor Plaza, Houston, TX 77030, USA

Tel: 713-798-6667

Email: stephenr@bcm.tmc.edu

NCBI Trace Archive: 22669760

Insert Length: 1750 Std Error: 0.25.

Location/Qualifiers

1. .1171

source

ORIGIN

Query Match 16.4%; Score 42.4; DB 8; Length 1171;  
Best Local Similarity 52.9%; Pred. No. 1.9;  
Matches 91; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

Qy 34 TGGAAATGCTAGCTATCCGTATGCTGGTACAGATGCCAGATGGCAGCATCAGAGGG 93  
Db TGGAGTCCCAAGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 848  
Qy 94 GACCTGCCACAGTGGAAATTCACGTACGTCAGCGCCGCGCCAGCTCAGCCCGGCATTGG 153  
Db GACCCCGCAGCGCCGCGCCAGAACTATCTGCGGGCCAAAGCGGACCCCCCGGTGGACCT 908  
Qy 154 GCGGGGAGCCCGGTGGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 205  
Db CGCGGGTTCCTCCCGTGGTCCAGCGGAACCCCTGGTGGACCCAGCGCGCTAC 960

RESULT 37  
DN757217/c  
LOCUS  
DEFINITION  
GL-Cf-14015 GLGC-LIB0001-of Canis familiaris Normalized Mixed  
Tissue cDNA Library Canis familiaris cDNA, mRNA sequence.

ACCESSION  
DN757217  
VERSION  
DN757217.1 GI:62146330  
KEYWORDS  
EST.  
SOURCE  
Canis familiaris (dog)  
Canis familiaris  
Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
Canis.

REFERENCE  
1 (bases 1 to 567)  
Liu, Q.  
Direct Submission Gene Logic Inc  
Unpublished (2005)  
JOURNAL  
Contact: Qing Liu  
Gene Logic Inc.  
610 Professional Drive, Gaithersburg, MD 20879, USA  
Tel: 301 987 1700  
Email: qlu@genelogic.com.

FEATURES  
source  
1..567  
Location/Qualifiers  
/organism="Canis familiaris"  
/mol\_type="mRNA"  
/strain="beagle"  
/db\_xref="taxon:9615"  
/lab\_host="EMPH108"  
/clone\_lib="GLGC-LIB0001-of Canis familiaris Normalized  
Mixed Tissue cDNA Library"  
/notes="Organ: heart, liver, kidney, testis, and brain;  
Vector: pCMVSPORT6.0; Site\_1: NotI; Site\_2: SalI"

ORIGIN

Query Match 15.6%; Score 40.2; DB 8; Length 567;  
Best Local Similarity 54.3%; Pred. No. 6.6;  
Matches 89; Conservative 0; Mismatches 71; Indels 4; Gaps 1;

Qy 39 TGCTCAGCTATCCGTATGCTGGTACCATGCCAGATGCCAGTGGCAGCATCAGAGGGGACCC 98  
Db TCCTCAGCGCAGCAACCTTTCTTGGGGACCATGCTCAGGGGCTGGCTGGAGCTAGCAGAAC 147  
Qy 99 TGCCAAGCTGGAATTCACGTACAGTACCGCGGCCAGCC----TCAGCCRCGCGCCATTGGG 154  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 146 TGCACACGGGAGCCCACTCCGGAAGCCTTNNCCACCGGNNCTGGCTCGGGGATTTCGC 87  
Qy 155 GCGGGGAGCCCGCTGGTGGAGCGAGTGACAGAGTGGAGCCACAG 198  
Db TCTGGGAGCCCTTGGGGGTGGGGGGTGGCNCNNNNNNNNCNGNG 43  
RESULT 38  
AJ394075/c  
LOCUS  
DEFINITION  
AJ394075 dkfz426 Gallus gallus cDNA clone 17p11r1, mRNA sequence.  
ACCESSION  
AJ394075  
VERSION  
AJ394075.1 GI:7123604  
KEYWORDS  
EST.  
SOURCE  
Gallus gallus (chicken)  
ORGANISM  
Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE  
1 (bases 1 to 797)  
AUTHORS  
Adraakmanov, I., Lodygin, D., Gerth, P., Arakawa, H., Law, A.,  
Plachy, J., Korn, B. and Buerstedde, J.M.  
TITLE  
A large database of chicken bursal ESTs as a resource for the  
analysis of vertebrate gene function  
JOURNAL  
Genome Res. 10 (12), 2062-2069 (2000)  
PUBMED  
11116100  
COMMENT  
Contact: Buerstedde JM  
Cellular Immunology  
Heinrich-Pette-Institut  
Martinistr. 52, 20251 Hamburg, Germany  
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.

FEATURES  
source  
1..797  
Location/Qualifiers  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="CB"  
/db\_xref="taxon:9031"  
/clone="17p11r1"  
/tissue\_type="Bursa of Fabricius"  
/cell\_type="bursal lymphocyte"  
/dev\_stage="2-3 weeks old"  
/clone\_lib="dkfz426"

ORIGIN

Query Match 15.4%; Score 39.8; DB 1; Length 797;  
Best Local Similarity 49.5%; Pred. No. 8.9;  
Matches 98; Conservative 1; Mismatches 99; Indels 0; Gaps 0;

Qy 14 GCAAGACGACTTCCGGGTGGGAATGCTCAGCTCATCCGCTATGCTGGCTACCATGTC 73  
Db GCAGCCACCACTGCCAGCAGCTGCTCTCTCTGTCGCTGCTGCTGCTGCTGCTGCTGCTG 439  
Qy 74 CAGATGGCAGCATCAGAGGGGACCTCGCAACGTTGGAATTCCTCAGTATCCCGGCCAG 133  
Db TTCCTCGTGGGAGGAGCTTTGACCCCTCCGAGGAGCGGACAGACACCTGCACAG 379  
Qy 134 CCTCAGCCRCGCGCATTTGGGGGGGAGCCCGCTGGTGGAGTGGAGTGGAGTGGAGCC 193  
Db CCACGGCCACTGTCAGCAGCCAGCTGAGCACCAGCTGCCAGGAATGCCAGTGGGAAGCA 319  
Qy 194 CAGAGGAGACAGCAGCC 211  
Db CTCAGGTACCACCTGCC 301

RESULT 39  
CN459880  
LOCUS  
DEFINITION  
UI-M-HB0-cow-f-04-0-UI.r1 NIH\_BMAP\_HB0 Mus musculus cDNA clone  
IMAGE:30648603 5', mRNA sequence.  
ACCESSION  
CN459880  
VERSION  
CN459880.1 GI:46465606  
KEYWORDS  
EST.

**SOURCE**  
Mus musculus (house mouse)

**ORGANISM**  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

**REFERENCE**  
1 (bases 1 to 771)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

**AUTHORS**  
Contact: Robert Strauberg, Ph.D.  
Email: [cgapbs@email.nih.gov](mailto:cgapbs@email.nih.gov)

**TITLE**  
cDNA Library preparation: Dr. James Lin University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at  
<http://genome.uiowa.edu/distribution/mouse1.html>  
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

**COMMENT**  
Seq primer: pYX-5.

**FEATURES**  
source  
Location/Qualifiers  
1..771  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:30648603"  
/tissue\_type="whole eye"  
/dev\_stage="embryo 12.5,13.5,14.5 dpc"  
/lab\_host="DH10B (T1 phage resistant)"  
/clone\_lib="NIH BMAP H80"  
/note="Organ: Eye; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Ronald, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is TTATTTGAAGT. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."

**ORIGIN**  
Query Match 15.3%; Score 39.6; DB 7; Length 771;  
Best Local Similarity 66.3%; Pred. No. 10;  
Matches 57; Conservative 0; Mismatches 29; Indels 0; Gaps 0;  
Qy 1 CAGCGAGTGTGTCAGACGACGATTCGGGTGTGGATGCTCAGCTACGCTATGCT 60  
Db 683 CAGCGTCCCTGCGCGGGAGACTTCGGATCTGGAACAGCCAGCTACGCTATGCG 742  
Qy 61 GGCTACACAGTCCAGATGCGCAGAT 86  
Db 743 GGCTATAGGCAGCAGGATGGCTCCGT 768

**RESULT 40**  
BJ733387  
LOCUS BJ733387 MF015DA cDNA Oryzias latipes cdna clone MF015DA022J07 5',  
DEFINITION mRNA sequence.  
ACCESSION BJ733387  
VERSION BJ733387.1 GI:45300699  
KEYWORDS EST.  
ORGANISM Oryzias latipes (Japanese medaka)  
Oryzias latipes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

**REFERENCE**  
1 (bases 1 to 721)  
AUTHORS Kohara, Y., Shin-i, T., Kimura, T., Narita, T., Jindo, T. and Takeda, H.  
TITLE Medaka EST project in Takeda's lab  
JOURNAL Unpublished (2001)  
COMMENT Contact: Tadasi Shin-i  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: [tshinigenes.nig.ac.jp](mailto:tshinigenes.nig.ac.jp).

**FEATURES**  
source  
Location/Qualifiers  
1..721  
/organism="Oryzias latipes"  
/mol\_type="mRNA"  
/strain="Hd-rR"  
/db\_xref="taxon:8090"  
/clone="MF015DA022J07"  
/sex="mixture of female and male"  
/tissue\_type="whole embryo"  
/dev\_stage="organogenesis stage 35"  
/clone\_lib="MF015DA cdna"

**ORIGIN**  
Query Match 15.3%; Score 39.4; DB 3; Length 721;  
Best Local Similarity 67.9%; Pred. No. 11;  
Matches 55; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
Qy 42 TCAGCTATCCGCTCTGCTGCTACGATGCCAGATGCCAGATCAGAGGGGACCTGC 101  
Db 5 TCAGCTGATTCTGTTACGAGGTTTACAAACAGCCTGACGGACAGATCCTGGGAGACCCGC 64  
Qy 102 CAACGTGGATTCACTCAGGT 122  
Db 65 CAATGTGGAGTTCACAGAT 85

Search completed: December 13, 2005, 18:11:36  
Job time : 3764 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 16:17:25 ; Search time 142 seconds  
(without alignments)  
3229.654 Million cell updates/sec

Title: US-10-713-137-1  
Perfect score: 258  
Sequence: 1 caggcgagtgatggcaagca.....ttgttccccagctgtgcatc 258

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:\*  
1: /cgn2\_6/prodata/1/ina/1 COMB.seq.\*  
2: /cgn2\_6/prodata/1/ina/5 COMB.seq.\*  
3: /cgn2\_6/prodata/1/ina/8A COMB.seq.\*  
4: /cgn2\_6/prodata/1/ina/8B COMB.seq.\*  
5: /cgn2\_6/prodata/1/ina/H COMB.seq.\*  
6: /cgn2\_6/prodata/1/ina/PCFUS COMB.seq.\*  
7: /cgn2\_6/prodata/1/ina/PP COMB.seq.\*  
8: /cgn2\_6/prodata/1/ina/RE COMB.seq.\*  
9: /cgn2\_6/prodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	257.6	99.8	47419	3	US-09-949-016-11841
2	257.6	99.8	47420	3	US-09-949-016-15484
3	120.4	46.7	3853	3	US-09-949-016-3742
4	120.4	46.7	3855	3	US-09-949-016-99
5	120.4	46.7	4062	3	US-09-126-109-11
6	120.4	46.7	4062	3	US-09-016-434-1478
7	120.4	46.7	4145	2	US-08-314-917-1
8	120.4	46.7	4145	2	US-08-265-046-1
9	120.4	46.7	4145	2	US-08-465-522-1
10	120.4	46.7	4145	6	PCT-US93-11401-1
11	120.4	46.7	4145	6	PCT-US95-07849-1
12	120.4	46.7	4164	3	US-09-023-655-1407
13	91.6	35.5	4041	2	US-08-147-812-4
14	91.6	35.5	4110	3	US-09-123-708-1
15	91.6	35.5	4110	3	US-09-123-624-1
16	91.6	35.5	4165	2	US-08-147-812-6
17	78.2	30.3	4079	3	US-09-016-434-1477
18	78.2	30.3	4353	2	US-08-365-486A-18
19	78.2	30.3	4353	3	US-08-880-342-18
20	75.6	29.3	5057	2	US-08-365-486A-12
21	75.6	29.3	5057	3	US-08-880-342-12
22	75.6	29.3	5108	2	US-07-642-002-1
23	75	29.1	4780	2	US-08-365-486A-20
24	75	29.1	4780	3	US-09-123-708-3

25	75	29.1	4780	3	US-09-123-624-3	Sequence 3, Appli
26	75	29.1	4780	3	US-08-880-342-20	Sequence 20, Appli
27	56.4	21.9	9208	3	US-09-068-506-1	Sequence 1, Appli
28	54.8	21.2	3612	3	US-09-068-506-2	Sequence 2, Appli
29	54.8	21.2	3690	3	US-09-016-434-1234	Sequence 1234, Ap
30	54.8	21.2	4035	3	US-09-016-434-1369	Sequence 1369, Ap
31	54.8	21.2	4099	3	US-08-896-053-5	Sequence 5, Appli
32	51.6	20.0	4097	3	US-09-123-708-5	Sequence 5, Appli
33	51.6	20.0	4097	3	US-09-123-624-5	Sequence 25, Appli
34	51.6	20.0	4491	3	US-08-809-917-25	Sequence 25, Appli
35	51.6	20.0	4491	3	US-09-419-371-25	Sequence 25, Appli
36	50	19.4	4089	2	US-07-908-245-1	Sequence 17, Appli
c 37	35.4	13.7	4603	2	US-08-258-261B-17	Sequence 17, Appli
c 38	35.4	13.7	4603	2	US-08-456-837-17	Sequence 17, Appli
c 39	35.4	13.7	4603	2	US-08-457-342-17	Sequence 17, Appli
c 40	35.4	13.7	4603	2	US-08-457-646A-17	Sequence 17, Appli
c 41	35.4	13.7	4603	2	US-08-458-076A-17	Sequence 17, Appli
c 42	35.4	13.7	4603	2	US-08-457-335A-17	Sequence 17, Appli
c 43	35.4	13.7	4603	2	US-08-728-214-17	Sequence 17, Appli
c 44	35.4	13.7	4603	3	US-09-028-934-17	Sequence 17, Appli
c 45	35.4	13.7	5698	2	US-08-761-258-11	Sequence 11, Appli

ALIGNMENTS

RESULT 1

US-09-949-016-11841  
; Sequence 11841, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11841  
; LENGTH: 47419  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-11841

Query Match	99.8%	Score 257.6;	DB 3;	Length 47419;
Best Local Similarity	99.6%	Pred. No. 7e-62;	0;	Indels 0;
Matches 257;	Conservative 1;	Mismatches 0;	Gaps 0;	
QY	1	CAGCGAGTGATGGCAAGCAGCATTC	CGGGTGTGGAATGCTCAGCTATCGCTATGCT	60
Db	21312	CAGCGAGTGATGGCAAGCAGCATTC	CGGGTGTGGAATGCTCAGCTATCGCTATGCT	21371
QY	61	GGTACCGAGTGCCAGATGGCAGCATC	AGAGGGACCTGCCACCTGGGATTCACCTCAG	120
Db	21372	GGTACCGAGTGCCAGATGGCAGCATC	AGAGGGACCTGCCACCTGGGATTCACCTCAG	21431
QY	121	GTATCCCGCCAGCCTCAGCCCGG	CGGAGCCCGTGGTGAGCCAGTG	180
Db	21432	GTATCCCGCCAGCCTCAGCCCGG	CGGAGCCCGTGGTGAGCCAGTG	21491
QY	181	ACAGAGTGAGCCAGAGGAGACAC	AGCCCGGGCTTACAGACTCAGAGG	240
Db	21492	ACAGAGTGAGCCAGAGGAGACAC	AGCCCGGGCTTACAGACTCAGAGG	21551
QY	241	GTTCCTCCAGCTGTGCATC	258	

```
Db 21552 GTTCCCGAGCTGTGCATC 21569

RESULT 2
US-09-949-016-15484
; Sequence 15484, Application US/09949016
; Patent No. 6812339
; ORGANISM: Human
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15484
; LENGTH: 47420
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15484

Query Match 99.8%; Score 257.6; DB 3; Length 47420;
Best Local Similarity 99.6%; Pred. No. 7e-62; Indels 0; Gaps 0;
Matches 257; Conservative 1; Mismatches 1;

Qy 1 CAGCGGAGTGATGCCAAGCAGCAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 21312 CAGCGGAGTGATGCCAAGCAGCAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 21371
Qy 61 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 120
Db 21372 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 21431
Qy 121 GTATCCCGGCCAGCCTCAGCCRCGCGCATTTGGGGCGGGGAGCCCGTGGTGAGCCGAGTG 180
Db 21432 GTATCCCGGCCAGCCTCAGCCRCGCGCATTTGGGGCGGGGAGCCCGTGGTGAGCCGAGTG 21491
Qy 181 ACAGAGTGGAGCCAGAGGAGACACGAGCCCGGGCTTACAGACTCAGAGGCCCGTCTT 240
Db 21492 ACAGAGTGGAGCCAGAGGAGACACGAGCCCGGGCTTACAGACTCAGAGGCCCGTCTT 21551
Qy 241 GTTCCCGAGCTGTGCATC 258
Db 21552 GTTCCCGAGCTGTGCATC 21569

RESULT 3
US-09-949-016-3742
; Sequence 3742, Application US/09949016
; Patent No. 6812339
; ORGANISM: Human
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3742
```

```
; LENGTH: 3853
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3742

Query Match 46.7%; Score 120.4; DB 3; Length 3853;
Best Local Similarity 99.2%; Pred. No. 5.6e-24; Indels 0; Gaps 0;
Matches 121; Conservative 0; Mismatches 1;

Qy 1 CAGCGGAGTGATGCCAAGCAGCAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 939 CAGCGGAGTGATGCCAAGCAGCAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 998
Qy 61 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 120
Db 999 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 1058
Qy 121 GT 122
Db 1059 CT 1060

RESULT 4
US-09-949-016-99
; Sequence 99, Application US/09949016
; Patent No. 6812339
; ORGANISM: Human
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 3855
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-99

Query Match 46.7%; Score 120.4; DB 3; Length 3855;
Best Local Similarity 99.2%; Pred. No. 5.6e-24; Indels 0; Gaps 0;
Matches 121; Conservative 0; Mismatches 1;

Qy 1 CAGCGGAGTGATGCCAAGCAGCAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 939 CAGCGGAGTGATGCCAAGCAGCAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 998
Qy 61 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 120
Db 999 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 1058
Qy 121 GT 122
Db 1059 CT 1060

RESULT 5
US-09-126-109-11
; Sequence 11, Application US/09126109
; Patent No. 6171856
; ORGANISM: Human
; GENERAL INFORMATION:
; APPLICANT: Thigpen, Anice
; APPLICANT: Hohmeier, Hans-Ewald
; APPLICANT: Newgard, Christopher B.
; APPLICANT: Unger, Roger H.
```



TITLE OF INVENTION: Oxide Synthase And Process for Preparing Same  
 NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Arnold B. Silverman  
 ADDRESSEE: Eckert Seamans Cherin & Mellott  
 STREET: 600 Grant Street, 42nd Floor  
 CITY: Pittsburgh  
 STATE: PA

```
; COUNTRY: USA
; ZIP: 15219
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/314,917
; APPLICATION NUMBER: US/08/314,917
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/981,344
; FILING DATE: 25-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Silverman, Arnold B.
; REGISTRATION NUMBER: 22,614
; REFERENCE/DOCKET NUMBER: 116972
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (412) 566-6000
; TELEFAX: (412) 566-6099
; TELEX: 866172
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4145 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; DESCRIPTION: Human Hepatocyte Inducible Nitric Oxide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Induced Human Hepatocyte RNA
; IMMEDIATE SOURCE:
; LIBRARY: Lambda Zap II cDNA
; CLONE: PHINOS
; CHROMOSOME/SEGMENT: unknown
; MAP POSITION: unknown
; UNITS: unknown
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 207..3668
; IDENTIFICATION METHOD: Experiment
; US-08-314-917-1
```

```
Query Match 46.7%; Score 120.4; DB 2; Length 4145;
Best Local Similarity 99.2%; Pred. No. 5.7e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAGCAGCTTCGGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 60
Db 951 CAGCGGAGTGATGGCAAGCAGCAGCTTCGGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 1010

Qy 61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
Db 1011 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 1070

Qy 121 GT 122
Db 1071 CT 1072
```

```
RESULT 8
US-08-265-046-1
; Sequence 1, Application US/08265046
; Patent No. 5658565
; GENERAL INFORMATION:
; APPLICANT: Timothy R. Billiar
; APPLICANT: Edith Tzeng
; APPLICANT: Andreas K. Nussler
```

```
; APPLICANT: David A. Geller
; APPLICANT: Richard L. Simmons
; TITLE OF INVENTION: Inducible Nitric Oxide Synthase
; TITLE OF INVENTION: Gene for Treatment of Disease
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lewis F. Gould, Jr.
; ADDRESSEE: Eckert Seamans Cherin & Mellott
; STREET: 1700 Market Street, Suite 3232
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,046
; FILING DATE: 24-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Gould, Lewis F. Jr.
; REGISTRATION NUMBER: 25,057
; REFERENCE/DOCKET NUMBER: 119130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 575-6020
; TELEFAX: (215) 575-6015
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4145 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; DESCRIPTION: Human Hepatocyte Inducible Nitric Oxide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Induced Human Hepatocyte RNA
; IMMEDIATE SOURCE:
; LIBRARY: Lambda Zap II cDNA
; CLONE: PHINOS
; CHROMOSOME/SEGMENT: unknown
; MAP POSITION: unknown
; UNITS: unknown
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 207..3668
; IDENTIFICATION METHOD: Experiment
; US-08-265-046-1
```

```
Query Match 46.7%; Score 120.4; DB 2; Length 4145;
Best Local Similarity 99.2%; Pred. No. 5.7e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAGCAGCTTCGGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 60
Db 951 CAGCGGAGTGATGGCAAGCAGCAGCTTCGGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 1010

Qy 61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
Db 1011 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 1070

Qy 121 GT 122
Db 1071 CT 1072
```

RESULT 9  
US-08-465-522-1  
; Sequence 1, Application US/08465522  
; Patent No. 5882908  
; GENERAL INFORMATION:  
; APPLICANT: Billiar, Timothy R.  
; APPLICANT: Nussler, Andreas K.  
; APPLICANT: Geller, David A.  
; APPLICANT: Simmons, Richard L.  
; TITLE OF INVENTION: cDNA Clone for Human Inducible Nitric  
; TITLE OF INVENTION: Oxide Synthase And Process for Preparing Same  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lewis F. Gould, Jr.  
; ADDRESSEE: Eckert Seamans Cherin & Mellott  
; STREET: 1700 Market St. Suite 3232  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/465,522  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gould, Jr., Lewis F.  
; REGISTRATION NUMBER: 25,057  
; REFERENCE/DOCKET NUMBER: 116972-6  
; TELEPHONE: (215) 575-6020  
; TELEFAX: (215) 575-6015  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4145 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; DESCRIPTION: Human Hepatocyte Inducible Nitric Oxide  
; DESCRIPTION: Synthase cDNA Clone  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; TISSUE TYPE: Induced Human Hepatocyte RNA  
; IMMEDIATE SOURCE:  
; LIBRARY: Lambda Zap II cDNA  
; CLONE: PHINOS  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT: unknown  
; MAP POSITION: unknown  
; UNITS: unknown  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 207..3668  
; IDENTIFICATION METHOD: Experiment  
US-08-465-522-1  
Query Match 46.7%; Score 120.4; DB 2; Length 4145;  
Best Local Similarity 99.2%; Pred. No. 5.7e-24;  
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 CAGCGGAGTGATGGCAAGCAGACTTCGCGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
Db 951 CAGCGGAGTGATGGCAAGCAGACTTCGCGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1010  
Qy 61 GGCTACCATGATGCCAGATGCCAGATCAGAGGGGACCTGCCAACGTGGGAATTCATCTCAG 120

Db 1011 GGCTACCATGATGCCAGATGCCAGATCAGAGGGGACCTGCCAACGTGGGAATTCATCTCAG 1070  
Qy 121 GT 122  
Db 1071 CT 1072  
RESULT 10  
PCT-US93-11401-1  
; Sequence 1, Application PCTUS9311401  
; GENERAL INFORMATION:  
; APPLICANT: Billiar, Timothy R.  
; APPLICANT: Nussler, Andreas K.  
; APPLICANT: Geller, David A.  
; APPLICANT: Simmons, Richard L.  
; TITLE OF INVENTION: cDNA Clone for Human Inducible Nitric  
; TITLE OF INVENTION: Oxide Synthase And Process for Preparing Same  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold B. Silverman  
; ADDRESSEE: Eckert Seamans Cherin & Mellott  
; STREET: 600 Grant Street, 42nd Floor  
; CITY: Pittsburgh  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 15219  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/11401  
; FILING DATE: 25-NOV-1992  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/981,344  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Silverman, Arnold B.  
; REGISTRATION NUMBER: 22,614  
; REFERENCE/DOCKET NUMBER: 116972  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (412) 566-6000  
; TELEFAX: (412) 566-6099  
; TELEX: 866172  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4145 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; TISSUE TYPE: Induced Human Hepatocyte RNA  
; IMMEDIATE SOURCE:  
; LIBRARY: Lambda Zap II cDNA  
; CLONE: PHINOS  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT: unknown  
; MAP POSITION: unknown  
; UNITS: unknown  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 207..3668  
; IDENTIFICATION METHOD: Experiment  
PCT-US93-11401-1  
Query Match 46.7%; Score 120.4; DB 6; Length 4145;  
Best Local Similarity 99.2%; Pred. No. 5.7e-24;  
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 951 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1010
QY 61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCTGCGAACGTGGGAATTCACCTCAG 120
Db 1011 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCTGCGAACGTGGGAATTCACCTCAG 1070
QY 121 GT 122
Db 1071 CT 1072

RESULT 11
PCT-US95-07849-1
; Sequence 1, Application PC/TUS9507849
; GENERAL INFORMATION:
; APPLICANT: University of Pittsburgh of the Commonwealth System of Higher
; APPLICANT: Education
; TITLE OF INVENTION: Inducible Nitric Oxide Synthase
; TITLE OF INVENTION: Gene for Treatment of Disease
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lewis F. Gould, Jr.
; ADDRESSEE: Eckert Seamans Cherin & Mellott
; STREET: 1700 Market Street, Suite 3232
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07849
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gould, Lewis F. Jr.
; REGISTRATION NUMBER: 25,057
; REFERENCE/DOCKET NUMBER: 119130-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 575-6020
; TELEFAX: (215) 575-6015
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4145 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; DESCRIPTION: Human Hepatocyte Inducible Nitric Oxide
; DESCRIPTION: Synthase cDNA Clone
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: Induced Human Hepatocyte RNA
; IMMEDIATE SOURCE:
; LIBRARY: Lambda Zap II cDNA
; CLONE: PHINOS
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: unknown
; MAP POSITION: unknown
; UNITS: unknown
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 207..3668
; IDENTIFICATION METHOD: Experiment
; PCT-US95-07849-1
```

```
Query Match 46.7%; Score 120.4; DB 6; Length 4145;
Best Local Similarity 99.2%; Pred. No. 5.7e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 951 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1010
QY 61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCTGCGAACGTGGGAATTCACCTCAG 120
Db 1011 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCTGCGAACGTGGGAATTCACCTCAG 1070
QY 121 GT 122
Db 1071 CT 1072

RESULT 12
US-09-023-655-1407
; Sequence 1407, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1407:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4164 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9441452
; US-09-023-655-1407

Query Match 46.7%; Score 120.4; DB 3; Length 4164;
Best Local Similarity 99.2%; Pred. No. 5.7e-24;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
|||||
```

Db 970 CAGCGGAGTGATGGCAAGCAAGCTTCCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 1029

Qy 61 GGCTACCAAGATCCAGATGGCAGCATCAGAGGGGACCTTGCACCAAGTGGAAATTCACCTCAG 120

Db 1030 GGCTACCAAGATCCAGATGGCAGCATCAGAGGGGACCTTGCACCAAGTGGAAATTCACCTCAG 1089

Qy 121 GT 122

Db 1090 CT 1091

## RESULT 13

US-08-147-812-4  
; Sequence 4, Application US/08147812  
; Patent No. 5766909  
; GENERAL INFORMATION:  
; APPLICANT: Xie, Qiao-wen  
; APPLICANT: Nathan, Carl F.  
; APPLICANT: Mumford, Richard A.  
; APPLICANT: Calaycay, Jimmy Ramos  
; TITLE OF INVENTION: DNA Encoding Inducible Nitric Oxide Synthase  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: 126 East Lincoln Avenue  
; CITY: Rahway  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07065

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: Macintosh Centris650  
OPERATING SYSTEM: Macintosh 7.0.1  
SOFTWARE: Microsoft Word 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/147,812  
FILING DATE: No. 5766909 Available  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/841,641  
FILING DATE: 02-FEB-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Wallen, John W III  
REGISTRATION NUMBER: 35,403  
REFERENCE/DOCKET NUMBER: 186581A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-3905  
TELEFAX: (908) 594-4720  
TELEX: 138825  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4041 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-147-812-4

Query Match 35.5%; Score 91.6; DB 2; Length 4041;  
Best Local Similarity 84.4%; Pred. No. 5.7e-16;  
Matches 103; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAAGCTTCCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 60

Db 982 CAGCGGAGTGACGGCAACATGATCTCAGGCTCTGGAAATTCACAGCTCATCCGCTACGCT 1041

Qy 61 GGCTACCAAGATCCAGATGGCAGCATCAGAGGGGACCTTGCACCAAGTGGAAATTCACCTCAG 120

Db 1042 GGCTACCAAGATCCAGATGGCAGCATCAGAGGGGATGCTGCCACCTTGGAGTTCAACCAG 1101

Qy 121 GT 122

Db 1102 TT 1103

## RESULT 14

US-09-123-708-1  
; Sequence 1, Application US/09123708  
; Patent No. 6146887  
; GENERAL INFORMATION:  
; APPLICANT: SCHRAEDER, Juergen  
; APPLICANT: GOEDECKE, Axel  
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC  
; TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS  
; FILE REFERENCE: 511169-2003  
; CURRENT APPLICATION NUMBER: US/09/123,708  
; CURRENT FILING DATE: 1998-07-28  
; EARLIER APPLICATION NUMBER: 08/553,503  
; EARLIER FILING DATE: 1996-03-01  
; EARLIER APPLICATION NUMBER: P4411402.8  
; EARLIER FILING DATE: 1994-03-31  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 4110  
; TYPE: DNA  
; ORGANISM: Cytomegalovirus

US-09-123-708-1

Query Match 35.5%; Score 91.6; DB 3; Length 4110;  
Best Local Similarity 84.4%; Pred. No. 5.8e-16;  
Matches 103; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
Qy 1 CAGCGGAGTGATGGCAAGCAAGCTTCCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 60  
Db 918 CAGCGGAGTGACGGCAACATGATCTCAGGCTCTGGAAATTCACAGCTCATCCGCTACGCT 977  
Qy 61 GGCTACCAAGATCCAGATGGCAGCATCAGAGGGGACCTTGCACCAAGTGGAAATTCACCTCAG 120  
Db 978 GGCTACCAAGATCCCGATGGCACCATCAGAGGGGATGCTGCCACCTTGGAGTTCAACCAG 1037  
Qy 121 GT 122

Db 1038 TT 1039

## RESULT 15

US-09-123-624-1  
; Sequence 1, Application US/09123624  
; Patent No. 6149936  
; GENERAL INFORMATION:  
; APPLICANT: SCHRAEDER, Juergen  
; APPLICANT: GOEDECKE, Axel  
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC  
; TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS  
; FILE REFERENCE: 511169-2004  
; CURRENT APPLICATION NUMBER: US/09/123,624  
; CURRENT FILING DATE: 1998-07-28  
; EARLIER APPLICATION NUMBER: 08/553,503  
; EARLIER FILING DATE: 1996-03-01  
; EARLIER APPLICATION NUMBER: 4411402.8  
; PRIOR FILING DATE: 1994-03-31  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 4110  
; TYPE: DNA  
; ORGANISM: Mus musculus

US-09-123-624-1

Query Match 35.5%; Score 91.6; DB 3; Length 4110;  
Best Local Similarity 84.4%; Pred. No. 5.8e-16;  
Matches 103; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
Qy 1 CAGCGGAGTGATGGCAAGCAAGCTTCCGGGTGTGGAAATGCTCAGCTCATCCGCTATGCT 60  
Db 918 CAGCGGAGTGACGGCAACATGATCTCAGGCTCTGGAAATTCACAGCTCATCCGCTACGCT 977

QY 61 GGCTACCATGATGCCAGATGCGAGATCAGAGGGAGCCCTGCCAAGCTGGAATTCACCTCAG 120  
|  
Db 978 GGCTACCATGATGCCAGATGCGAGATCAGAGGGAGCCCTGCCAAGCTGGAATTCACCTCAG 1037  
  
QY 121 GT 122  
|  
Db 1038 TT 1039

## RESULT 16

US-08-147-812-6  
; Sequence 6, Application US/08147812  
; Patent No. 5766909  
; GENERAL INFORMATION:  
; APPLICANT: Xie, Qiao-wen  
; APPLICANT: Nathan, Carl F.  
; APPLICANT: Mumford, Richard A.  
; APPLICANT: Calaycav, Jimmy Ramos  
; TITLE OF INVENTION: DNA Encoding Inducible Nitric Oxide Synthase  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: 126 East Lincoln Avenue  
; CITY: Rahway  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07065

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: Macintosh Centris650  
; OPERATING SYSTEM: Macintosh 7.0.1  
; SOFTWARE: Microsoft Word 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/147,812  
; FILING DATE: No. 5766909 Available  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/841,641  
; FILING DATE: 02-FEB-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wallen, John W III  
; REGISTRATION NUMBER: 35,403  
; REFERENCE/DOCKET NUMBER: 186581A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 594-3905  
; TELEFAX: (908) 594-4720  
; TELEX: 138825

; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4165 bases  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-147-812-6

Query Match 35.5%; Score 91.6; DB 2; Length 4165;  
Best Local Similarity 84.4%; Pred. No. 5.8e-16;  
Matches 103; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGCCAAGCAGCACTCCGGGTGTGGAATGCTCAGGCTCATCCGCTATGCT 60  
|  
Db 982 CAGCGGAGTGATGCCAAGCAGCACTCCGGGTGTGGAATGCTCAGGCTCATCCGCTATGCT 1041  
  
QY 61 GGCTACCATGCGAGATGCGAGATCAGAGGGAGCCCTGCCAAGCTGGAATTCACCTCAG 120  
|  
Db 1042 GGCTACCATGCGCGATGCGACCATCAGAGGGAGTGTCCACCTTGGAGTTCAACCCAG 1101  
  
QY 121 GT 122  
|  
Db 1102 TT 1103

## RESULT 17

US-09-016-434-1477  
; Sequence 1477, Application US/09016434  
; Patent No. 6500938  
; GENERAL INFORMATION:  
; APPLICANT: Janice Au-Young  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1490  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/016,434  
; FILING DATE: HERewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0002 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166

; INFORMATION FOR SEQ ID NO: 1477:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4079 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: G951318  
US-09-016-434-1477

Query Match 30.3%; Score 78.2; DB 3; Length 4079;  
Best Local Similarity 77.2%; Pred. No. 3e-12;  
Matches 95; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGCCAAGCAGCACTCCGGGTGTGGAATGCTCAGGCTCATCCGCTATGCT 60  
|  
Db 1412 CAGAGGACAGACGGCAAGCAGCACTCCGAGTCTGGAATCCAGGCTCATCCGCTACGCT 1471  
  
QY 61 GGCTACCATGCGAGATGCGAGATCAGAGGGAGCCCTGCCAAGCTGGAATTCACCTCAG 120  
|  
Db 1472 GGCTACCATGCGAGCTCAGCGCTCCACCTGGGGGACCCAGCCCAATGTGCAGTTTCACAGAG 1531  
  
QY 121 GTA 123  
|  
Db 1532 ATA 1534

## RESULT 18

US-08-365-486A-18  
; Sequence 18, Application US/08365486A  
; Patent No. 5834306  
; GENERAL INFORMATION:  
; APPLICANT: Webster, Keith A.  
; APPLICANT: Bishopric, Nanette H.  
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated



```
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365,486A
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5057 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: rat bnos cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 349..4638
; US-08-365-486A-12

Query Match 29.3%; Score 75.6; DB 2; Length 5057;
Best Local Similarity 76.2%; Pred. No. 1.7e-11;
Matches 93; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGTGCGAAGCAGCACTTCCGGGTGGGAATGCTCAGCTCATCCGCTATGCT 60
Db 1738 CAGAGGACTACGCGCAACATGACTCCGAGTGTGGAACTCGCAGCTCATCCGCTACGG 1797
Qy 61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAAATTCACCTCAG 120
Db 1798 GGCTACAAGCAGCAGATGGCTCTACCTTGGGGGATCCAGCCAAATGTGCAGTTTCACGGAG 1857
Qy 121 GT 122
Db 1858 AT 1859

RESULT 21
US-08-880-342-12
; Sequence 12, Application US/08880342
; Patent No. 6218179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Laderoute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA

; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365,486
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5057 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: rat bnos cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 349..4638
; US-08-365-486A-12

Query Match 29.3%; Score 75.6; DB 3; Length 5057;
Best Local Similarity 76.2%; Pred. No. 1.7e-11;
Matches 93; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGTGCGAAGCAGCACTTCCGGGTGGGAATGCTCAGCTCATCCGCTATGCT 60
Db 1738 CAGAGGACTACGCGCAACATGACTCCGAGTGTGGAACTCGCAGCTCATCCGCTACGG 1797
Qy 61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAAATTCACCTCAG 120
Db 1798 GGCTACAAGCAGCAGATGGCTCTACCTTGGGGGATCCAGCCAAATGTGCAGTTTCACGGAG 1857
Qy 121 GT 122
Db 1858 AT 1859

RESULT 22
US-07-642-002-1
; Sequence 1, Application US/07642002
; Patent No. 5268465
; GENERAL INFORMATION:
; APPLICANT: Brett, David S.
; APPLICANT: Hwang, Paul M.
; APPLICANT: Reed, Randall
; APPLICANT: Snyder, Solomon H.
; TITLE OF INVENTION: Purification and Molecular Cloning of Nitric
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: One Thomas Circle, NW
; CITY: Washington
```



STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/642,002  
FILING DATE: 19910118  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kagan, Sarah A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 1107.033576  
TELEPHONE: (202) 296-5500  
TELEFAX: (202) 296-7830  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5108 base pairs  
TYPE: NUCLEIC ACID  
STRADEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: N  
ANTI-SENSE: N  
ORIGINAL SOURCE:  
ORGANISM: Rattus rattus  
TISSUE TYPE: Brain  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 400..4686  
OTHER INFORMATION:  
US-07-642-002-1

Query Match 29.3%; Score 75.6; DB 2; Length 5108;  
Best Local Similarity 76.2%; Pred. No. 1.7e-11;  
Matches 93; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
|||||  
Db 1789 CAGGAGCTGACGGCAACATGATCTCCGAGTGTGGAATCCTCGAGCTCATCCGCTACGGG 1848  
|||||

QY 61 GGCTACCATGATGCGAGATGCGAGCATCAGAGGGGACCCCTGCCAACTGGAATTCATCTAG 120  
|||||  
Db 1849 GGCTACCATGATGCGAGATGCGAGCATCAGAGGGGACCCCTGCCAACTGGAATTCATCTAG 1908  
|||||

QY 121 GT 122  
Db 1909 AT 1910

RESULT 23  
US-08-365-486A-20  
Sequence 20, Application US/08365486A  
Patent No. 5834306  
GENERAL INFORMATION:  
APPLICANT: Webster, Keith A.  
APPLICANT: Bishopric, Nanette H.  
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated  
TITLE OF INVENTION: Therapeutic Constructs  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Avenue, Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/365,486A  
FILING DATE: 23-DEC-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Sholtz, Charles K.  
REGISTRATION NUMBER: 38,615  
REFERENCE/DOCKET NUMBER: 8255-0018  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4780 base pairs  
TYPE: nucleic acid  
STRADEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: Human NOS-SN gene, Nakane, et al,  
INDIVIDUAL ISOLATE: FEBS Lett 316:175 (1993)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 431..4732  
US-08-365-486A-20

Query Match 29.1%; Score 75; DB 2; Length 4780;  
Best Local Similarity 75.6%; Pred. No. 2.4e-11;  
Matches 93; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
|||||  
Db 1832 CAGAGGACAGAGCGGCAAGCAGCAGCTTCCGAGTGTGGAATCCTCGAGCTCATCCGCTACGCT 1891  
|||||

QY 61 GGCTACCATGATGCGAGATGCGAGCATCAGAGGGGACCCCTGCCAACTGGAATTCATCTAG 120  
|||||  
Db 1892 GGCTACCATGATGCGAGATGCGAGCATCAGAGGGGACCCCTGCCAACTGGAATTCATCTAG 1951  
|||||

QY 121 GTA 123  
Db 1952 ATA 1954

RESULT 24  
US-09-123-708-3  
Sequence 3, Application US/09123708  
Patent No. 6146887  
GENERAL INFORMATION:  
APPLICANT: SCHRADER, Juergen  
APPLICANT: GOEDECKE, Axel  
TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC  
TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS  
FILE REFERENCE: 511169-2003  
CURRENT APPLICATION NUMBER: US/09/123,708  
CURRENT FILING DATE: 1998-07-28  
EARLIER APPLICATION NUMBER: 08/553,503  
EARLIER FILING DATE: 1996-03-01  
EARLIER APPLICATION NUMBER: P4411402.8  
EARLIER FILING DATE: 1994-03-31  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
TYPE: DNA  
LENGTH: 4780  
ORGANISM: Cytomegalovirus  
US-09-123-708-3

Query Match 29.1%; Score 75; DB 3; Length 4780;

STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/642,002  
FILING DATE: 19910118  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kagan, Sarah A.  
REGISTRATION NUMBER: 32,141  
REFERENCE/DOCKET NUMBER: 1107.033576  
TELEPHONE: (202) 296-5500  
TELEFAX: (202) 296-7830  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5108 base pairs  
TYPE: NUCLEIC ACID  
STRADEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: N  
ANTI-SENSE: N  
ORIGINAL SOURCE:  
ORGANISM: Rattus rattus  
TISSUE TYPE: Brain  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 400..4686  
OTHER INFORMATION:  
US-07-642-002-1

Query Match 29.3%; Score 75.6; DB 2; Length 5108;  
Best Local Similarity 76.2%; Pred. No. 1.7e-11;  
Matches 93; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCAGCTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
|||||  
Db 1789 CAGGAGCTGACGGCAACATGATCTCCGAGTGTGGAATCCTCGAGCTCATCCGCTACGGG 1848  
|||||

QY 61 GGCTACCATGATGCGAGATGCGAGCATCAGAGGGGACCCCTGCCAACTGGAATTCATCTAG 120  
|||||  
Db 1849 GGCTACCATGATGCGAGATGCGAGCATCAGAGGGGACCCCTGCCAACTGGAATTCATCTAG 1908  
|||||

QY 121 GT 122  
Db 1909 AT 1910

RESULT 23  
US-08-365-486A-20  
Sequence 20, Application US/08365486A  
Patent No. 5834306  
GENERAL INFORMATION:  
APPLICANT: Webster, Keith A.  
APPLICANT: Bishopric, Nanette H.  
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated  
TITLE OF INVENTION: Therapeutic Constructs  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Avenue, Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk





```
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016.434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1369:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4035 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9434699
US-09-016-434-1369

Query Match 21.2%; Score 54.8; DB 3; Length 4035;
Best Local Similarity 65.6%; Pred. No. 9.7e-06;
Matches 80; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGAAGCAGCAGCTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 748 CAGCGCTGCCCTGCGCGAGGAGACTTCGGAATCTGGAACAGCCAGCTGGTGGCTACGCG 807

Qy 61 GGCTACCATGTCAGATGCGCAGCATCAGAGGGGACCCCTGCCAACGTGGAAATTCACCTCAG 120
Db 808 GGCTACCGGCAGCAGGAGCGCTCTGTGCGGGGGACCCAGCCACGCTGGAGATCACCGAG 867

Qy 121 GT 122
Db 868 CT 869

RESULT 31
US-08-896-053-5
; Sequence 5, Application US/08896053
; Patent No. 6720309
; GENERAL INFORMATION:
; APPLICANT: Janssens, Stefans
; APPLICANT: Bloch, Kenneth D.
; APPLICANT: Collen, D sir
; TITLE OF INVENTION: Method of Inducing Vasodilation and
; TITLE OF INVENTION: Treating Pulmonary Hypertension Using Adenoviral-Mediated
; TITLE OF INVENTION: Transfer of the Nitric Oxide Synthase Gene
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896.053
```

```
; FILING DATE: 17-JUL-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,912
; FILING DATE: 17-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Millonig, Robert C.
; REGISTRATION NUMBER: 34,395
; REFERENCE/DOCKET NUMBER: 0609.4280001/JAG/RCM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4099 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-896-053-5

Query Match 21.2%; Score 54.8; DB 3; Length 4099;
Best Local Similarity 65.6%; Pred. No. 9.7e-06;
Matches 80; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGAAGCAGCAGCTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 743 CAGCGCTGCCCTGCGCGAGGAGACTTCGGAATCTGGAACAGCCAGCTGGTGGCTACGCG 802

Qy 61 GGCTACCATGTCAGATGCGCAGCATCAGAGGGGACCCCTGCCAACGTGGAAATTCACCTCAG 120
Db 803 GGCTACCGGCAGCAGGAGCGCTCTGTGCGGGGGACCCAGCCACGCTGGAGATCACCGAG 862

Qy 121 GT 122
Db 863 CT 864

RESULT 32
US-09-123-708-5
; Sequence 5, Application US/09123708
; Patent No. 6146887
; GENERAL INFORMATION:
; APPLICANT: SCHRADER, Juergen
; APPLICANT: GOEDECKE, Axel
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC
; TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
; FILE REFERENCE: 511169-2003
; CURRENT APPLICATION NUMBER: US/09/123,708
; CURRENT FILING DATE: 1998-07-28
; EARLIER APPLICATION NUMBER: 08/553,503
; EARLIER FILING DATE: 1996-03-01
; EARLIER APPLICATION NUMBER: P4411402.8
; EARLIER FILING DATE: 1994-03-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 4097
; TYPE: DNA
; ORGANISM: Cytomegalovirus
US-09-123-708-5

Query Match 20.0%; Score 51.6; DB 3; Length 4097;
Best Local Similarity 62.3%; Pred. No. 7.5e-05;
Matches 81; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGAAGCAGCAGCTTCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 760 CAGCGCGCGCGCGCGCGAGACTTCGGAATCTGGAACAGCCAGCTGGTGGCTACGCA 819

Qy 61 GGCTACCATGTCAGATGCGCAGCATCAGAGGGGACCCCTGCCAACGTGGAAATTCACCTCAG 120
Db 820 GGCTACAGACAGCAGGATGGCTCTGTGCGTGGGGACCCAGCCACGCTGGAGATCACCGAG 879
```

QY 121 GTACCGGCC 130  
DB 880 CTCTGCATCC 889

RESULT 33  
US-09-123-624-5  
; Sequence 5, Application US/09123624  
; Patent No. 6149936  
; GENERAL INFORMATION:  
; APPLICANT: SCHRAEDER, Jurgen  
; APPLICANT: CODECKE, Axel  
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC  
; TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS  
; FILE REFERENCE: 511169-2004  
; CURRENT APPLICATION NUMBER: US/09/123,624  
; CURRENT FILING DATE: 1998-07-28  
; PRIOR APPLICATION NUMBER: 08/553,503  
; PRIOR FILING DATE: 1996-03-01  
; PRIOR APPLICATION NUMBER: 4411402.8  
; PRIOR FILING DATE: 1994-03-31  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 4097  
; TYPE: DNA  
; ORGANISM: Bos taurus  
US-09-123-624-5

Query Match 20.0%; Score 51.6; DB 3; Length 4097;  
Best Local Similarity 62.3%; Pred. No. 7.5e-05;  
Matches 81; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCAGCTTCGGGGTGTGGAATGCTCAGCTATCGCTATGCT 60  
DB 760 CAGCGGCGCCGCGCGGAGACTTCGGATCTGGAACAGCCAGCTGGTGGCTACGCA 819  
QY 61 GGTACAGATGCCAGATGCGCAGCATCAGAGGGGACCTGCCAAGCTGGAATTCATCTAG 120  
DB 820 GGCTACAGACAGCAGGATGCTGTGGTGGGGGCCAGCCAGCAACGTGGAGATCACGGAG 879

QY 121 GTACCGGCC 130  
DB 880 CTCTGCATCC 889

RESULT 34  
US-08-809-917-25  
; Sequence 25, Application US/08809917  
; Patent No. 6689557  
; GENERAL INFORMATION:  
; APPLICANT:  
; APPLICANT: APPLICANT  
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES  
; TITLE OF INVENTION: ASSOCIATED WITH LONG-TERM MEMORY  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/809,917  
; FILING DATE:  
; CLASSIFICATION:

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/13198  
; FILING DATE:  
; APPLICATION NUMBER: US 08/361,063  
; FILING DATE: 21-DEC-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/319,866  
; FILING DATE: 07-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia  
; REGISTRATION NUMBER: 32,227  
; REFERENCE/DOCKET NUMBER: CSHL94-03A2 PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 861-6240  
; TELEFAX: (617) 861-9540  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4491 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-809-917-25

Query Match 20.0%; Score 51.6; DB 3; Length 4491;  
Best Local Similarity 63.9%; Pred. No. 7.6e-05;  
Matches 78; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCAGCTTCGGGGTGTGGAATGCTCAGCTATCGCTATGCT 60  
DB 1320 CAACGCACAGATGCCAAGCATGATTATCGCATTTGGGAATAACCAATTAATATCTTATGCC 1379  
QY 61 GGTACAGATGCCAGATGCGCAGCATCAGAGGGGACCTGCCAAGCTGGAATTCATCTAG 120  
DB 1380 GGCTACAGACAGCAGGATGCTGTGGTGGGGGCCAGCCAGCAACGTGGAGATCACGGAG 1439

QY 121 GT 122  
DB 1440 GT 1441

RESULT 35  
US-09-419-371-25  
; Sequence 25, Application US/09419371  
; Patent No. 6890516  
; GENERAL INFORMATION:  
; APPLICANT: Tully, Timothy P.  
; APPLICANT: Yin, Jerry Chi-Ping  
; TITLE OF INVENTION: Cloning and Characterizing of Genes  
; TITLE OF INVENTION: Associated With Long-Term Memory  
; FILE REFERENCE: CSHL94-03A3Z  
; CURRENT APPLICATION NUMBER: US/09/419,371  
; CURRENT FILING DATE: 1999-10-14  
; PRIOR APPLICATION NUMBER: 08/809,917  
; PRIOR FILING DATE: 1997-07-07  
; PRIOR APPLICATION NUMBER: PCT/US95/13198  
; PRIOR FILING DATE: 1995-10-06  
; PRIOR APPLICATION NUMBER: 08/361,063  
; PRIOR FILING DATE: 1994-12-21  
; PRIOR APPLICATION NUMBER: 08/319,866  
; PRIOR FILING DATE: 1994-10-07  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 25  
; LENGTH: 4491  
; TYPE: DNA  
; ORGANISM: Drosophila  
US-09-419-371-25

Query Match 20.0%; Score 51.6; DB 3; Length 4491;  
Best Local Similarity 63.9%; Pred. No. 7.6e-05;  
Matches 78; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

```
Qy 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGTGTGGAAATGCTCAGCTCAGCTCCGCTATGCT 60
Db 1320 CAAGCCACAGATGCCAAGCATGATTATCGCATTTGGAATAACCAATTAATCTTATGCCC 1379

Qy 61 GGCTACCAGATGCCAGATGGCAGCAGCAGAGGGACCCCTGCCAACGCTGGAATTCACATCAG 120
Db 1380 GGCTACAGCAGCGCGGATGGAAAAATCATTGGCGATCCCATGAATGTGGAGTTTACAGAG 1439

Qy 121 GT 122
Db 1440 GT 1441

RESULT 36
US-07-908-245-1
; Sequence 1, Application US/07908245
; Patent No. 5498539
; GENERAL INFORMATION:
; APPLICANT: Harrison, David G.
; APPLICANT: Alexander, R. Wayne
; APPLICANT: Murphy, T.J.
; APPLICANT: Nishida, Ken'ichi
; TITLE OF INVENTION: Endothelial Nitric Oxide Synthase
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kilpatrick & Cody
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: U.S.
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/908,245
; FILING DATE: 19920702
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: EMU 111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-815-6508
; TELEFAX: 404-815-6555
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4089 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bovine
; TISSUE TYPE: Aorta
; CELL TYPE: Endothelial
US-07-908-245-1

Query Match 19.4%; Score 50; DB 2; Length 4089;
Best Local Similarity 61.5%; Pred. No. 0.00021;
Matches 80; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAGCACTTCGGGTGTGGAAATGCTCAGCTCAGCTCCGCTATGCT 60
Db 732 CAGCGCGCCCGCGGAGTCTTCGGATCTGGAAACAGCAGCTGGTGGCTACGCA 791

Qy 61 GGCTACCAGATGCCAGATGGCAGCAGCAGAGGGACCCCTGCCAACGCTGGAATTCACATCAG 120
Db 792 GGCTACAGCAGCAGGATGGCTCTGTGCTGGGGACCCAGGCCAATGTGGAGATCACGGAG 851
```

```
Qy 121 GTACCCGGCC 130
Db 852 CTCTGCATCC 861
```

```
RESULT 37
US-08-258-261B-17/C
; Sequence 17, Application US/08258261B
; Patent No. 5639949
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James M.
; APPLICANT: Beck, James Joseph
; APPLICANT: Hill, Dwight Steven
; APPLICANT: Ryals, John Andrew
; APPLICANT: Gaffney, Thomas Deane
; APPLICANT: Lam, Stephen Ting
; APPLICANT: Hammer, Phillip E.
; APPLICANT: Uknes, Scott Joseph
; TITLE OF INVENTION: Genes for the synthesis of
; TITLE OF INVENTION: antipathogenic substances
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/258,261B
; FILING DATE: 08-JUN-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/457,205
; FILING DATE: 01-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8614
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4603 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 230..1594
; OTHER INFORMATION: /gene= "phz1"
; OTHER INFORMATION: /label= ORF1
; OTHER INFORMATION: /note= "Open Reading Frame #1 for DNA sequence"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1598..2758
; OTHER INFORMATION: /gene= "phz2"
; OTHER INFORMATION: /label= ORF2
; OTHER INFORMATION: /note= "Open Reading Frame #2 for DNA sequence"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2764..3597
; OTHER INFORMATION: /gene= "phz3"
; OTHER INFORMATION: /label= ORF3
```



STATE: NY  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/08/457,342  
APPLICATION NUMBER: US/08/457,342  
FILING DATE: 01-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/457,205  
FILING DATE: 01-JUN-1995  
APPLICATION NUMBER: 08/258,261  
FILING DATE: 08-Jun-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129  
REFERENCE/DOCKET NUMBER: CGC 1506/CIP3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8614  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4603 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 230..1594  
OTHER INFORMATION: /gene= "phz1"  
OTHER INFORMATION: /label= ORF1  
OTHER INFORMATION: /note= "Open Reading Frame #1 for DNA sequence"  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1598..2758  
OTHER INFORMATION: /gene= "phz2"  
OTHER INFORMATION: /label= ORF2  
OTHER INFORMATION: /note= "Open Reading Frame #2 for DNA sequence"  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 2764..3597  
OTHER INFORMATION: /gene= "phz3"  
OTHER INFORMATION: /label= ORF3  
OTHER INFORMATION: /note= "Open Reading Frame #3 for DNA sequence"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 3597..4262  
OTHER INFORMATION: /label= ORF4  
OTHER INFORMATION: /note= "Open Reading Frame #4 of DNA sequence. This information is repeated in SEQ ID NO:21 due to overlapping ORFs."  
OTHER INFORMATION:  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..4603  
OTHER INFORMATION: /note= "Four open reading frames"  
OTHER INFORMATION:  
OTHER INFORMATION: Example 18 of the specification."  
US-08-457-342-17  
Query Match 13.7%; Score 35.4; DB 2; Length 4603;  
Best Local Similarity 57.8%; Pred.No.2.4;  
Matches 63; Conservative 0; Mismatches 46; Indels 0; Gaps 0;  
Qy 1 CAGCGAGTGATGCGACGACGACTTCGGGTGTGGAATGCTCAGCTATCCGCTATGCT 60  
169 CACGCGAGTAATGCTTTCGCCAGGGGTTTCAGCGCGGGTTCGCACAGGGCTTTTGTAGCGGCT 110  
Qy 61 GGCTACCAGATGCCAGATGCGCAGCATCAGAGGGGACCTGCGCAACGTGG 109

Db 109 GGCGACCTGATGCGAGCGCGCGCATCGGAAGCGCACTCGCTGACGCTCG 61  
RESULT 40  
US-08-457-646A-17/c  
Sequence 17, Application US/08457646A  
Patent No. 5679560  
GENERAL INFORMATION:  
APPLICANT: Schupp, Thomas  
APPLICANT: Ligon, James M.  
APPLICANT: Beck, James Joseph  
APPLICANT: Hill, Dwight Steven  
APPLICANT: Ryals, John Andrew  
APPLICANT: Gaffney, Thomas Deane  
APPLICANT: Lam, Stephen Ting  
APPLICANT: Hammer, Phillip E.  
APPLICANT: Uknes, Scott Joseph  
TITLE OF INVENTION: Genes for the synthesis of  
antipathogenic substances  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ciba-Geigy Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: NY  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/08/457,646A  
APPLICATION NUMBER: US/08/457,646A  
FILING DATE: 01-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/457,205  
FILING DATE: 01-JUN-1995  
APPLICATION NUMBER: 08/258,261  
FILING DATE: 08-Jun-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129  
REFERENCE/DOCKET NUMBER: CGC 1506/CIP3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8614  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4603 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 230..1594  
OTHER INFORMATION: /gene= "phz1"  
OTHER INFORMATION: /label= ORF1  
OTHER INFORMATION: /note= "Open Reading Frame #1 for DNA sequence"  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1598..2758  
OTHER INFORMATION: /gene= "phz2"  
OTHER INFORMATION: /label= ORF2  
OTHER INFORMATION: /note= "Open Reading Frame #2 for DNA sequence"  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 2764..3597  
OTHER INFORMATION: /gene= "phz3"  
OTHER INFORMATION: /label= ORF3  
OTHER INFORMATION: /note= "Open Reading Frame #3 for DNA sequence"  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 3597..4262  
OTHER INFORMATION: /label= ORF4  
OTHER INFORMATION: /note= "Open Reading Frame #4 of DNA sequence. This information is repeated in SEQ ID NO:21 due to overlapping ORFs."  
OTHER INFORMATION:  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..4603  
OTHER INFORMATION: /note= "Four open reading frames"  
OTHER INFORMATION:  
OTHER INFORMATION: Example 18 of the specification."  
US-08-457-342-17  
Query Match 13.7%; Score 35.4; DB 2; Length 4603;  
Best Local Similarity 57.8%; Pred.No.2.4;  
Matches 63; Conservative 0; Mismatches 46; Indels 0; Gaps 0;  
Qy 1 CAGCGAGTGATGCGACGACGACTTCGGGTGTGGAATGCTCAGCTATCCGCTATGCT 60  
169 CACGCGAGTAATGCTTTCGCCAGGGGTTTCAGCGCGGGTTCGCACAGGGCTTTTGTAGCGGCT 110  
Qy 61 GGCTACCAGATGCCAGATGCGCAGCATCAGAGGGGACCTGCGCAACGTGG 109



```

;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3597..4262
; OTHER INFORMATION: /label= ORF4
; OTHER INFORMATION: /note= "Open Reading Frame #4 of DNA sequence. This information
; OTHER INFORMATION: is repeated in SEQ ID NO:21 due to overlapping ORFs."
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..4503
; OTHER INFORMATION: /note= "Four open reading frames
; OTHER INFORMATION:
; OTHER INFORMATION: Example 18 of the specification."
;
; US-08-457-646A-17

```

Query Match	13.7%	Score 35.4;	DB 2;	Length 4603;
Best Local Similarity	57.8%;	Pred. No. 2.4;		
Matches	63;	Conservative 0;	Mismatches 46;	Indels 0; Gaps 0;

  

Qy	1	CAGCGAGTGATGGCAAGCA	CGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT	60
Db	169	CACGCGAGTAATGCTTGTCCAGGGTTCAGGCGGGGTGCGACAGGCTTTGTGTAGCGGCT	110	
Qy	61	GGCTACAGATGCCAGATGCGCAGCATCAGAGGGGACCTGCCAACGTGG	109	
Db	109	GGGCACCTGATGAGGCGCGGCGGATCGGAAGGGCACTCGCTCAGCTCG	61	

Search completed: December 13, 2005, 18:14:07  
Job time : 144 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 16:24:48 ; Search time 796 Seconds  
(without alignments)  
2680.276 Million cell updates/sec

Title: US-10-713-137-1

Perfect score: 258

Sequence: 1 cagcgagtgatggcaagca.....tgttccccagctgtgcatc 258

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	257.6	99.8	258	US-10-713-137-1	Sequence 1, Appli
2	256.8	99.5	55689	US-10-741-601-5684	Sequence 5684, Ap
3	256.8	99.5	55689	US-10-741-600-17734	Sequence 17734, A
4	200.6	77.8	201	US-10-741-601-19182	Sequence 19182, A
5	200.6	77.8	201	US-10-741-600-51219	Sequence 51219, A
6	200.2	77.6	201	US-10-741-601-19156	Sequence 19156, A
7	200.2	77.6	201	US-10-741-600-51193	Sequence 51193, A
8	191.2	74.1	201	US-10-741-601-19177	Sequence 19177, A
9	191.2	74.1	201	US-10-741-600-51214	Sequence 51214, A
10	120.4	46.7	1152	US-10-220-282A-3	Sequence 3, Appli
11	120.4	46.7	3462	US-10-220-282A-1	Sequence 1, Appli
12	120.4	46.7	3855	US-10-210-682-1	Sequence 1, Appli
13	120.4	46.7	4062	US-10-305-720-1478	Sequence 1478, Ap
14	120.4	46.7	4062	US-10-631-467-38	Sequence 38, Appl
15	120.4	46.7	4062	US-10-631-467-155	Sequence 155, App
16	120.4	46.7	4133	US-10-741-601-228	Sequence 228, App
17	120.4	46.7	4133	US-10-741-600-621	Sequence 621, App
18	120.4	46.7	4145	US-10-182-049-3	Sequence 3, Appli
19	120.4	46.7	4145	US-10-182-049-10	Sequence 10, Appl
20	120.4	46.7	4164	US-10-641-643-1407	Sequence 1407, App
21	120.4	46.7	4221	US-10-741-601-229	Sequence 229, App
22	120.4	46.7	4221	US-10-741-600-622	Sequence 622, App
23	118.8	46.0	4150	US-10-688-845-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1

US-10-713-137-1  
; Sequence 1, Application US/10713137  
; Publication No. US20050106573A1  
; GENERAL INFORMATION:  
; APPLICANT: Pasha, Abdul Qadar Mohammad  
; APPLICANT: Ahsan, Aarif  
; TITLE OF INVENTION: A method of detection of predisposition  
; FILE REFERENCE: to high altitude pulmonary edema (HAPE)  
; FILE REFERENCE: 09755-0018US1  
; CURRENT APPLICATION NUMBER: US/10/713,137  
; CURRENT FILING DATE: 2003-11-13  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 258  
; TYPE: DNA  
; ORGANISM: Human  
US-10-713-137-1

Query Match 99.8%; Score 257.6; DB 9; Length 258;  
Best Local Similarity 100.0%; Pred. No. 1.3e-70;  
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CAGCGAGTGATGGCAAGCAGCTTCGGGTGTGGATGCTCAGCTCATCGCTATGCT	60
DB	1		60
QY	61	GGCTACCAATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACCTGGAAATTCCTCAG	120
DB	61		120
QY	121	GTATCCCGGGCCCAAGCTCAGCCRCGGGCCATTTGGGGGGGGAGCCCCCGTGTGAGCGAGTG	180
DB	121		180
QY	181	ACAGAGTGAGGCCAGAGAGACACGACGCCCCGGGTTCACAGCTCAGAGGGCCCTCTT	240
DB	181		240
QY	241	GTTCCTCCAGCTGTGCATC	258
DB	241		258

RESULT 2



```
Query Match 77.8%; Score 200.6; DB 8; Length 201;
Best Local Similarity 100.0%; Pred. No. 8.6e-53;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 TCAGCTCATCCGCTATGCTGCTACCAAGATGCCAGATGGCAGATGCAGAGGGACCCCTGC 101
Db 1 TCAGCTCATCCGCTATGCTGCTACCAAGATGCCAGATGGCAGATGCAGAGGGACCCCTGC 60

Qy 102 CAAGTGAATTAATCACTAGGTACCGGCCAGCCTCAGCCCGCCATTGGGGCGGGGA 161
Db 61 CAAGTGAATTAATCACTAGGTACCGGCCAGCCTCAGCCCGCCATTGGGGCGGGGA 120

Qy 162 GCCCGTGGTGGAGGAGTGCAGAGTGGAGCCAGAGGAGACACGACGCCCGGCTTACA 221
Db 121 GCCCGTGGTGGAGGAGTGCAGAGTGGAGCCAGAGGAGACACGACGCCCGGCTTACA 180

Qy 222 GACTCACAGGGCCCGCTTTGT 242
Db 181 GACTCACAGGGCCCGCTTTGT 201

RESULT 6
US-10-741-601-19156
; Sequence 19156, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19156
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-741-601-19156

Query Match 77.6%; Score 200.2; DB 7; Length 201;
Best Local Similarity 99.0%; Pred. No. 1.2e-52;
Matches 199; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 44 AGCTCATCCGCTATGCTGCTACCAAGATGCCAGATGGCAGATGCAGAGGGACCCCTGCCA 103
Db 1 AGCTCATCCGCTATGCTGCTACCAAGATGCCAGATGGCAGATGCAGAGGGACCCCTGCCA 60

Qy 104 AGCTGGAATTAATCACTAGGTACCGGCCAGCCTCAGCCCGCCATTGGGGCGGGAGC 163
Db 61 AGCTGGAATTAATCACTAGGTACCGGCCAGCCTCAGCCCGCCATTGGGGCGGGAGC 120

Qy 164 CCCGTGGTGGAGGAGTGCAGAGTGGAGCCAGAGGAGACACGACGCCCGGCTTACAGA 223
Db 121 CCCGTGGTGGAGGAGTGCAGAGTGGAGCCAGAGGAGACACGACGCCCGGCTTACAGA 180

Qy 224 CTCACAGGGCCCGCTTTGTTTC 244
Db 181 CTCACAGGGCCCGCTTTGTTTC 201

RESULT 7
US-10-741-600-51193
; Sequence 51193, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997

Query Match 77.8%; Score 200.6; DB 8; Length 201;
Best Local Similarity 100.0%; Pred. No. 8.6e-53;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 TCAGCTCATCCGCTATGCTGCTACCAAGATGCCAGATGGCAGATGCAGAGGGACCCCTGC 101
Db 1 TCAGCTCATCCGCTATGCTGCTACCAAGATGCCAGATGGCAGATGCAGAGGGACCCCTGC 60

Qy 102 CAAGTGAATTAATCACTAGGTACCGGCCAGCCTCAGCCCGCCATTGGGGCGGGGA 161
Db 61 CAAGTGAATTAATCACTAGGTACCGGCCAGCCTCAGCCCGCCATTGGGGCGGGGA 120

Qy 162 GCCCGTGGTGGAGGAGTGCAGAGTGGAGCCAGAGGAGACACGACGCCCGGCTTACA 221
Db 121 GCCCGTGGTGGAGGAGTGCAGAGTGGAGCCAGAGGAGACACGACGCCCGGCTTACA 180

Qy 222 GACTCACAGGGCCCGCTTTGT 242
Db 181 GACTCACAGGGCCCGCTTTGT 201

RESULT 8
US-10-741-601-19177
; Sequence 19177, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19177
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-741-601-19177

Query Match 74.1%; Score 191.2; DB 7; Length 201;
Best Local Similarity 99.0%; Pred. No. 7.5e-50;
Matches 190; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 67 CAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAGGTACCC 126
Db 1 CAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAGGTACCC 60

Qy 127 GSCCCAGCCTCAGCCRCGCCGCTTTGGGGCGGGAGACCCCGTGTGAGCAGTGAAGAG 186
Db 61 GSCCCAGCCTCAGCCRCGCCGCTTTGGGGCGGGAGACCCCGTGTGAGCAGTGAAGAG 120

Qy 187 TGGAGCCAGAGGAGACACGACGCCCGGCTTACAGATCAGAGGGCCCGCTTTGTTCC 246
Db 121 TGGAGCCAGAGGAGACACGACGCCCGGCTTACAGATCAGAGGGCCCGCTTTGTTCC 180

Qy 247 CAGCTGTGCATC 258
Db 181 CAGCTGTGCATC 192

RESULT 9
US-10-741-600-51214
; Sequence 51214, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51193
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-51193

Query Match 77.6%; Score 200.2; DB 8; Length 201;
Best Local Similarity 99.0%; Pred. No. 1.2e-52;
Matches 199; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 44 AGCTCATCCGCTATGCTGCTACCAAGATGCCAGATGGCAGATGCAGAGGGACCCCTGCCA 103
Db 1 AGCTCATCCGCTATGCTGCTACCAAGATGCCAGATGGCAGATGCAGAGGGACCCCTGCCA 60

Qy 104 ACGTGGAAATTAATCACTAGGTACCGGCCAGCCTCAGCCCGCCATTGGGGCGGGAGC 163
Db 61 ACGTGGAAATTAATCACTAGGTACCGGCCAGCCTCAGCCCGCCATTGGGGCGGGAGC 120

Qy 164 CCCGTGGTGGAGGAGTGCAGAGTGGAGCCAGAGGAGACACGACGCCCGGCTTACAGA 223
Db 121 CCCGTGGTGGAGGAGTGCAGAGTGGAGCCAGAGGAGACACGACGCCCGGCTTACAGA 180

Qy 224 CTCACAGGGCCCGCTTTGTTTC 244
Db 181 CTCACAGGGCCCGCTTTGTTTC 201
```

```
RESULT 8
US-10-741-601-19177
; Sequence 19177, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19177
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-741-601-19177
```

```
Query Match 74.1%; Score 191.2; DB 7; Length 201;
Best Local Similarity 99.0%; Pred. No. 7.5e-50;
Matches 190; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 67 CAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAGGTACCC 126
Db 1 CAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAGGTACCC 60

Qy 127 GSCCCAGCCTCAGCCRCGCCGCTTTGGGGCGGGAGACCCCGTGTGAGCAGTGAAGAG 186
Db 61 GSCCCAGCCTCAGCCRCGCCGCTTTGGGGCGGGAGACCCCGTGTGAGCAGTGAAGAG 120

Qy 187 TGGAGCCAGAGGAGACACGACGCCCGGCTTACAGATCAGAGGGCCCGCTTTGTTCC 246
Db 121 TGGAGCCAGAGGAGACACGACGCCCGGCTTACAGATCAGAGGGCCCGCTTTGTTCC 180

Qy 247 CAGCTGTGCATC 258
Db 181 CAGCTGTGCATC 192
```

```
RESULT 9
US-10-741-600-51214
; Sequence 51214, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
```

; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; FILE REFERENCE: CU001499  
; CURRENT APPLICATION NUMBER: US/10/741.600  
; NUMBER OF SEQ ID NOS: 73997  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 51214  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-741-600-51214

Query Match 74.1%; Score 191.2; DB 8; Length 201;  
Best Local Similarity 99.0%; Pred. No. 7.5e-50;  
Matches 190; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 67 CAGATGCCAGATGCCAGCATCAGAGGGGACCTGCCAACGTGGAATTCACCTAGGTACCC 126  
Db 1 CAGATGCCAGATGCCAGCATCAGAGGGGACCTGCCAACGTGGAATTCACCTAGGTACCC 60  
QY 127 GGCCCGACCTCAGCCCGCCATTGGGGGGGAGCCCGTGGTGAGCGAGTGACAGAG 186  
Db 61 GGCCCGACCTCAGCCCGCCATTGGGGGGGAGCCCGTGGTGAGCGAGTGACAGAG 120  
QY 187 TGAGGCCAGAGAGACACGCGCGGGTTACAGACTCACAGGCGCGTCTTGTTCCTC 246  
Db 121 TGAGGCCAGAGAGACACGCGCGGGTTACAGACTCACAGGCGCGTCTTGTTCCTC 180  
QY 247 CAGCTGTGCATC 258  
Db 181 CAGCTGTGCATC 192

RESULT 10  
US-10-220-282A-3  
; Sequence 3, Application US/10220282A  
; Publication No. US20040053323A1  
; GENERAL INFORMATION:  
; APPLICANT: ISHII, YOSHINORI  
; APPLICANT: UEDA, YOSHIKO  
; APPLICANT: IWAMI, MORITA  
; APPLICANT: ARAKAWA, HIROYUKI  
; APPLICANT: NOTSU, YOSHITADA  
; TITLE OF INVENTION: SCREENING METHODS FOR INHIBITORS OF INDUCIBLE NITROGEN OXIDE SYNT  
; FILE REFERENCE: 227899USOPCT  
; CURRENT APPLICATION NUMBER: US/10/220,282A  
; CURRENT FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: PCT/JP01/01865  
; PRIOR FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: JP 2000-72480  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 3  
; LENGTH: 1152  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1152)  
; OTHER INFORMATION:  
US-10-220-282A-3

Query Match 46.7%; Score 120.4; DB 7; Length 1152;  
Best Local Similarity 99.2%; Pred. No. 1.1e-27;  
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
Db 379 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 438

QY 61 GGCTACCAGATGCCAGATGCCAGCATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 120  
Db 439 GGCTACCAGATGCCAGATGCCAGCATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 498  
QY 121 GT 122  
Db 499 CT 500

RESULT 11  
US-10-220-282A-1  
; Sequence 1, Application US/10220282A  
; Publication No. US20040053323A1  
; GENERAL INFORMATION:  
; APPLICANT: ISHII, YOSHINORI  
; APPLICANT: UEDA, YOSHIKO  
; APPLICANT: IWAMI, MORITA  
; APPLICANT: ARAKAWA, HIROYUKI  
; APPLICANT: NOTSU, YOSHITADA  
; TITLE OF INVENTION: SCREENING METHODS FOR INHIBITORS OF INDUCIBLE NITROGEN OXIDE SYNT  
; FILE REFERENCE: 227899USOPCT  
; CURRENT APPLICATION NUMBER: US/10/220,282A  
; CURRENT FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: PCT/JP01/01865  
; PRIOR FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: JP 2000-72480  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 1  
; LENGTH: 3462  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3462)  
; OTHER INFORMATION:  
US-10-220-282A-1

Query Match 46.7%; Score 120.4; DB 7; Length 3462;  
Best Local Similarity 99.2%; Pred. No. 1.1e-27;  
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
Db 745 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 804

QY 61 GGCTACCAGATGCCAGATGCCAGCATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 120  
Db 805 GGCTACCAGATGCCAGATGCCAGCATCAGAGGGGACCTGCCAACGTGGAATTCACCTCAG 864  
QY 121 GT 122  
Db 865 CT 866

RESULT 12  
US-10-210-682-1  
; Sequence 1, Application US/10210682  
; Publication No. US20030092039A1  
; GENERAL INFORMATION:  
; APPLICANT: Olson-Munoz, Marilyn C.  
; APPLICANT: Donald, Glen  
; TITLE OF INVENTION: Screening Nutraceuticals  
; FILE REFERENCE: FORS-07289  
; CURRENT APPLICATION NUMBER: US/10/210,682  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: 60/309,279  
; PRIOR FILING DATE: 2001-08-01  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patentin version 3.1

```
; SEQ ID NO 1
; LENGTH: 3855
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-210-682-1

Query Match          46.7%; Score 120.4; DB 5; Length 3855;
Best Local Similarity 80.3%; Pred. No. 1.1e-27;
Matches 98; Conservative 23; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 939 CAGCGGAGUGAUGGCAAGCAGACUUCGCGGUGUGAAUGCUCAGCUCAUCGCUAUGCU 998
QY 61 GGCTACCAAGTCCAGATGCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
Db 999 GGCURACCAAGUAGCCAGUAGGCGACUAGAGGGGACCCUGCCAAAGUGGAAUUCACUCAG 1058
QY 121 GT 122
Db 1059 CU 1060

RESULT 13
US-10-305-720-1478
; Sequence 1478, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1478
; TYPE: DNA
; LENGTH: 4062
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g951320
US-10-305-720-1478

Query Match          46.7%; Score 120.4; DB 6; Length 4062;
Best Local Similarity 99.2%; Pred. No. 1.1e-27;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 850 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 909
QY 61 GGCTACCAAGTCCAGATGCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
Db 910 GGCTACCAAGTCCAGATGCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 969
QY 121 GT 122
Db 970 CT 971

RESULT 14
US-10-631-467-38
; Sequence 38, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive P
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
```

```
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 38
; LENGTH: 4062
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-631-467-38

Query Match          46.7%; Score 120.4; DB 9; Length 4062;
Best Local Similarity 99.2%; Pred. No. 1.1e-27;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 850 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 909
QY 61 GGCTACCAAGTCCAGATGCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
Db 910 GGCTACCAAGTCCAGATGCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 969
QY 121 GT 122
Db 970 CT 971

RESULT 15
US-10-631-467-155
; Sequence 155, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive i
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 155
; LENGTH: 4062
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-631-467-155

Query Match          46.7%; Score 120.4; DB 9; Length 4062;
Best Local Similarity 99.2%; Pred. No. 1.1e-27;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 850 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 909
QY 61 GGCTACCAAGTCCAGATGCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
Db 910 GGCTACCAAGTCCAGATGCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 969
QY 121 GT 122
Db 970 CT 971

RESULT 16
US-10-741-601-228
; Sequence 228, Application US/10741601
```

```
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741.601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 228
; LENGTH: 4133
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-228

Query Match          46.7%; Score 120.4; DB 7; Length 4133;
Best Local Similarity 99.2%; Pred. No. 1.1e-27;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 939 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 998
QY 61 GGCTACCAGATGCCAGATGCCAGATCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
Db 999 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 1058
QY 121 GT 122
Db 1059 CT 1060

RESULT 17
US-10-741-600-621
; Sequence 621, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741.600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 621
; LENGTH: 4133
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-621

Query Match          46.7%; Score 120.4; DB 8; Length 4133;
Best Local Similarity 99.2%; Pred. No. 1.1e-27;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 939 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 998
QY 61 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
Db 999 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 1058
QY 121 GT 122
Db 1059 CT 1060

RESULT 18
US-10-182-049-3
; Sequence 3, Application US/10182049
; Publication No. US20050113322A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF INDUCIBLE NITRIC OXIDE SYNTHASE EXPRESSION
; FILE REFERENCE: RTSP-0360
; CURRENT APPLICATION NUMBER: US/10/182,049
; CURRENT FILING DATE: 2002-07-27
; PRIOR APPLICATION NUMBER: 09/490,208
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 3
; LENGTH: 4145
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (207)...(3668)
US-10-182-049-3

Query Match          46.7%; Score 120.4; DB 9; Length 4145;
Best Local Similarity 99.2%; Pred. No. 1.1e-27;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 951 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1010
QY 61 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
Db 1011 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 1070
QY 121 GT 122
Db 1071 CT 1072

RESULT 19
US-10-182-049-10
; Sequence 10, Application US/10182049
; Publication No. US20050113322A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF INDUCIBLE NITRIC OXIDE SYNTHASE EXPRESSION
; FILE REFERENCE: RTSP-0360
; CURRENT APPLICATION NUMBER: US/10/182,049
; CURRENT FILING DATE: 2002-07-27
; PRIOR APPLICATION NUMBER: 09/490,208
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 10
; LENGTH: 4145
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)...(4110)
US-10-182-049-10

Query Match          46.7%; Score 120.4; DB 9; Length 4145;
Best Local Similarity 99.2%; Pred. No. 1.1e-27;
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db 951 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1010
QY 61 GGCTACCAGATGCCAGATGCCAGATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
```



Db 1011 GGCTACCATGCGCAGATGCGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTCAG 1070

QY 121 GT 122  
Db 1071 CT 1072

RESULT 20

US-10-641-643-1407  
; Sequence 1407, Application US/10641643  
; Publication No. US20040077003A1  
; GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.  
; Susan G. Stuart  
; Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL  
; GENE EXPRESSION

; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO

; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/641,643  
; FILING DATE: 14-Aug-2003  
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: <Unknown>

; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:

; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166

; INFORMATION FOR SEQ ID NO: 1407:  
; SEQUENCE CHARACTERISTICS:

; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: g441452

; SEQUENCE DESCRIPTION: SEQ ID NO: 1407 :  
US-10-641-643-1407

Query Match 46.7%; Score 120.4; DB 7; Length 4164;  
Best Local Similarity 99.2%; Pred. No. 1.1e-27;  
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
Db 970 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1029

QY 61 GGCTACCATGCGCAGATGCGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTCAG 120  
Db 1030 GGCTACCATGCGCAGATGCGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTCAG 1089

QY 121 GT 122  
Db 1090 CT 1091

RESULT 21

US-10-741-601-229  
; Sequence 229, Application US/10741601  
; Publication No. US20040166519A1  
; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; STENOSIS, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001500  
; CURRENT APPLICATION NUMBER: US/10/741,601  
; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 26415  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 229

; LENGTH: 4221  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-10-741-601-229

Query Match 46.7%; Score 120.4; DB 7; Length 4221;  
Best Local Similarity 99.2%; Pred. No. 1.1e-27;  
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
Db 1009 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1068

QY 61 GGCTACCATGCGCAGATGCGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTCAG 120  
Db 1069 GGCTACCATGCGCAGATGCGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTCAG 1128

QY 121 GT 122  
Db 1129 CT 1130

RESULT 22

US-10-741-600-622  
; Sequence 622, Application US/10741600  
; Publication No. US20050026169A1  
; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001499  
; CURRENT APPLICATION NUMBER: US/10/741,600  
; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 73997  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 622

; LENGTH: 4221  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-10-741-600-622

Query Match 46.7%; Score 120.4; DB 8; Length 4221;  
Best Local Similarity 99.2%; Pred. No. 1.1e-27;  
Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
Db 1009 CAGCGGAGTGATGGCAAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 1068

QY 61 GGCTACCATGCGCAGATGCGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTCAG 120  
Db 1069 GGCTACCATGCGCAGATGCGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTCAG 1128

QY 121 GT 122  
Db 1129 CT 1130

RESULT 23

```
US-10-688-845-37
; Sequence 37, Application US/10688845
; Publication No. US20040247578A1
; GENERAL INFORMATION:
; APPLICANT: Lotze, Michael T
; APPLICANT: Tahara, Hideaki
; TITLE OF INVENTION: Methods And Reagents For Inducing Immunity
; FILE REFERENCE: UPT-004
; CURRENT APPLICATION NUMBER: US/10/688,845
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/418,865
; PRIOR FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 4150
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-688-845-37

Query Match      46.0%; Score 118.8; DB 8; Length 4150;
Best Local Similarity 98.4%; Pred. No. 3.5e-27;
Matches 120; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGCGAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 979 CAGCGGAGTGATGCGAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCACTATGCT 1038
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGGAATTCACCTCAG 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 1039 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGGAATTCACCTCAG 1098
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 121 GT 122
Db |
Qy 1099 CT 1100
Db |

RESULT 24
US-10-929-182-33
; Sequence 33, Application US/10929182
; Publication No. US20050064483A1
; GENERAL INFORMATION:
; APPLICANT: Zang, Jingwu
; APPLICANT: Hong, Jian
; TITLE OF INVENTION: Gene Expression Profiling Technology for Treatment Evaluation of
; FILE REFERENCE: Multiple Sclerosis
; FILE REFERENCE: HO-P02859US1
; CURRENT APPLICATION NUMBER: US/10/929,182
; CURRENT FILING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: US 60/498,731
; PRIOR FILING DATE: 2003-08-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33
; LENGTH: 3444
; TYPE: DNA
; ORGANISM: HUMAN
US-10-929-182-33

Query Match      36.1%; Score 93.2; DB 9; Length 3444;
Best Local Similarity 85.2%; Pred. No. 3.6e-19;
Matches 104; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 736 CAGCGGAACGATGGAGGACATGACTTCCGGATCTGGAATTCAGATCTCCAGCTCATCCGCTACGCT 795
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGGAATTCACCTCAG 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 796 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGGAATTCACCTCAG 855
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 121 GT 122
Db |

US-10-688-845-37
; Sequence 37, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 123
; LENGTH: 3690
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (256)..(3690)
; OTHER INFORMATION:
US-09-870-759-123

Query Match      35.5%; Score 91.6; DB 3; Length 3690;
Best Local Similarity 84.4%; Pred. No. 1.1e-18;
Matches 103; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 982 CAGCGGAGTGACGGCAACATGACTTCAGGCTCTGGAATTCACAGCTCATCCGCTACGCT 1041
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 61 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGGAATTCACCTCAG 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 1042 GGCTACCAGATGCCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGGAATTCACCTCAG 1101
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 121 GT 122
Db |
Qy 1102 TT 1103
Db |

RESULT 26
US-09-751-708A-123
; Sequence 123, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 123
; LENGTH: 3690
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (256)..(3690)
; OTHER INFORMATION:
US-09-751-708A-123

Query Match      35.5%; Score 91.6; DB 3; Length 3690;
Best Local Similarity 84.4%; Pred. No. 1.1e-18;
Matches 103; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
```

Db 982 CAGCGGAGTGACGGCAACATGACTTCAGGCTCTGGAATTCACAGCTCATCCGGTACGCT 1041  
Qy 61 GGCTACCAAGATGCCAGATGCGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTCAG 120  
Db 1042 GGCTACCAAGATGCCAGATGCGCAGCATCAGAGGGGATGCTGCCACCTTGGAGTTACCCAG 1101  
Qy 121 GT 122  
Db 1102 TT 1103

RESULT 27  
US-10-428-817A-119  
; Sequence 119, Application US/10428817A  
; Publication No. US20040214783A1  
; GENERAL INFORMATION:  
; APPLICANT: TERMAN, David S  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE  
; FILE REFERENCE: 38373-189118  
; CURRENT APPLICATION NUMBER: US/10/428,817A  
; CURRENT FILING DATE: 2003-05-05  
; PRIOR APPLICATION NUMBER: US 60/378,988  
; PRIOR FILING DATE: 2002-05-08  
; PRIOR APPLICATION NUMBER: US 60/389,366  
; PRIOR FILING DATE: 2002-06-15  
; PRIOR APPLICATION NUMBER: US 60/406,697  
; PRIOR FILING DATE: 2002-08-28  
; PRIOR APPLICATION NUMBER: US 60/406,750  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US 60/415,310  
; PRIOR FILING DATE: 2002-10-01  
; PRIOR APPLICATION NUMBER: US 60/415,400  
; PRIOR FILING DATE: 2002-10-02  
; PRIOR APPLICATION NUMBER: US 60/438,686  
; PRIOR FILING DATE: 2003-01-09  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 119  
; LENGTH: 3690  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (256)...(3690)  
US-10-428-817A-119

Query Match 35.5%; Score 91.6; DB 8; Length 3690;  
Best Local Similarity 84.4%; Pred. No. 1.1e-18;  
Matches 103; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
Qy 1 CAGCGGAGTGATGGCAAGCAGCATCTCCGGGTGTGGAATGCTCAGCTCATCCGGTATGCT 60  
Db 982 CAGCGGAGTGACGGCAACATGACTTCAGGCTCTGGAATTCACAGCTCATCCGGTACGCT 1041  
Qy 61 GGCTACCAAGATGCCAGATGCGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTCAG 120  
Db 1042 GGCTACCAAGATGCCAGATGCGCAGCATCAGAGGGGATGCTGCCACCTTGGAGTTACCCAG 1101  
Qy 121 GT 122  
Db 1102 TT 1103

RESULT 28  
US-10-937-758A-100  
; Sequence 100, Application US/10937758A  
; Publication No. US20050112141A1  
; GENERAL INFORMATION:  
; APPLICANT: TERMAN, David S  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE  
; FILE REFERENCE: 650884  
; CURRENT APPLICATION NUMBER: US/10/937,758A

; CURRENT FILING DATE: 2004-09-08  
; PRIOR APPLICATION NUMBER: 09/650,884  
; PRIOR FILING DATE: 2000-08-30  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 100  
; LENGTH: 3690  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (256)...(3690)  
; OTHER INFORMATION:  
US-10-937-758A-100

Query Match 35.5%; Score 91.6; DB 9; Length 3690;  
Best Local Similarity 84.4%; Pred. No. 1.1e-18;  
Matches 103; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
Qy 1 CAGCGGAGTGATGGCAAGCAGCATCTCCGGGTGTGGAATGCTCAGCTCATCCGGTATGCT 60  
Db 982 CAGCGGAGTGACGGCAACATGACTTCAGGCTCTGGAATTCACAGCTCATCCGGTACGCT 1041  
Qy 61 GGCTACCAAGATGCCAGATGCGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTCAG 120  
Db 1042 GGCTACCAAGATGCCAGATGCGCAGCATCAGAGGGGATGCTGCCACCTTGGAGTTACCCAG 1101  
Qy 121 GT 122  
Db 1102 TT 1103

RESULT 29  
US-10-182-049-18  
; Sequence 18, Application US/10182049  
; Publication No. US20050113322A1  
; GENERAL INFORMATION:  
; APPLICANT: Isis Pharmaceuticals, Inc.  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: Lex M. Cowbert  
; TITLE OF INVENTION: ANTISENSE MODULATION OF INDUCIBLE NITRIC OXIDE SYNTHASE EXPRESSION  
; FILE REFERENCE: RTSP-0360  
; CURRENT APPLICATION NUMBER: US/10/182,049  
; CURRENT FILING DATE: 2002-07-27  
; PRIOR APPLICATION NUMBER: 09/490,208  
; PRIOR FILING DATE: 2000-01-24  
; NUMBER OF SEQ ID NOS: 182  
; SEQ ID NO 18  
; LENGTH: 3690  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (256)...(3690)  
US-10-182-049-18

Query Match 35.5%; Score 91.6; DB 9; Length 3690;  
Best Local Similarity 84.4%; Pred. No. 1.1e-18;  
Matches 103; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
Qy 1 CAGCGGAGTGATGGCAAGCAGCATCTCCGGGTGTGGAATGCTCAGCTCATCCGGTATGCT 60  
Db 982 CAGCGGAGTGACGGCAACATGACTTCAGGCTCTGGAATTCACAGCTCATCCGGTACGCT 1041  
Qy 61 GGCTACCAAGATGCCAGATGCGCAGCATCAGAGGGGACCCCTGCCAAGCTGGAATTCACCTCAG 120  
Db 1042 GGCTACCAAGATGCCAGATGCGCAGCATCAGAGGGGATGCTGCCACCTTGGAGTTACCCAG 1101  
Qy 121 GT 122  
Db 1102 TT 1103

RESULT 30  
US-10-631-467-966  
; Sequence 966, Application US/10631467  
; Publication No. US20050208496A1  
; GENERAL INFORMATION:  
; APPLICANT: Genox Research Inc.  
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive p  
; TITLE OF INVENTION: disease  
; FILE REFERENCE: 3462.1005-000  
; CURRENT APPLICATION NUMBER: US/10/631.467  
; CURRENT FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: JP 2003-077212  
; PRIOR FILING DATE: 2003-03-20  
; PRIOR APPLICATION NUMBER: JP 2002-229312  
; PRIOR FILING DATE: 2002-08-06  
; NUMBER OF SEQ ID NOS: 2086  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 966  
; LENGTH: 3991  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-631-467-966

Query Match 35.5%; Score 91.6; DB 9; Length 3991;  
Best Local Similarity 84.4%; Pred. No. 1.1e-18;  
Matches 103; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGCCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
Db 911 CAGCGGAGTGACGCGCAACATGACTTCAGGCTCTGGAATTCACAGCTCATCCGCTAGCT 970

Qy 61 GGCTACCAGATGCCAGATGCGAGCATCAGAGGGACCCCTGCCAACGTGGAATTCACCTCAG 120  
Db 971 GGCTACCAGATGCCGCGATGGCACCATCAGAGGGGATGCTGCCACCTTGGAGTTACCCAG 1030

Qy 121 GT 122  
Db 1031 TT 1032

RESULT 31  
US-10-631-467-1064  
; Sequence 1064, Application US/10631467  
; Publication No. US20050208496A1  
; GENERAL INFORMATION:  
; APPLICANT: Genox Research Inc.  
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive p  
; TITLE OF INVENTION: disease  
; FILE REFERENCE: 3462.1005-000  
; CURRENT APPLICATION NUMBER: US/10/631.467  
; CURRENT FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: JP 2003-077212  
; PRIOR FILING DATE: 2003-03-20  
; PRIOR APPLICATION NUMBER: JP 2002-229312  
; PRIOR FILING DATE: 2002-08-06  
; NUMBER OF SEQ ID NOS: 2086  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1064  
; LENGTH: 3991  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-631-467-1064

Query Match 35.5%; Score 91.6; DB 9; Length 3991;  
Best Local Similarity 84.4%; Pred. No. 1.1e-18;  
Matches 103; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGCCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
Db 911 CAGCGGAGTGACGCGCAACATGACTTCAGGCTCTGGAATTCACAGCTCATCCGCTAGCT 970

Qy 61 GGCTACCAGATGCCAGATGCGAGCATCAGAGGGACCCCTGCCAACGTGGAATTCACCTCAG 120  
Db 971 GGCTACCAGATGCCGCGATGGCACCATCAGAGGGGATGCTGCCACCTTGGAGTTACCCAG 1030

Qy 121 GT 122  
Db 1031 TT 1032

Db 971 GGCTACCAGATGCCGCGATGGCACCATCAGAGGGGATGCTGCCACCTTGGAGTTACCCAG 1030

Qy 121 GT 122  
Db 1031 TT 1032

RESULT 32  
US-10-305-720-1477  
; Sequence 1477, Application US/10305720  
; Publication No. US20040010136A1  
; GENERAL INFORMATION:  
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.  
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression  
; FILE REFERENCE: PA-0002-1 CON  
; CURRENT APPLICATION NUMBER: US/10/305,720  
; CURRENT FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: 09/016,434  
; PRIOR FILING DATE: 1998-01-30  
; NUMBER OF SEQ ID NOS: 1490  
; SOFTWARE: PERL Program  
; SEQ ID NO 1477  
; LENGTH: 4079  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g951318  
US-10-305-720-1477

Query Match 30.3%; Score 78.2; DB 6; Length 4079;  
Best Local Similarity 77.3%; Pred. No. 1.8e-14;  
Matches 95; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAGCACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60  
Db 1412 CAGAGGACAGAGCGGCAAGCAGCACTTCCGAGTCTGGAATCTCCAGCTCATCCGCTAGCT 1471

Qy 61 GGCTACCAGATGCCAGATGCGAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120  
Db 1472 GGCTACAAGCAGCGCTCAGCGCTCCACCCTGGGGGACCCAGCAATGTGCAGTTTCACAGAG 1531

Qy 121 GTA 123  
Db 1532 ATA 1534

RESULT 33  
US-10-475-049A-1  
; Sequence 1, Application US/10475049A  
; Publication No. US20050019854A1  
; GENERAL INFORMATION:  
; APPLICANT: Gross, Rene  
; APPLICANT: Lajoix, Anne-Dominique  
; APPLICANT: Ribes, Gerard  
; TITLE OF INVENTION: Novel Method For Screening Inhibitors of  
; TITLE OF INVENTION: the Linkage Between the Neuronal Nitric Oxide Synthase  
; TITLE OF INVENTION: Associated Protein and the Protein Inhibiting Neuronal  
; TITLE OF INVENTION: Nitric Oxide Synthase  
; FILE REFERENCE: 50319/005001  
; CURRENT APPLICATION NUMBER: US/10/475,049A  
; CURRENT FILING DATE: 2003-10-17  
; PRIOR APPLICATION NUMBER: PCT/FR02/01327  
; PRIOR FILING DATE: 2002-04-17  
; PRIOR APPLICATION NUMBER: FR 01/05248  
; PRIOR FILING DATE: 2001-04-18  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 4290  
; TYPE: DNA  
; ORGANISM: Rattus rattus

```
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(4287)
; OTHER INFORMATION:
; US-10-475-049A-1

Query Match      29.3%; Score 75.6; DB 8; Length 4290;
Best Local Similarity 76.2%; Pred. No. 1.2e-13;
Matches 93; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 1 CAGCGAGTGATGGCAAGCAGACACTTCGGGTGTGGAATGCTCAGTCAATCCGCTATGCT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1390 CAGAGGACTGACGGCAACATGACTTCCGAGTGTGGAATCGCAGCTCATCCGCTACGGC 1449

QY 61 GGCTACCATGCGCAGATCGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1450 GGCTACAGAGCCAGATGGCTCTACCTTGGGGATCCAGCCAAATGTGAGTTACGGAG 1509

QY 121 GT 122
Db 1510 AT 1511

RESULT 34
US-09-925-065A-56987
; Sequence 56987, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 937086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56987
; LENGTH: 700
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-56987

Query Match      22.3%; Score 57.6; DB 4; Length 700;
Best Local Similarity 66.4%; Pred. No. 4.9e-08;
Matches 81; Conservative 1; Mismatches 40; Indels 0; Gaps 0;

QY 1 CAGCGAGTGATGGCAAGCAGACACTTCGGGTGTGGAATGCTCAGTCAATCCGCTATGCT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 508 CAGCGCTGCCCTGGCCGAGGAGACTTCCGAATCTGGAACAGCCAGCTGGTGCCTACGGC 567

QY 61 GGCTACCATGCGCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 568 GGCTACCGGACGACGAGTGGCTCTGTGCGGGGGGACCCAGCCAACTGGAGATCACCGAG 627

QY 121 GT 122
Db 628 GT 629

RESULT 35
US-10-889-121-8
; Sequence 8, Application US/10889121
; Publication No. US20040253685A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Sessa, William C.
; TITLE OF INVENTION: eNOS MUTATIONS USEFUL FOR GENE THERAPY AND THERAPEUTIC SCREENING
; FILE REFERENCE: 044574-5046-01
; CURRENT APPLICATION NUMBER: US/10/889,121
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US 09/956,699
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: PCT/US00/09913
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 60/129,550
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 3612
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-889-121-8

Query Match      21.2%; Score 54.8; DB 8; Length 3612;
Best Local Similarity 65.6%; Pred. No. 3.7e-07;
Matches 80; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 1 CAGCGAGTGATGGCAAGCAGACACTTCGGGTGTGGAATGCTCAGTCAATCCGCTATGCT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 697 CAGCGCTGCCCTGGCCGAGGAGACTTCCGAATCTGGAACAGCCAGCTGGTGCCTACGGC 756

QY 61 GGCTACCATGCGCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 757 GGCTACCGGACGAGGAGCGCTCTGTGCGGGGGGACCCAGCCAACTGGAGATCACCGAG 816

QY 121 GT 122
Db 817 CT 818

RESULT 36
US-10-305-720-1234
; Sequence 1234, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1234
; LENGTH: 3690
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g189259
US-10-305-720-1234

Query Match      21.2%; Score 54.8; DB 6; Length 3690;
Best Local Similarity 65.6%; Pred. No. 3.7e-07;
Matches 80; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 1 CAGCGAGTGATGGCAAGCAGACACTTCGGGTGTGGAATGCTCAGTCAATCCGCTATGCT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 717 CAGCGCTGCCCTGGCCGAGGAGACTTCCGAATCTGGAACAGCCAGCTGGTGCCTACGGC 776

QY 61 GGCTACCATGCGCAGATGGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTCACCTCAG 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 777 GGCTACCGGACGAGGAGCGCTCTGTGCGGGGGGACCCAGCCAACTGGAGATCACCGAG 836

QY 121 GT 122
```

```
Db      837 CT 838

RESULT 37
US-10-720-1369
; Sequence 1369, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1369
; LENGTH: 4035
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g434699
US-10-720-1369

Query Match      21.2%; Score 54.8; DB 6; Length 4035;
Best Local Similarity 65.6%; Pred. No. 3.7e-07;
Matches 80; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy      1 CAGCGGAGTGATGGCAAGCAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
      |||||
Db      748 CAGCGCTGCCCTGGCCGAGGAGACTTCCGAATCTGGAACAGCCAGCTGGTGGCTACGCG 807
      |||||

Qy      61 GGCTACAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGGAATTCACCTCAG 120
      |||||
Db      808 GGCTACCGGACGAGGAGCGCTCTGTGCGGGGGGACCCAGCCACGTTGGAGATCACCGAG 867
      |||||

Qy      121 GT 122
      |
Db      868 CT 869

RESULT 38
US-10-172-118-414
; Sequence 414, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 414
; LENGTH: 4077
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: M93718
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-414
```

```
Query Match      21.2%; Score 54.8; DB 6; Length 4077;
Best Local Similarity 65.6%; Pred. No. 3.7e-07;
Matches 80; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy      1 CAGCGGAGTGATGGCAAGCAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
      |||||
Db      743 CAGCGCTGCCCTGGCCGAGGAGACTTCCGAATCTGGAACAGCCAGCTGGTGGCTACGCG 802
      |||||

Qy      61 GGCTACAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGGAATTCACCTCAG 120
      |||||
Db      803 GGCTACCGGACGAGGAGCGCTCTGTGCGGGGGGACCCAGCCACGTTGGAGATCACCGAG 862
      |||||

Qy      121 GT 122
      |
Db      863 CT 864

RESULT 39
US-10-342-887-414
; Sequence 414, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 414
; LENGTH: 4077
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-414

Query Match      21.2%; Score 54.8; DB 7; Length 4077;
Best Local Similarity 65.6%; Pred. No. 3.7e-07;
Matches 80; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy      1 CAGCGGAGTGATGGCAAGCAGCAGACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCT 60
      |||||
Db      743 CAGCGCTGCCCTGGCCGAGGAGACTTCCGAATCTGGAACAGCCAGCTGGTGGCTACGCG 802
      |||||

Qy      61 GGCTACAGATGCCAGATGGCAGCATCAGAGGGGACCCTGCCAACGTGGGAATTCACCTCAG 120
      |||||
Db      803 GGCTACCGGACGAGGAGCGCTCTGTGCGGGGGGACCCAGCCACGTTGGAGATCACCGAG 862
      |||||

Qy      121 GT 122
      |
Db      863 CT 864

RESULT 40
US-10-889-121-9
; Sequence 9, Application US/10889121
; Publication No. US20040253685A1
; GENERAL INFORMATION:
; APPLICANT: Seesla, William C.
; TITLE OF INVENTION: eNOS MUTATIONS USEFUL FOR GENE THERAPY AND THERAPEUTIC SCREENING
; FILE REFERENCE: 04574-5046-01
; CURRENT APPLICATION NUMBER: US/10/889,121
```

Wed Dec 14 07:48:57 2005

```
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: US 09/956,699
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: PCT/US00/09913
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 60/129,550
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 4077
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-889-121-9

Query Match      21.2%; Score 54.8; DB 8; Length 4077;
Best Local Similarity 65.6%; Pred. No. 3.7e-07;
Matches 80; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY      1 CAGCGGAGTGCATGGCAAGCACGACTTCGGGTGTGGAATGCTCAGCTCATCGCTATGCT 60
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
743 CAGCGTGCCTGGCCGAGGAGACTTCCGAATCTGGAACAGCCAGCTGTGCGCTACGCG 802
QY      61 GGCTACCGAGATGCCAGATGCGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACCTCAG 120
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
803 GGCTACCGGAGCAGCAGGCGCTCTGTGCGGGGGGACCAGCCAAACGTGGAGATCACCGAG 862
QY      121 GT 122
Db      ||
863 CT 864
```

Search completed: December 13, 2005, 18:27:38  
Job time : 798 secs

**THIS PAGE BLANK (USPTO)**



November 2005

Published\_Applications\_Nucleic Acid and Published\_Applications\_Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions **.rnpbm** (Published\_Applications\_NA\_Main) and **.rnpbn** (Published\_Applications\_NA\_New).

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions **.rapbm** (Published\_Applications\_AA\_Main) and **.rapbn** (Published\_Applications\_AA\_New).

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 16:32:55 ; Search time 238 Seconds  
(without alignments)  
405.271 Million cell updates/sec

Title: US-10-713-137-1

Perfect score: 258

Sequence: 1 cagcggatgaggaagca.....ttgtcccccagctgtgcac 258

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3392430 seqs, 186927314 residues

Total number of hits satisfying chosen parameters: 6784860

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq2:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq3:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

\*Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32.8	12.7	3001	7	US-11-145-703-194
2	32.2	12.5	2827	6	US-10-750-185-59391
3	31	12.0	154452	7	US-11-121-086-74
4	31	12.0	168516	7	US-11-121-086-3
5	30.6	11.9	2840	6	US-10-750-185-60778
6	30	11.6	4745	6	US-10-909-125-837
7	29.8	11.6	1678	6	US-10-750-185-43745
8	29.8	11.6	171162	7	US-11-112-908-38
9	29.4	11.4	1009	6	US-10-750-185-63750
10	29.4	11.4	1676	6	US-10-750-185-31860
11	29.4	11.4	3138	6	US-10-750-185-62600
12	29.4	11.4	179666	7	US-11-121-086-67
13	29.2	11.3	164810	7	US-11-121-086-4
14	29	11.2	3772	7	US-10-821-234-671
15	29	11.2	162289	7	US-11-121-086-20
16	28.8	11.2	600	6	US-10-750-185-868
17	28.8	11.2	1564	6	US-10-750-185-56551
18	28.6	11.1	861	6	US-10-750-185-54914
19	28.6	11.1	1196	6	US-10-750-185-34965
20	28.6	11.1	1543	6	US-10-750-185-25939
21	28.6	11.1	171486	7	US-11-121-086-105
22	28.4	11.0	2335	6	US-10-750-185-45463
23	28.4	11.0	172543	7	US-11-121-086-6

C 24	28.2	10.9	2333	6	US-10-645-441-6	Sequence 6, Appli
C 25	28.2	10.9	2532	6	US-10-645-441-11	Sequence 11, Appli
C 26	28.2	10.9	3745	6	US-10-750-185-26897	Sequence 26897, A
C 27	28.2	10.9	4226	6	US-10-750-185-61399	Sequence 61399, A
C 28	28	10.9	1215	6	US-10-750-185-56711	Sequence 56711, A
C 29	28	10.9	3132	6	US-10-392-234A-33	Sequence 33, Appli
C 30	27.8	10.8	792	6	US-10-821-234-551	Sequence 551, App
C 31	27.8	10.8	2233	6	US-10-750-185-44988	Sequence 44988, A
C 32	27.8	10.8	2498	6	US-10-131-826A-483	Sequence 483, App
C 33	27.8	10.8	4305	7	US-11-080-991-67	Sequence 67, Appli
C 34	27.8	10.8	163162	7	US-11-121-086-66	Sequence 66, Appli
C 35	27.8	10.8	179892	7	US-11-112-908-39	Sequence 39, Appli
C 36	27.6	10.7	2085	6	US-10-496-711-1	Sequence 1, Appli
C 37	27.6	10.7	149419	7	US-11-112-908-49	Sequence 49, Appli
C 38	27.6	10.7	161726	7	US-11-112-908-48	Sequence 48, Appli
C 39	27.6	10.7	161726	7	US-11-112-908-52	Sequence 52, Appli
C 40	27.6	10.7	163162	7	US-11-121-086-66	Sequence 66, Appli
C 41	27.6	10.7	166111	7	US-11-112-908-47	Sequence 47, Appli
C 42	27.4	10.6	600	6	US-10-750-185-20492	Sequence 20492, A
C 43	27.4	10.6	1934	6	US-10-750-185-32804	Sequence 32804, A
C 44	27.4	10.6	2236	6	US-10-131-826A-381	Sequence 381, App
C 45	27.4	10.6	126552	7	US-11-121-086-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-11-145-703-194  
; Sequence 194, Application US/11145703  
; Publication No. US20050260667A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilya  
; APPLICANT: Bougueleret, Lydie  
; APPLICANT: Bihain, Bernard  
; APPLICANT: Essioux, Laurent  
; TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS  
; FILE REFERENCE: 53 US16 DIV  
; CURRENT APPLICATION NUMBER: US/11/145,703  
; CURRENT FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: US/10/147,603  
; PRIOR FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: 09/539,333  
; PRIOR FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: US 60/126,903  
; PRIOR FILING DATE: 1999-03-30  
; PRIOR APPLICATION NUMBER: US 60/131,971  
; PRIOR FILING DATE: 1999-04-30  
; PRIOR APPLICATION NUMBER: US 60/132,065  
; PRIOR FILING DATE: 1999-04-30  
; PRIOR APPLICATION NUMBER: US 60/143,928  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: US 60/145,915  
; PRIOR FILING DATE: 1999-07-27  
; PRIOR APPLICATION NUMBER: US 60/146,453  
; PRIOR FILING DATE: 1999-07-29  
; PRIOR APPLICATION NUMBER: US 60/146,452  
; PRIOR FILING DATE: 1999-07-29  
; PRIOR APPLICATION NUMBER: US 60/162,288  
; PRIOR FILING DATE: 1999-10-28  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 234  
; SOFTWARE: Patent.pm  
; SEQ ID NO 194  
; LENGTH: 3001  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 1501  
; OTHER INFORMATION: 99-26223-225 : polymorphic base G or T

```

; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: 1481..1500
; OTHER INFORMATION: 99-26223-225.mis1,
;
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: 1502..1520
; OTHER INFORMATION: 99-26223-225.mis2, complement
;
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1277..1297
; OTHER INFORMATION: upstream amplification primer
;
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1842..1862
; OTHER INFORMATION: downstream amplification primer, complement
;
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: 1489..1513
; OTHER INFORMATION: 99-26223-225 probe
;
; US-11-145-703-194
;
; Query Match      12.7%; Score 32.8; DB 7; Length 3001;
; Best Local Similarity 51.4%; Pred. No. 1.7;
; Matches 76; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
;
Qy 62 GCTACCAAGATGCCAGATGCGCAGCATCAGAGGGGACCCTGCCAACGTGGAATTCACCTCAGG 121
Db 862 GCAAGAAGATGCAAAATTTACTCTCTAACTTTGAACCATATAAAACATTTCCAGGCAATCAAG 921
;
Qy 122 TACCGCGCCAGCCTCAGCRRCCGGCCATTGGGGGGGAGCCCCGTGTGAGCGACTGA 181
Db 922 AACACTTCCCTGCTCTACTTCCAGACACAGAAGAGAGACAGAGAGAGATGTGAGAGA 981
;
Qy 182 CAGAGTGGAGCCCGCAGAGGAGACAGCGCAG 209
Db 982 CAGAAATGTGAGGAGAGAGAAACATGTAG 1009
;
RESULT 2
US-10-750-185-59391
; Sequence 59391, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59391
; LENGTH: 2827
; TYPE: DNA
; ORGANISM: Bovine 19866880650684
; US-10-750-185-59391
;
; Query Match      12.5%; Score 32.2; DB 6; Length 2827;
; Best Local Similarity 46.3%; Pred. No. 2.4;
; Matches 106; Conservative 0; Mismatches 123; Indels 0; Gaps 0;
;
Qy 22 GACTTCCGGGTGTGGAATGCTCAGCTCATCCGCTATGCTGTACCAAGATGCCAGATGGC 81
Db 1014 GAATTCCTGCTGGGCAAGGCCATGGCCCTCATCTTTGTGGGCGCGTGTGCCCGAGGGTGC 1073

```

```

Qy 82 AGCATCAGAGGGGACCCCTGCCACGTGGAATTCACCTCAGTACCGCGGCCAGCCTCAGCC 141
Db 1074 ACCATGCTGACGCCCGTGCCAAATGCACTGGGGAGAGAGACCACATTCATTCCTCCACG 1133
;
Qy 142 RCCGGCCATTGGGGCGGGAGCCCCGTGGTGACCGAGTGACAGAGTGGAGCCCGCAGAGGAG 201
Db 1134 TGTGGCTGTGCACCAGGCTGTGTCCAAGTGAGGCTGAGAGAAGCTACAGCCGGGATGAG 1193
;
Qy 202 ACACGAGCCCGGGCTTACAGACTCAGAGGCCCCGTGTTGTTCCCGCAGC 250
Db 1194 GCAGGCATGACAGCAAGGTGCTGGACACCGCCCATGCAGGCCCTTCATC 1242
;
RESULT 3
US-11-121-086-74
; Sequence 74, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 74
; LENGTH: 154452
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-121-086-74
;
; Query Match      12.0%; Score 31; DB 7; Length 154452;
; Best Local Similarity 58.4%; Pred. No. 7.7;
; Matches 52; Conservative 1; Mismatches 36; Indels 0; Gaps 0;
;
Qy 127 GCGCCAGCCTCAGCRRCCGGCCATTGGGGCGGGAGCCCCGTGTGAGCGGAGTACAGAG 186
Db 117867 GCGCCTGCGGCTGCGCATGCCCTCGGGTTCGAGCGCGACGGGGCGGCGCGCGGCG 117926
;
Qy 187 TGGAGCCCGCAGGAGACAGCGCCCGG 215
Db 117927 TCCAGCGCGCGCGGAGAGACGCGGAGG 117955
;
RESULT 4
US-11-121-086-3
; Sequence 3, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 168516
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-121-086-3
;
; Query Match      12.0%; Score 31; DB 7; Length 168516;
; Best Local Similarity 56.7%; Pred. No. 7.7;
; Matches 55; Conservative 1; Mismatches 41; Indels 0; Gaps 0;
;
Qy 121 GTACCGCGCCAGCCTCAGCCRCGCGCATTTGGGGCGGGAGCCCCCGTGTGAGCGAGTG 180

```

Accession	Sequence	Position
98271	GTTCGCGCAGGACCGACAGGGACAGAGGGCGGGCTGGTCTGACGACGTG	98330
181	ACAGTGTGAGCCGACGAGAGACACGACGCCCGGGCT	217
98331	GCAGGGGTGTGGCCACGGCAGGAGGCACCTGACGCT	98367

```

RESULT 5
US-10-750-185-60778/c
; Sequence 60778, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 60778
; LENGTH: 2840
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-60778

```

```

RESULT 6
US-10-909-125-837/c
; Sequence 837, Application US/10909125
; Publication No. US20050261218A1
; GENERAL INFORMATION:
; APPLICANT: Esau, Christine
; APPLICANT: Lollo, Bridget
; APPLICANT: Bennett, C. Frank
; APPLICANT: Freier, Susan M.
; APPLICANT: Griffey, Richard H.
; APPLICANT: Baker, Brenda F.
; APPLICANT: Vickers, Timothy
; APPLICANT: Marcussen, Eric G.
; APPLICANT: Koller, Erich
; APPLICANT: Swayze, Eric
; APPLICANT: Jain, Ravi
; APPLICANT: Bhat, Balkrishen
; APPLICANT: Peralta, Eigen
; TITLE OF INVENTION: Oligomeric Compounds And Compositions For Use In Modulation
; TITLE OF INVENTION: Of Small Non-Coding RNAs
; FILE REFERENCE: ISIS0080-100 (CORE0016US)
; CURRENT APPLICATION NUMBER: US/10/909,125
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: US 60/492,056
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US 60/516,303

```

```

RESULT 7
US-10-750-185-43745
; Sequence 43745, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: Denise, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750.185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 43745
; LENGTH: 1678
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-43745

```

```

RESULT 8
US-11-112-908-38/c
; Sequence 38, Application US/1112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers

```

```
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,759
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38
; LENGTH: 171162
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-38

Query Match      11.6%; Score 29.8; DB 7; Length 171162;
Best Local Similarity 48.0%; Pred. No. 17;
Matches 82; Conservative 1; Mismatches 88; Indels 0; Gaps 0;

QY      46 CTCATCCGCTATGCTGCTACAGATGCCAGATGCAGATGCAGATGCAGAGGAGCCCTGCCAAC 105
Db      12535 CCCACACCCCGCGCGCGCGCTCCACCTGCTCCACCCCGCGCGCGCGCGCGCGCGCGCG 12476

QY      106 GTGGAATTACTCAGGTACCGCGCCCGCCCTCAGCCRCGCCCATTTGGGGCGGGAGCGCC 165
Db      12475 CGGCCCGCGCGCTGTGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 12416

QY      166 CGTGTGAGCAGTGCAGAGTGGAGCCCGAGAGAGACACCGACCGCGCGCGCGCGCGCG 216
Db      12415 GCGAGAGGGCGAGCGCCAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 12365

RESULT 9
US-10-750-185-63750/c
; Sequence 63750, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63750
; LENGTH: 1009
; TYPE: DNA
; ORGANISM: Bovine 19866880851319
US-10-750-185-63750

Query Match      11.4%; Score 29.4; DB 6; Length 1009;
Best Local Similarity 49.0%; Pred. No. 13;
Matches 75; Conservative 1; Mismatches 77; Indels 0; Gaps 0;

QY      98 CTGCCAAGCTGAATTCAGTACCGCGCCCGCCAGCTCAGCCRCGCCCATTTGGGGCG 157
Db      782 CTGCCACCTCCGCGGTTGGGTGGACCCGCTCGGGCTGAGGGGCACTCAGAGGGCT 723

QY      158 GGGAGCCCCGTGGTGGAGCGAGTGACAGAGTGGAGCGCCAGAGAGACACGACGACCGCGGCT 217
Db      722 CTGAGCCAGAGAGGGTGGGCCCAAGATTCCACTTAAACAATCTGGGGGTCTCTTAT 663
```

```
QY      218 TACAGATCAGAGGCGCGCTCTTGTTCGCCAGC 250
Db      662 TCCTGTAAAGAGGGCGCCCTAGGTCCCCCAGC 630

RESULT 10
US-10-750-185-31860/c
; Sequence 31860, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31860
; LENGTH: 1676
; TYPE: DNA
; ORGANISM: Bovine 19866881075748
US-10-750-185-31860

Query Match      11.4%; Score 29.4; DB 6; Length 1676;
Best Local Similarity 52.9%; Pred. No. 14;
Matches 63; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY      64 TACAGATGCCAGATGCAGCATCAGAGGGGAGCCCTGCCAACCTGGAATTCACCTCAGGTA 123
Db      629 TACAGAGACCTTATTCGAGGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 570

QY      124 CCGCGCCCGAGCTCAGCCRCGCCCATTTGGGGCGGGAGCGCCGCTGGTGGAGCGAGTGAC 182
Db      569 CACAGCTCCGCTGTGCCCCAGAGCCAGTGTACTGTGAGAGCTGTGATGGTCTTGAGAC 511

RESULT 11
US-10-750-185-62600/c
; Sequence 62600, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62600
; LENGTH: 3138
; TYPE: DNA
; ORGANISM: Bovine 19866881144324
US-10-750-185-62600

Query Match      11.4%; Score 29.4; DB 6; Length 3138;
Best Local Similarity 55.7%; Pred. No. 15;
```

Matches 54; Conservative 1; Mismatches 42; Indels 0; Gaps 0;

QY 53 GCTATCTGCTACCATGCGGAGATGCGAGCATCAGAGGGGACCTGCGCAAGTGGAT 112  
DB 1370 GCTACACCTCTCCAGCTGCCATTTTTCGCAAGTGCAGAAACTGCCCATGAGGCGAG 1311

QY 113 TCACCTAGGTACCGCGCCGAGCCTCAGCCRCGCGCCA 149  
DB 1310 CAGAAGCAACACCCAGCAGAGCCTCAGCCCAATGCACA 1274

RESULT 12  
US-11-121-086-67/c  
; Sequence 67, Application US/11121086  
; Publication No. US20050266459A1  
; GENERAL INFORMATION:  
; APPLICANT: POULSEN, TIM S.  
; APPLICANT: NIELSEN, KIRSTEN V.  
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES  
; FILE REFERENCE: 09138.6000-00000  
; CURRENT APPLICATION NUMBER: US/11/121,086  
; CURRENT FILING DATE: 2005-05-04  
; PRIOR APPLICATION NUMBER: 60/567,570  
; PRIOR FILING DATE: 2004-05-04  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 67  
; LENGTH: 179666  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-121-086-67

Query Match 11.4%; Score 29.4; DB 7; Length 179666;  
Best Local Similarity 54.3%; Pred. No. 22; Indels 0; Gaps 0;  
Matches 57; Conservative 1; Mismatches 47; Indels 0; Gaps 0;

QY 135 CTCAGCCRCGCGCATTTGGGGGAGCGCCCGTGTGAGCGAGTGACAGAGTGGAGCCCC 194  
DB 165368 CACACCGGGCGGGAGTGGGAAACGGGAGCCAGATCGGAGCCAGCATGGAGCAGCGAC 165309

QY 195 AGAGGAGACACGCGCCCGGCTTACAGACTCAGAGCCCGCT 239  
DB 165308 AGAGCAGCGATAGAGCGCTGGGTGGAGCGGCGGCTCAGCT 165264

RESULT 13  
US-11-121-086-4  
; Sequence 4, Application US/11121086  
; Publication No. US20050266459A1  
; GENERAL INFORMATION:  
; APPLICANT: POULSEN, TIM S.  
; APPLICANT: NIELSEN, KIRSTEN V.  
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES  
; FILE REFERENCE: 09138.6000-00000  
; CURRENT APPLICATION NUMBER: US/11/121,086  
; CURRENT FILING DATE: 2005-05-04  
; PRIOR APPLICATION NUMBER: 60/567,570  
; PRIOR FILING DATE: 2004-05-04  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 4  
; LENGTH: 164810  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-121-086-4

Query Match 11.3%; Score 29.2; DB 7; Length 164810;  
Best Local Similarity 57.8%; Pred. No. 24; Indels 0; Gaps 0;  
Matches 52; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 156 CGGGGAGCCCGTGGTGGAGCGAGTGACAGAGTGGAGCCCGCAGAGAGACACGCGAGCCCGG 215  
DB 131807 CGGGGAGCCCGTGGAGGAGGCGCCACTGCTGAGGCTGGAGCAGGAGGAGGAGG 131866

QY 216 CTTACAGACTCAGAGGCGCGCTTGTGTTCC 245  
DB 131867 CTGACTGCTCTCTGGGCTTAGTTTCTCC 131896

RESULT 14  
US-10-821-234-671  
; Sequence 671, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Suean  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pt\_seq\_genes Version 1.0  
; SEQ ID NO 671  
; LENGTH: 3772  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-821-234-671

Query Match 11.2%; Score 29; DB 6; Length 3772;  
Best Local Similarity 49.7%; Pred. No. 19; Indels 0; Gaps 0;  
Matches 71; Conservative 1; Mismatches 71; Indels 0; Gaps 0;

QY 93 GCACCTGCGCAACGTGGAATTCACCTCAGGTACCGCGCCAGCTCAGCCRCGCGCATTTG 152  
DB 1545 GGAGCTGGCTGTCTTGGCATCCCGCAGAGCTGTCTGCTGTGAGCCCGGCTGT 1604

QY 153 GGGCGGGAGCGCCCGTGTGTGAGCGAGTGACAGAGTGGAGCCCGCAGAGAGACACGCGAGCCC 212  
DB 1605 GGGCGCTCCCGGGTGTGAGCGGAGGAGCGCGGCGAGGAGCGGCGAGGCGGCTTACGCCCT 1664

QY 213 GGGCTTACAGACTCAGAGGCGCC 235  
DB 1665 GTGCTGGAGCGCTGCAGGTCTC 1687

RESULT 15  
US-11-121-086-20/c  
; Sequence 20, Application US/11121086  
; Publication No. US20050266459A1  
; GENERAL INFORMATION:  
; APPLICANT: POULSEN, TIM S.  
; APPLICANT: NIELSEN, KIRSTEN V.  
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES  
; FILE REFERENCE: 09138.6000-00000  
; CURRENT APPLICATION NUMBER: US/11/121,086  
; CURRENT FILING DATE: 2005-05-04  
; PRIOR APPLICATION NUMBER: 60/567,570  
; PRIOR FILING DATE: 2004-05-04  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 20  
; LENGTH: 162289  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-121-086-20

Query Match 11.2%; Score 29; DB 7; Length 162289;  
Best Local Similarity 50.4%; Pred. No. 27; Indels 0; Gaps 0;  
Matches 71; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 46 CTCATCGCTATCTCGTGTACCATGCGCAGATGGCAGATGGCAGGAGGAGCCCTGCCAAC 105  
DB 131807 CTCATCGCTATCTCGTGTACCATGCGCAGATGGCAGATGGCAGGAGGAGGAGGAGG 131866

D	b		108108	CTCAGCCCCCTCACTGGGACGCCTGTGTGCCCTGTGTGCCCTCAGTAGGAGACGAGGTCAAT	108049
Q	y		106	GTGGAATTCACTCAGTACCAGCCAGCCCTCAGCRCRCCGSCCATTTGGGCGGGAGGCC	165
D	b		108048	GGCAGCTTCACGACGACAGGCTTACCAGGCAAAGCACACACAGACGTGTCTGGGCA	107989
Q	y		166	CGTGCTGACGAGTGACAGAG	186
D	b		107988	CGTGGTGACACATGACAGAG	107968
 RESULT 16 US-10-750-185-868/c					
; Sequence 868, Application US/10750185					
; Publication No. US20050260603A1					
; GENERAL INFORMATION:					
; APPLICANT: MMI GENOMICS, INC.					
; APPLICANT: DENISE, Sue K.					
; APPLICANT: KERR, Richard					
; APPLICANT: ROSENFELD, David					
; APPLICANT: HOLM, Tom					
; APPLICANT: BATES, Stephen					
; APPLICANT: FANTIN, Dennis					
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS					
; FILE REFERENCE: MMII100-2					
; CURRENT APPLICATION NUMBER: US/10/750,185					
; CURRENT FILING DATE: 2003-12-31					
; PRIOR APPLICATION NUMBER: US 60/437,482					
; PRIOR FILING DATE: 2002-12-31					
; NUMBER OF SEQ ID NOS: 64922					
; SOFTWARE: PatentIn version 3.1					
; SEQ ID NO 868					
; LENGTH: 600					
; TYPE: DNA					
; ORGANISM: Bovine MMBT07408					
US-10-750-185-868					
 Query Match            11.2%; Score 28.8; DB 6; Length 600;					
Best Local Similarity   56.7%; Pred.No.18;					
Matches   51; Conservative   1; Mismatches   38; Indels   0; Gaps   0;					
Q	y		79	GGCAGCATCAGAGGGGACCCCTGCCAACGTGGAATTACTCAGGTACCCGGCCAGCCTCA	138
D	b		359	GGTATGCTCAGCTGGGACCAGGACACGTGATTCTGGACAGAGGTCCCTCGAGGGCCAGY	300
Q	y		139	GCRCGCGCCATTGGGGCGGGAGCCCCTG	168
D	b		299	GCACCCCTCAATTGGGGCAGCCCCCTCCCT	270
 RESULT 17 US-10-750-185-56551/c					
; Sequence 56551, Application US/10750185					
; Publication No. US20050260603A1					
; GENERAL INFORMATION:					
; APPLICANT: MMI GENOMICS, INC.					
; APPLICANT: DENISE, Sue K.					
; APPLICANT: KERR, Richard					
; APPLICANT: ROSENFELD, David					
; APPLICANT: HOLM, Tom					
; APPLICANT: BATES, Stephen					
; APPLICANT: FANTIN, Dennis					
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS					
; FILE REFERENCE: MMII100-2					
; CURRENT APPLICATION NUMBER: US/10/750,185					
; CURRENT FILING DATE: 2003-12-31					
; PRIOR APPLICATION NUMBER: US 60/437,482					
; PRIOR FILING DATE: 2002-12-31					
; NUMBER OF SEQ ID NOS: 64922					
; SOFTWARE: PatentIn version 3.1					
; SEQ ID NO 56551					
; LENGTH: 1564					
; TYPE: DNA					









Db 303 CCTGCCCGGCTGAGCTGCAGACCGCTGAAGAAAGCCGAGGCGGCATGCGCAGGC 362  
Qy 201 GACAGGAGCCGGCTTACAGACTACAGAGCCCGCTTGTTCCTCCAGCTG 252  
Db 363 GGTGCTGACCGGCGCTGCAGGTGCGAGACACGAGCGCGGTTCCTGCTG 414

RESULT 30  
US-10-821-234-551  
; Sequence 551, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462,047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pt\_seq\_genes Version 1.0  
; SEQ ID NO 551  
; LENGTH: 792  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-821-234-551

Query Match 10.8%; Score 27.8; DB 6; Length 792;  
Best Local Similarity 54.6%; Pred. No. 36;  
Matches 53; Conservative 1; Mismatches 43; Indels 0; Gaps 0;

Qy 140 CCRCCGGCCATTGGGGGGGAGCCCGCTGTGTGAGCGAGTGACAGAGTGGAGGCCAGG 199  
Db 77 CCATGGGCTCGGGGAACCCGCGCTGTGTGTGTGCTGCTCCAGCGCCAGGAGG 136

Qy 200 AGACAGCGAGCCCGGCTTACAGACTACAGAGGCCG 236  
Db 137 CCACCTGCAGCGCTGTGTCTCCAGACTGATGTCAACCCG 173

RESULT 31  
US-10-750-185-44988/c  
; Sequence 44988, Application US/10750185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: Denise, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-2  
; CURRENT APPLICATION NUMBER: US/10/750,185  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIN version 3.1  
; SEQ ID NO 44988  
; LENGTH: 2233  
; TYPE: DNA  
; ORGANISM: Bovine 19866880984581  
US-10-750-185-44988

Query Match 10.8%; Score 27.8; DB 6; Length 2233;  
Best Local Similarity 49.6%; Pred. No. 40;  
Matches 68; Conservative 1; Mismatches 68; Indels 0; Gaps 0;

Qy 20 ACAGTTCGGGTGTGGAATGCTCAGCTCATCGCTATGCTGGCTACCCAGATGCCAGATG 79  
Db 1440 ATGAGTACAAGGTACCTTAAGTTCTCTGGGCTTCCCGATGGCTCAGCAGGTAAAGAATCTG 1381  
Qy 80 GCAGCATCAGAGGGACCCCTGCCAACGTGGAATTCATCAGGTACCCGGCCCGCCCTCAG 139  
Db 1380 CCTGCAGTGCAGGAGATCCAGACAACTGGGTTTGACCCCTGGGTGCGGAAGAGCCCCCTG 1321

Qy 140 CCRCCGGCCATTGGGGC 156  
Db 1320 GAGGAGGCCATTGTGAC 1304

RESULT 32  
US-10-131-826A-483  
; Sequence 483, Application US/10131826A  
; Publication No. US20050245730A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C128  
; CURRENT APPLICATION NUMBER: US/10/131,826A  
; CURRENT FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059115  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059117  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059122  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059184  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059352  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/059588  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 483  
; LENGTH: 2498  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-131-826A-483

Query Match 10.8%; Score 27.8; DB 6; Length 2498;  
Best Local Similarity 54.6%; Pred. No. 40;  
Matches 53; Conservative 1; Mismatches 43; Indels 0; Gaps 0;

Qy 140 CCRCCGGCCATTGGGGGGGAGGCCCGCTGTGTGAGCGAGTGCAGAGTGGAGGCCAGG 199

Db 93 CCATGGCTCGGGAAACCCCGCCGGTGGTGTGTTGCTGCCAGCAGGGCCAGGAG 152  
QY 200 AGACAGCAGCCCGGGCTTACAGACTCACAGGCCCG 236  
Db 153 CCACCTGCAGCCTGGTGTCTCCAGACTGATGTACCCG 189

RESULT 33  
US-11-080-991-67  
; Sequence 67, Application US/11080991  
; Publication No. US20050266437A1  
; GENERAL INFORMATION:  
; APPLICANT: Veiby, Pether Ole  
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR  
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST  
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST  
; FILE REFERENCES: MRI-039  
; CURRENT FILING DATE: 2005-03-11  
; PRIOR APPLICATION NUMBER: US/11/080,991  
; PRIOR FILING DATE: 2002-06-21  
; PRIOR FILING DATE: 2005-03-11  
; PRIOR FILING DATE: 2002-06-21  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 67  
; LENGTH: 4305  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-080-991-67

Query Match 10.8%; Score 27.8; DB 7; Length 4305;  
Best Local Similarity 50.4%; Pred. No. 42;  
Matches 65; Conservative 1; Mismatches 53; Indels 0; Gaps 0;  
QY 79 GGCAGCATCAGAGGGACCTGTCACAGTGGAAATTCATCAGTACCCGCCCGAGCTCA 138  
Db 687 GTCATCACCAGCTGCACCCGGGCGACGCGCTCTCTGTGAGGCGGTGCGCGCTCGCC 746  
QY 139 GCRCCGGCCATTGGGGCGGGAGCCCGTGTGAGCGAGTGACAGAGTGAGGCCAGAG 198  
Db 747 GAGCCAGCAGCAGTGTGCGCGCTGCTGAGACGTGCTGACGTGAGTGGGGCCGGGA 806  
QY 199 GAGACAGC 207  
Db 807 GGGCCGCGC 815

RESULT 34  
US-11-121-086-66  
; Sequence 66, Application US/11121086  
; Publication No. US20050266459A1  
; GENERAL INFORMATION:  
; APPLICANT: POULSEN, TIM S.  
; APPLICANT: NIELSEN, KIRSTEN V.  
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES  
; FILE REFERENCES: 09138, 6000-00000  
; CURRENT APPLICATION NUMBER: US/11/121,086  
; CURRENT FILING DATE: 2005-05-04  
; PRIOR APPLICATION NUMBER: 60/567,570  
; PRIOR FILING DATE: 2004-05-04  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 66  
; LENGTH: 163162  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-121-086-66

Query Match 10.8%; Score 27.8; DB 7; Length 163162;  
Best Local Similarity 62.0%; Pred. No. 59;  
Matches 44; Conservative 0; Mismatches 27; Indels 0; Gaps 0;  
QY 67 CAGATGCCAGTGCAGCATCAGAGGGGACCTGCCAACGTGGAAATTCACCTCAGGTACCC 126

Db 32805 CAGAGGCTGTATCTGTATGATGGGACGCTGCCGACCAACTGTCTTCTGCTCCC 32864  
QY 127 GCGCCAGCCTC 137  
Db 32865 AGCACAGCCTC 32875

RESULT 35  
US-11-112-908-39/c  
; Sequence 39, Application US/11112908  
; Publication No. US20050260659A1  
; GENERAL INFORMATION:  
; APPLICANT: Harris, Cole  
; APPLICANT: Davis, Lisa M.  
; TITLE OF INVENTION: Breast Cancer Biomarkers  
; FILE REFERENCES: 04-164-US  
; CURRENT APPLICATION NUMBER: US/11/112,908  
; CURRENT FILING DATE: 2005-04-22  
; PRIOR APPLICATION NUMBER: US 60/564,758  
; PRIOR FILING DATE: 2004-04-23  
; PRIOR APPLICATION NUMBER: US 60/575,978  
; PRIOR FILING DATE: 2004-06-01  
; PRIOR APPLICATION NUMBER: US 60/631,702  
; PRIOR FILING DATE: 2004-11-30  
; PRIOR APPLICATION NUMBER: US 60/633,826  
; PRIOR FILING DATE: 2004-12-07  
; NUMBER OF SEQ ID NOS: 511  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 39  
; LENGTH: 179892  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-112-908-39

Query Match 10.8%; Score 27.8; DB 7; Length 179892;  
Best Local Similarity 54.6%; Pred. No. 59;  
Matches 53; Conservative 1; Mismatches 43; Indels 0; Gaps 0;  
QY 122 TACCGGGCCAGCCTCAGCCCGCCATTGGGGCGGGAGCCCGTGGTGAGCGAGTGA 181  
Db 155215 TGCCCCCCCCCTGCCAGCAGCAGATGCCACTGACCATCAGGAGCGGGGGTGTGAGCCA 155156  
QY 182 CAGAGTGGAGCCCGAGAGGAGACACGACGCGCGGCTT 218  
Db 155155 GGGGTTGACGGGCTGGCGGTGAGCTGGCTGGGTT 155119

RESULT 36  
US-10-496-711-1/c  
; Sequence 1, Application US/10496711  
; Publication No. US20050256649A1  
; GENERAL INFORMATION:  
; APPLICANT: SmithKline Beecham Corporation  
; TITLE OF INVENTION: HIGH THROUGHPUT CORRELATION OF  
; TITLE OF INVENTION: POLYMORPHIC FORMS WITH MULTIPLE PHENOTYPES WITHIN CLINICAL  
; TITLE OF INVENTION: POPULATIONS  
; FILE REFERENCES: PU4699WO  
; CURRENT APPLICATION NUMBER: US/10/496,711  
; CURRENT FILING DATE: 2004-05-26  
; PRIOR APPLICATION NUMBER: 60/344892  
; PRIOR FILING DATE: 2002-12-21  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2085  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-496-711-1

Query Match 10.7%; Score 27.6; DB 6; Length 2085;  
Best Local Similarity 56.7%; Pred. No. 45;  
Matches 51; Conservative 0; Mismatches 39; Indels 0; Gaps 0;



Db 98434 GAAGCGGGCGCTTCCCTCCGAGAGGCGACGAGGGCGGCCACGACGAGGGTGGCTCG 98375  
Qy 196 GAGGAGACAGCGAGCC 211  
Db 98374 GTGAGCCTGGCGCCC 98359

RESULT 40  
US-11-121-086-66/c  
; Sequence 66, Application US/11121086  
; Publication No. US2005026459A1  
; GENERAL INFORMATION:  
; APPLICANT: POULSEN, TIM S.  
; APPLICANT: NIELSEN, KIRSTEN V.  
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES  
; FILE REFERENCE: 09138.6000-00000  
; CURRENT APPLICATION NUMBER: US/11/121,086  
; CURRENT FILING DATE: 2005-05-04  
; PRIOR APPLICATION NUMBER: 60/567,570  
; PRIOR FILING DATE: 2004-05-04  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 66  
; LENGTH: 163162  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-121-086-66

Query Match 10.7%; Score 27.6; DB 7; Length 163162;  
Best Local Similarity 51.6%; Pred. No. 67;  
Matches 63; Conservative 0; Mismatches 59; Indels 0; Gaps 0;  
Qy 95 ACCCTGCCAACGTGGAATTCACTCAGGTACCGGCGCCAGCCTCAGCCRCGCGCCATTGGG 154  
Db 52052 ACCGCGCATAAAGTTGGGGGCTCCCGAGGCGGCTCCCGAGACCGCGCCCTCACCTCG 51993  
Qy 155 GCGGGAGAGCCCGTGTGAGCGAGTGACAGAGTGGAGCCCGAGAGGAGACAGCGAGCCCGG 214  
Db 51992 CCGCGTGTCTCATGTCTAGCCCCCGAGCGCCCGCCCGCTCCACAGGCGCGCCCGG 51933  
Qy 215 GC 216  
Db 51932 CC 51931

Search completed: December 13, 2005, 18:31:57  
Job time : 249 secs

**THIS PAGE BLANK (USPTO)**



```

RESULT 2
US-11-036-317-523844
; Sequence 523844, Application US/11036317
; Publication NO. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

```

```
; SEQ ID NO 523844
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-523844

Query Match          70.0%; Score 16.8; DB 10; Length 25;
Best Local Similarity 90.0%; Pred. No. 8e+02; 2; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATGCACAGCTGGGGAACAA 20
   |||||
Db 6 GCTGCACAGCTGAGNACAA 25

RESULT 3
US-10-719-956-683762/c
; Sequence 683762, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 683762
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-683762

Query Match          65.8%; Score 15.8; DB 7; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATGCACAGCTGGGGAACAA 20
   |||||
Db 19 ATGCACAGCTGGGGTACAA 1

RESULT 4
US-10-719-900-83698/c
; Sequence 83698, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 83698
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-83698

Query Match          65.8%; Score 15.8; DB 8; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CACAGCTGGGGAACAGAC 23
   |||||
Db 24 CACAGCTGGGAATCAAGAC 6

RESULT 5
US-10-719-900-743593/c
; Sequence 743593, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 743593
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-743593

Query Match          65.8%; Score 15.8; DB 8; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCACAGCTGGGGAACAA 22
   |||||
Db 25 GCACAGATGGGCACAA 7

RESULT 6
US-10-719-900-904575/c
; Sequence 904575, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 904575
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-904575

Query Match          65.8%; Score 15.8; DB 8; Length 25;
Best Local Similarity 89.5%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CACAGCTGGGGAACAGAC 23
   |||||
Db 20 CACAGCTGGGGATGAAGAC 2

RESULT 7
US-10-719-900-979803/c
; Sequence 979803, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 979803
```

; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-719-900-979803

Query Match 65.8%; Score 15.8; DB 8; Length 25;  
Best Local Similarity 89.5%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GCACAGCTGGGGAACAAGA 22  
| | | | | | | | | | | | | | | | | | | | | |  
Db 22 GCACAGATGGGCAACAAGA 4

RESULT 8  
US-11-036-317-296939/c  
; Sequence 296939, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; APPLICANT: Blume, John  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036,317  
; CURRENT FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536,639  
; PRIOR FILING DATE: 2004-01-13  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 296939  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-296939

Query Match 65.0%; Score 15.6; DB 10; Length 25;  
Best Local Similarity 81.8%; Pred. No. 2.9e+03;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ATGCACAGCTGGGGAACAAGAC 23  
| | | | | | | | | | | | | | | | | | | | | |  
Db 25 ATGCTCATCTGTGGACCAAGAC 4

RESULT 9  
US-11-036-317-498568  
; Sequence 498568, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; APPLICANT: Blume, John  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036,317  
; CURRENT FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536,639  
; PRIOR FILING DATE: 2004-01-13  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 498568  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-498568

Query Match 65.0%; Score 15.6; DB 10; Length 25;  
Best Local Similarity 81.8%; Pred. No. 2.9e+03;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GATGCACAGCTGGGGAACAAGA 22  
| | | | | | | | | | | | | | | | | | | | | |  
Db 4 GCTGCACCTGCTGAGGAACAACA 25

RESULT 10  
US-11-036-317-810975  
; Sequence 810975, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; APPLICANT: Blume, John  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036,317  
; CURRENT FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536,639  
; PRIOR FILING DATE: 2004-01-13  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 810975  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-810975

Query Match 65.0%; Score 15.6; DB 10; Length 25;  
Best Local Similarity 81.8%; Pred. No. 2.9e+03;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TGCACAGCTGGGGAACAAGACG 24  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 TGCTCAGCACTGGGAACAAGACG 22

RESULT 11  
US-10-874-242-35  
; Sequence 35, Application US/10874242  
; Publication No. US20050026252A1  
; GENERAL INFORMATION:  
; APPLICANT: ESTES, SCOTT  
; APPLICANT: ZHANG, WEIQUN  
; TITLE OF INVENTION: NOVEL PROMOTERS AND USES THEREOF  
; FILE REFERENCE: 07680.0027-00000  
; CURRENT APPLICATION NUMBER: US/10/874,242  
; CURRENT FILING DATE: 2004-06-24  
; PRIOR APPLICATION NUMBER: 60/480,768  
; PRIOR FILING DATE: 2003-06-24  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 35  
; LENGTH: 26  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: forward primer for amplifying beta-actin promoter containing  
; OTHER INFORMATION: Intron 1  
US-10-874-242-35

Query Match 65.0%; Score 15.6; DB 8; Length 26;  
Best Local Similarity 81.8%; Pred. No. 2.9e+03;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ATGCACAGCTGGGGAACAAGAC 23  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 AGGCCAGCCTTGGGACCAAGAC 22

RESULT 12  
US-10-719-900-741411/c  
; Sequence 741411, Application US/10719900  
; Publication No. US20050026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Wei  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900

```
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 741411
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-741411
```

```
Query Match 63.3%; Score 15.2; DB 8; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 GATGCACAGCTGGGGAACAA 20
    ||||| ||||| ||||| ||||| |||||
Db 22 GATGCCCATCTTGGGAACAA 3
```

```
RESULT 13
US-10-719-900-841215/c
; Sequence 841215, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 841215
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-841215
```

```
Query Match 63.3%; Score 15.2; DB 8; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 3 TGCACAGCTGGGGAACAGA 22
    ||||| ||||| ||||| ||||| |||||
Db 20 TGCACAGCTAGGAAGAA 1
```

```
RESULT 14
US-10-809-189-92895
; Sequence 92895, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92895
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-92895
```

```
Query Match 63.3%; Score 15.2; DB 9; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 GATGCACAGCTGGGGAACAA 20
    ||||| ||||| ||||| ||||| |||||
Db 4 GCTGCAGAGCTGGGGAGAA 23
```

```
RESULT 15
US-11-036-317-523845
; Sequence 523845, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 523845
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-523845
```

```
Query Match 63.3%; Score 15.2; DB 10; Length 25;
Best Local Similarity 85.0%; Pred. No. 4.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 GATGCACAGCTGGGGAACAA 20
    ||||| ||||| ||||| ||||| |||||
Db 6 GCTGCACCTGCTGAGGAGCAA 25
```

```
RESULT 16
US-10-719-900-599645
; Sequence 599645, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 599645
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-599645
```

```
Query Match 62.5%; Score 15; DB 8; Length 25;
Best Local Similarity 78.3%; Pred. No. 5.4e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 GATGCACAGCTGGGGAACAAAGAC 23
    ||||| ||||| ||||| ||||| |||||
Db 2 GAGGCAGAGCTGGGTACCAACAC 24
```

```
RESULT 17
US-10-809-189-57613/c
; Sequence 57613, Application US/10809189
; Publication No. US20050048531A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57613
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-57613

Query Match      62.5%; Score 15; DB 9; Length 25;
Best Local Similarity 78.3%; Pred. No. 5.4e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 ATGCACAGCTGGGGAACAAGACG 24
Db      23 ATGCAGAAATAGGGACAAGATG 1

RESULT 18
US-10-956-157-14605/c
; Sequence 14605, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14605
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-14605

Query Match      62.5%; Score 15; DB 9; Length 25;
Best Local Similarity 78.3%; Pred. No. 5.4e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 GATGCACAGCTGGGGAACAAGAC 23
Db      23 GATTCACACCTGAGAAACAAGTC 1

RESULT 19
US-10-956-2771/c
; Sequence 2771, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 648791
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-648791

Query Match      61.7%; Score 14.8; DB 8; Length 25;
Best Local Similarity 88.9%; Pred. No. 6.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GATGCACAGCTGGGGAC 18
Db      18 GATGCACAGCTGGGGACC 1

; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 692355
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-692355/c
; Sequence 692355, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 692355
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-692355

Query Match      61.7%; Score 14.8; DB 7; Length 25;
Best Local Similarity 88.9%; Pred. No. 6.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      6 ACAGCTGGGGAACAAGAC 23
Db      22 ACAGATGGAGACAAGAC 5

RESULT 20
US-10-719-956-692355/c
; Sequence 692355, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 692355
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-692355

Query Match      61.7%; Score 14.8; DB 7; Length 25;
Best Local Similarity 88.9%; Pred. No. 6.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      6 ACAGCTGGGGAACAAGAC 23
Db      22 ACAGATGGAGACAAGAC 5

RESULT 21
US-10-719-900-648791/c
; Sequence 648791, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 648791
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-648791

Query Match      61.7%; Score 14.8; DB 8; Length 25;
Best Local Similarity 88.9%; Pred. No. 6.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GATGCACAGCTGGGGAC 18
Db      18 GATGCACAGCTGGGGACC 1
```

```
RESULT 22
US-10-956-157-315950/c
; Sequence 315950, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 315950
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-315950

Query Match      61.7%; Score 14.8; DB 9; Length 25;
Best Local Similarity 88.9%; Pred. No. 6.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TGCACAGCTGGGGAACAA 20
    ||||| ||||| ||||| ||
DB 18 TGCACAGCTGGGGAAGAA 1

RESULT 23
US-11-036-317-436639/c
; Sequence 436639, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 436639
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-436639

Query Match      61.7%; Score 14.8; DB 10; Length 25;
Best Local Similarity 88.9%; Pred. No. 6.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CACAGCTGGGGAACAGA 22
    ||||| ||||| ||||| ||
DB 24 CACAGCTGGGGACTAAGA 7

RESULT 24
US-10-719-956-198953/c
; Sequence 198953, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 198953
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-198953

Query Match      60.8%; Score 14.6; DB 7; Length 25;
Best Local Similarity 81.0%; Pred. No. 8.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 TGCACAGCTGGGGAACAAGAC 23
    ||||| ||||| ||||| ||||
DB 24 TGCACAGCTGGTCAAGATGAC 4

RESULT 25
US-10-719-956-198954/c
; Sequence 198954, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 198954
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-198954

Query Match      60.8%; Score 14.6; DB 7; Length 25;
Best Local Similarity 81.0%; Pred. No. 8.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 TGCACAGCTGGGGAACAAGAC 23
    ||||| ||||| ||||| ||||
DB 24 TGCACAGCTGGTCAAGATGAC 4

RESULT 26
US-10-719-900-58299/c
; Sequence 58299, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 58299
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-58299

Query Match      60.8%; Score 14.6; DB 8; Length 25;
Best Local Similarity 81.0%; Pred. No. 8.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 TGCACAGCTGGGGAACAAGAC 23
    ||||| ||||| ||||| ||||
DB 24 TGCACAGCTGGGTCAAGATC 4
```

```
RESULT 27
US-10-719-900-267621/c
; Sequence 267621, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 267621
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-267621

Query Match      60.8%; Score 14.6; DB 8; Length 25;
Best Local Similarity 81.0%; Pred. No. 8.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      3  TGCACAGCTGGGGAACAAGAC 23
      ||||| ||||| ||||| |||||
Db      24  TGCACAGCTGGTCAAGAGGAC 4

RESULT 28
US-10-719-900-267622/c
; Sequence 267622, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 267622
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-267622

Query Match      60.8%; Score 14.6; DB 8; Length 25;
Best Local Similarity 81.0%; Pred. No. 8.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      3  TGCACAGCTGGGGAACAAGAC 23
      ||||| ||||| ||||| |||||
Db      24  TGCACAGCTGGTCAAGAGGAC 4

RESULT 29
US-10-956-157-14604/c
; Sequence 14604, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14604
```

```
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-14604

Query Match      60.8%; Score 14.6; DB 9; Length 25;
Best Local Similarity 81.0%; Pred. No. 8.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1  GATGCACAGCTGGGGAACAAG 21
      ||||| ||||| ||||| |||||
Db      21  GATTCACACCTGAGAAACAAG 1

RESULT 30
US-10-956-157-14606/c
; Sequence 14606, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14606
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-14606

Query Match      60.8%; Score 14.6; DB 9; Length 25;
Best Local Similarity 81.0%; Pred. No. 8.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1  GATGCACAGCTGGGGAACAAG 21
      ||||| ||||| ||||| |||||
Db      22  GATTCACACCTGAGAAACAAG 2

RESULT 31
US-11-036-317-81764
; Sequence 81764, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 81764
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-81764

Query Match      60.8%; Score 14.6; DB 10; Length 25;
Best Local Similarity 81.0%; Pred. No. 8.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2  ATGCACAGCTGGGGAACAAGA 22
      ||||| ||||| ||||| |||||
Db      3  AGGCACAGCTGGATAGCAAGA 23
```

```
RESULT 32
US-11-036-317-189892/c
; Sequence 189892, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 189892
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-189892
Query Match 60.8%; Score 14.6; DB 10; Length 25;
Best Local Similarity 81.0%; Pred. No. 8.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 TGCACAGCTGGGGAACAAGAC 23
Db 25 TGCATCTGTGGACCAAGAC 5
|||||
|||||

RESULT 33
US-11-036-317-552223
; Sequence 552223, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 552223
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-552223
Query Match 60.8%; Score 14.6; DB 10; Length 25;
Best Local Similarity 81.0%; Pred. No. 8.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 ATGCACAGCTGGGGAACAAGA 22
Db 3 AGGCACAGCTGGATAGCAAGA 23
|||||
|||||

RESULT 34
US-11-036-317-770140/c
; Sequence 770140, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
```

```
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 770140
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-770140
Query Match 60.8%; Score 14.6; DB 10; Length 25;
Best Local Similarity 81.0%; Pred. No. 8.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 ATGCACAGCTGGGGAACAAGA 22
Db 25 AAGCACAGCTGGGTAAAGAGGA 5
|||||
|||||

RESULT 35
US-10-349-143-1997
; Sequence 1997, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 1997
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-7877-363 : polymorphic base A or G
US-10-349-143-1997
Query Match 60.8%; Score 14.6; DB 6; Length 47;
Best Local Similarity 73.9%; Pred. No. 8.2e+03;
Matches 17; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 GATGCACAGCTGGGGAACAAGAC 23
Db 24 RATGCACACCTGTTTCACAAGAC 46
|||||
|||||

RESULT 36
US-10-719-900-520335
; Sequence 520335, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 520335
; LENGTH: 25
```



```
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-520335

Query Match      60.0%; Score 14.4; DB 8; Length 25;
Best Local Similarity 75.0%; Pred. No. 1e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GATGCACAGCTGGGGAACAAGCAG 24
    ||||| ||||| ||||| |||||
Db 1 GATTCACAGCCGAGGACACAGCAGG 24

RESULT 37
US-10-719-900-520337
; Sequence 520337, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 520337
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-520337

Query Match      60.0%; Score 14.4; DB 8; Length 25;
Best Local Similarity 75.0%; Pred. No. 1e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GATGCACAGCTGGGGAACAAGCAG 24
    ||||| ||||| ||||| |||||
Db 1 GATTCACAGCCGCTGGACACAGCAGG 24

RESULT 38
US-11-036-317-46464/c
; Sequence 46464, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 46464
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-46464

Query Match      60.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGCACAGCTGGGGGAC 18
    ||||| ||||| |||||
Db 25 TGCACAGCTGGGGATC 10

RESULT 39
US-11-036-317-183105/c
; Sequence 183105, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 183105
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-183105

Query Match      60.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 CAGCTGGGGGAACAAGA 22
    ||||| ||||| |||||
Db 18 CAGCTGGGGGAACAAGA 3

RESULT 40
US-11-036-317-271344/c
; Sequence 271344, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 271344
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-271344

Query Match      60.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 CAGCTGGGGGAACAAGA 22
    ||||| ||||| |||||
Db 17 CAGCTGGGGGAACAAGA 2

Search completed: December 13, 2005, 16:17:15
Job time : 661 secs
```

**THIS PAGE BLANK (SEE ...)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 13:14:34 ; Search time 104.5 Seconds  
(without alignments)  
408.244 Million cell updates/sec

Title: US-10-713-137-3

Perfect score: 24

Sequence: 1 gatgcacagctggggaagacg 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1299706

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*

1: /cgn2\_6/ptodata/1/ina/1 COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5 COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/H COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/PCTUS COMB.seq.\*  
7: /cgn2\_6/ptodata/1/ina/PP COMB.seq.\*  
8: /cgn2\_6/ptodata/1/ina/RE COMB.seq.\*  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	15.2	63.3	25	3	US-09-396-196G-92895
c 2	15	62.5	25	3	US-09-396-196G-57613
c 3	15	62.5	38	2	US-08-537-811-13
4	14.6	60.8	47	3	US-09-422-978-1997
5	14.2	59.2	25	3	US-09-396-196G-103166
6	14.2	59.2	50	3	US-10-131-827-6696
c 7	14.2	59.2	50	3	US-10-131-827-7086
8	14	58.3	25	3	US-09-396-196G-32344
9	14	58.3	47	3	US-09-422-978-1898
10	14	58.3	50	3	US-10-131-827-6394
c 11	14	58.3	50	3	US-10-131-827-6784
c 12	13.8	57.5	17	3	US-09-866-108A-8469
c 13	13.8	57.5	20	3	US-09-194-478-5
14	13.8	57.5	25	3	US-09-866-108A-13361
15	13.8	57.5	25	3	US-09-866-108A-13362
16	13.8	57.5	25	3	US-09-866-108A-13363
17	13.8	57.5	25	3	US-09-866-108A-13364
18	13.8	57.5	25	3	US-09-866-108A-13365
19	13.8	57.5	25	3	US-09-866-108A-13366
20	13.8	57.5	25	3	US-09-866-108A-13367
21	13.8	57.5	25	3	US-09-866-108A-13368
22	13.8	57.5	25	3	US-09-866-108A-13369
c 23	13.8	57.5	47	3	US-09-422-978-3853
c 24	13.6	56.7	25	3	US-09-396-196G-57614

25 13.6 56.7 27 3 US-09-101-927-5 Sequence 5, Appli  
26 13.6 56.7 31 3 US-08-679-645-361 Sequence 361, App  
27 13.6 56.7 34 3 US-09-644-858-6 Sequence 6, Appli  
c 28 13.6 56.7 49 3 US-09-220-557-11 Sequence 11, Appl  
c 29 13.6 56.7 49 3 US-10-219-227-11 Sequence 11, Appl  
30 13.4 55.8 25 3 US-09-396-196G-88421 Sequence 88421, A  
31 13.4 55.8 25 3 US-09-396-196G-95727 Sequence 95727, A  
c 32 13.4 55.8 25 3 US-09-396-196G-107466 Sequence 107466,  
33 13.4 55.8 30 3 US-09-033-333-17 Sequence 17, Appl  
c 34 13.4 55.8 30 3 US-09-033-428-18 Sequence 18, Appl  
c 35 13.4 55.8 30 3 US-09-033-556-40 Sequence 40, Appl  
36 13.4 55.8 30 3 US-09-614-495-17 Sequence 17, Appl  
c 37 13.4 55.8 30 3 US-09-898-883-18 Sequence 18, Appl  
c 38 13.4 55.8 30 3 US-08-462-159B-6 Sequence 6, Appli  
c 39 13.4 55.8 30 3 US-09-814-292-38 Sequence 38, Appl  
c 40 13.4 55.8 30 3 US-09-875-228-24 Sequence 24, Appl  
c 41 13.4 55.8 45 3 US-09-897-259C-6 Sequence 6, Appli  
c 42 13.4 55.8 47 3 US-09-338-907-332 Sequence 332, App  
c 43 13.4 55.8 47 3 US-09-218-207-332 Sequence 332, App  
c 44 13.2 55.0 25 3 US-09-396-196G-14507 Sequence 14507, A  
c 45 13.2 55.0 25 3 US-09-396-196G-22239 Sequence 22239, A

## ALIGNMENTS

## RESULT 1

US-09-396-196G-92895 ; Sequence 92895, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396.196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 92895  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: mus musculus  
US-09-396-196G-92895

Query Match 63.3%; Score 15.2; DB 3; Length 25;

Best Local Similarity 85.0%; Pred. No. 8.9e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GATGCACAGCTGGGGAACAA 20

Db 4 GCTGCAGAGCTGGGGAAGAA 23

## RESULT 2

US-09-396-196G-57613/c ; Sequence 57613, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396.196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17

1. **Background**  
 2. **Methods**  
 3. **Results**  
 4. **Conclusions**  
 5. **References**  
 6. **Abbreviations**  
 7. **Keywords**  
 8. **Introduction**  
 9. **Discussion**  
 10. **Conclusion**  
 11. **References**  
 12. **Abbreviations**  
 13. **Keywords**  
 14. **Introduction**  
 15. **Discussion**  
 16. **Conclusion**  
 17. **References**  
 18. **Abbreviations**  
 19. **Keywords**  
 20. **Introduction**  
 21. **Discussion**  
 22. **Conclusion**  
 23. **References**  
 24. **Abbreviations**  
 25. **Keywords**  
 26. **Introduction**  
 27. **Discussion**  
 28. **Conclusion**  
 29. **References**  
 30. **Abbreviations**  
 31. **Keywords**  
 32. **Introduction**  
 33. **Discussion**  
 34. **Conclusion**  
 35. **References**  
 36. **Abbreviations**  
 37. **Keywords**  
 38. **Introduction**  
 39. **Discussion**  
 40. **Conclusion**  
 41. **References**  
 42. **Abbreviations**  
 43. **Keywords**  
 44. **Introduction**  
 45. **Discussion**  
 46. **Conclusion**  
 47. **References**  
 48. **Abbreviations**  
 49. **Keywords**  
 50. **Introduction**  
 51. **Discussion**  
 52. **Conclusion**  
 53. **References**  
 54. **Abbreviations**  
 55. **Keywords**  
 56. **Introduction**  
 57. **Discussion**  
 58. **Conclusion**  
 59. **References**  
 60. **Abbreviations**  
 61. **Keywords**  
 62. **Introduction**  
 63. **Discussion**  
 64. **Conclusion**  
 65. **References**  
 66. **Abbreviations**  
 67. **Keywords**  
 68. **Introduction**  
 69. **Discussion**  
 70. **Conclusion**  
 71. **References**  
 72. **Abbreviations**  
 73. **Keywords**  
 74. **Introduction**  
 75. **Discussion**  
 76. **Conclusion**  
 77. **References**  
 78. **Abbreviations**  
 79. **Keywords**  
 80. **Introduction**  
 81. **Discussion**  
 82. **Conclusion**  
 83. **References**  
 84. **Abbreviations**  
 85. **Keywords**  
 86. **Introduction**  
 87. **Discussion**  
 88. **Conclusion**  
 89. **References**  
 90. **Abbreviations**  
 91. **Keywords**  
 92. **Introduction**  
 93. **Discussion**  
 94. **Conclusion**  
 95. **References**  
 96. **Abbreviations**  
 97. **Keywords**  
 98. **Introduction**  
 99. **Discussion**  
 100. **Conclusion**  
 101. **References**  
 102. **Abbreviations**  
 103. **Keywords**  
 104. **Introduction**  
 105. **Discussion**  
 106. **Conclusion**  
 107. **References**  
 108. **Abbreviations**  
 109. **Keywords**  
 110. **Introduction**  
 111. **Discussion**  
 112. **Conclusion**  
 113. **References**  
 114. **Abbreviations**  
 115. **Keywords**  
 116. **Introduction**  
 117. **Discussion**  
 118. **Conclusion**  
 119. **References**  
 120. **Abbreviations**  
 121. **Keywords**  
 122. **Introduction**  
 123. **Discussion**  
 124. **Conclusion**  
 125. **References**  
 126. **Abbreviations**  
 127. **Keywords**  
 128. **Introduction**  
 129. **Discussion**  
 130. **Conclusion**  
 131. **References**  
 132. **Abbreviations**  
 133. **Keywords**  
 134. **Introduction**  
 135. **Discussion**  
 136. **Conclusion**  
 137. **References**  
 138. **Abbreviations**  
 139. **Keywords**  
 140. **Introduction**  
 141. **Discussion**  
 142. **Conclusion**  
 143. **References**  
 144. **Abbreviations**  
 145. **Keywords**  
 146. **Introduction**  
 147. **Discussion**  
 148. **Conclusion**  
 149. **References**  
 150. **Abbreviations**  
 151. **Keywords**  
 152. **Introduction**  
 153. **Discussion**  
 154. **Conclusion**  
 155. **References**  
 156. **Abbreviations**  
 157. **Keywords**  
 158. **Introduction**  
 159. **Discussion**  
 160. **Conclusion**  
 161. **References**  
 162. **Abbreviations**  
 163. **Keywords**  
 164. **Introduction**  
 165. **Discussion**  
 166. **Conclusion**  
 167. **References**  
 168. **Abbreviations**  
 169. **Keywords**  
 170. **Introduction**  
 171. **Discussion**  
 172. **Conclusion**  
 173. **References**  
 174. **Abbreviations**  
 175. **Keywords**  
 176. **Introduction**  
 177. **Discussion**  
 178. **Conclusion**  
 179. **References**  
 180. **Abbreviations**  
 181. **Keywords**  
 182. **Introduction**  
 183. **Discussion**  
 184. **Conclusion**  
 185. **References**  
 186. **Abbreviations**  
 187. **Keywords**  
 188. **Introduction**  
 189. **Discussion**  
 190. **Conclusion**  
 191. **References**  
 192. **Abbreviations**  
 193. **Keywords**  
 194. **Introduction**  
 195. **Discussion**  
 196. **Conclusion**  
 197. **References**  
 198. **Abbreviations**  
 199. **Keywords**  
 200. **Introduction**  
 201. **Discussion**  
 202. **Conclusion**  
 203. **References**  
 204. **Abbreviations**  
 205. **Keywords**  
 206. **Introduction**  
 207. **Discussion**  
 208. **Conclusion**  
 209. **References**  
 210. **Abbreviations**  
 211. **Keywords**  
 212. **Introduction**  
 213. **Discussion**  
 214. **Conclusion**  
 215. **References**  
 216. **Abbreviations**  
 217. **Keywords**  
 218. **Introduction**  
 219. **Discussion**  
 220. **Conclusion**  
 221. **References**  
 222. **Abbreviations**  
 223. **Keywords**  
 224. **Introduction**  
 225. **Discussion**  
 226. **Conclusion**  
 227. **References**  
 228. **Abbreviations**  
 229. **Keywords**  
 230. **Introduction**  
 231. **Discussion**  
 232. **Conclusion**  
 233. **References**  
 234. **Abbreviations**  
 235. **Keywords**  
 236. **Introduction**  
 237. **Discussion**  
 238. **Conclusion**  
 239. **References**  
 240. **Abbreviations**  
 241. **Keywords**  
 242. **Introduction**  
 243. **Discussion**  
 244. **Conclusion**  
 245. **References**  
 246. **Abbreviations**  
 247. **Keywords**  
 248. **Introduction**  
 249. **Discussion**  
 250. **Conclusion**  
 251. **References**  
 252. **Abbreviations**  
 253. **Keywords**  
 254. **Introduction**  
 255. **Discussion**  
 256. **Conclusion**  
 257. **References**  
 25



```
US-10-131-827-6394
; Sequence 6394, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: CHRONIC INFLAMMATORY DISEASES
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 3.1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6394
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-6394

Query Match      58.3%; Score 14; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCTGGGGAACAAGA 22
   |||||
DB 31 GCTGGGGAACAAGA 44

RESULT 11
US-10-131-827-6784/c
; Sequence 6784, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: CHRONIC INFLAMMATORY DISEASES
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6784
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-6784

Query Match      58.3%; Score 14; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GCTGGGGAACAAGA 22
   |||||
DB 20 GCTGGGGAACAAGA 7

RESULT 12
US-09-866-108A-8469
; Sequence 8469, Application US/09866108A
; Patent No. 6686188
```

```
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 8469
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-8469

Query Match      57.5%; Score 13.8; DB 3; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.8e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 AGCTGGGGAACAAGACG 24
   |||||
DB 1 AGCTGGGGAACAATGACG 17

RESULT 13
US-09-194-478-5/c
; Sequence 5, Application US/09194478
; Patent No. 6284463
; GENERAL INFORMATION:
; APPLICANT: Hasebe, Masahisa
; APPLICANT: Goto, Masanori
; APPLICANT: Tosu, Mariko
; TITLE OF INVENTION: Method for Detection of Mutations
; FILE REFERENCE: PU96-1684
; CURRENT APPLICATION NUMBER: US/09/194,478
; CURRENT FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: PCT/SE97/00839
; PRIOR FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: SWEDEN 9602062-3
; PRIOR FILING DATE: 1996-05-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: synthetic construct
```

```
US-09-194-478-5
Query Match          57.5%; Score 13.8; DB 3; Length 20;
Best Local Similarity 88.2%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      6 ACAGCTGGGGAACAAGA 22
      ||||| ||||| |||||
Db      20 ACAGCTGGAGAAGA 4

RESULT 14
US-09-866-108A-13361
; Sequence 13361, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13362
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13362

Query Match          57.5%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      8 AGCTGGGGAACAAGACG 24
      ||||| ||||| |||||
Db      8 AGCTGGAGAATGACG 24

RESULT 16
US-09-866-108A-13363
; Sequence 13363, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
```

```
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13363
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13363

Query Match      57.5%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4e+03; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      8 AGCTGGGGAACAAGACG 24
      ||||| ||||| |||||
Db      7 AGCTGGAGAACATGACG 23

RESULT 17
US-09-866-108A-13364
; Sequence 13364, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13364
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13365

Query Match      57.5%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4e+03; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      8 AGCTGGGGAACAAGACG 24
      ||||| ||||| |||||
Db      5 AGCTGGAGAACATGACG 21

RESULT 18
US-09-866-108A-13365
; Sequence 13365, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13365
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13365

Query Match      57.5%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4e+03; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      8 AGCTGGGGAACAAGACG 24
      ||||| ||||| |||||
Db      5 AGCTGGAGAACATGACG 21

RESULT 19
US-09-866-108A-13366
; Sequence 13366, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
```



```
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866.108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13366
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13366

Query Match      57.5%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      8 AGCTGGGGAACAAGACG 24
        ||||| ||||| |||||
Db      4 AGCTGGAGACATGACG 20

RESULT 20
US-09-866-108A-13367
; Sequence 13367, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866.108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13366
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13366

Query Match      57.5%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      8 AGCTGGGGAACAAGACG 24
        ||||| ||||| |||||
Db      4 AGCTGGAGACATGACG 20

RESULT 20
US-09-866-108A-13367
; Sequence 13367, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866.108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13366
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13367
```

```
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13367
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13367

Query Match      57.5%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      8 AGCTGGGGAACAAGACG 24
        ||||| ||||| |||||
Db      3 AGCTGGAGACATGACG 19

RESULT 21
US-09-866-108A-13368
; Sequence 13368, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866.108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13368
; LENGTH: 25
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13368

Query Match      57.5%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 0; Gaps 0;

QY 8 AGCTGGGGACACAGACG 24
    ||||| ||||| |||||
Db 2 AGCTGGAGAACATGACG 18

RESULT 22
US-09-866-108A-13369
; Sequence 13369, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13369
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13369

Query Match      57.5%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 0; Gaps 0;

QY 8 AGCTGGGGACACAGACG 24
    ||||| ||||| |||||
Db 1 AGCTGGAGAACATGACG 17

RESULT 23
US-09-422-978-3853/C
; Sequence 3853, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Rickles, Richard J
; TITLE OF INVENTION: Cell-Based Assay
; FILE REFERENCE: 336A PCT/US
```

; CURRENT APPLICATION NUMBER: US/09/101,927  
; CURRENT FILING DATE: 1998-07-15  
; EARLIER APPLICATION NUMBER: PCT/US97/026735  
; EARLIER FILING DATE: 1997-02-21  
; EARLIER APPLICATION NUMBER: 60/012,218  
; EARLIER FILING DATE: 1996-02-23  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 27  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-101-927-5

Query Match 56.7%; Score 13.6; DB 3; Length 27;  
Best Local Similarity 80.0%; Pred. No. 5e+03; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 4

Qy 1 GATGCACAGCTGGGGAACAA 20  
Db 4 GATCCGAGCTGGGGAAGAA 23

RESULT 26  
US-08-679-645-361  
; Sequence 361, Application US/08679645  
; Patent No. 6350934  
; GENERAL INFORMATION:  
; APPLICANT: Zwick, Michael G.  
; APPLICANT: Edington, Brent E.  
; APPLICANT: McSwiggen, James A.  
; APPLICANT: Merlo, Patricia Ann Owens  
; APPLICANT: Guo, Lining  
; APPLICANT: Skokut, Thomas A.  
; APPLICANT: Young, Scott A.  
; APPLICANT: Folkerts, Otto  
; APPLICANT: Merlo, Donald J.  
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR  
; TITLE OF INVENTION: MODULATION OF GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1263  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/679,645  
; FILING DATE: July 12, 1996  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/001,135  
; FILING DATE: July 13, 1995  
; APPLICATION NUMBER: 08/300,726  
; FILING DATE: September 2, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 219/247  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 361:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 31 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; OTHER INFORMATION: The letter "N" stands for any base.  
US-08-679-645-361

Query Match 56.7%; Score 13.6; DB 3; Length 31;  
Best Local Similarity 66.7%; Pred. No. 5.1e+03;  
Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GATGCACAGCTGGGGAACAAG 21  
Db 5 GAUGCACUGAUGAAGAAAG 25

RESULT 27  
US-09-644-858-6  
; Sequence 6, Application US/09644858  
; Patent No. 6933364  
; GENERAL INFORMATION:  
; APPLICANT: Tosho Corporation  
; APPLICANT: Hattori, Yoshiyuki  
; APPLICANT: Akamizu, Takashi  
; TITLE OF INVENTION: SECRETORY THYROID STIMULATING HORMONE RECEPTOR, AND METHOD FOR  
; TITLE OF INVENTION: ANTI-THYROID STIMULATING HORMONE RECEPTOR ANTIBODY USING THE S  
; FILE REFERENCE: PA21-0046  
; CURRENT APPLICATION NUMBER: US/09/644,858  
; CURRENT FILING DATE: 2000-08-24  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6  
; LENGTH: 34  
; TYPE: DNA  
; ORGANISM: Artificial/Unknown  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: ()...()  
; OTHER INFORMATION: sense primer sHTSHR-2  
US-09-644-858-6

Query Match 56.7%; Score 13.6; DB 3; Length 34;  
Best Local Similarity 80.0%; Pred. No. 5.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 CACAGCTGGGGAACAAGC 24  
Db 10 CGCAGCTGAAGACAAGAGG 29

RESULT 28  
US-09-220-557-11/c  
; Sequence 11, Application US/09220557A  
; Patent No. 6515206  
; GENERAL INFORMATION:  
; APPLICANT: Chaudhuri, Sumita  
; TITLE OF INVENTION: PLASTID TRANSFORMATION OF BRASSICA  
; FILE REFERENCE: 15398/00/US  
; CURRENT APPLICATION NUMBER: US/09/220,557A  
; CURRENT FILING DATE: 1998-12-23  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 49  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-09-220-557-11

Query Match 56.7%; Score 13.6; DB 3; Length 49;

Best Local Similarity 80.0%; Pred. No. 5.4e+03; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 4;

QY 5 CACAGCTGGGGAACAAGACG 24  
||||| ||||| ||||| ||  
Db 39 CACAGCGAGGGAGCAAGTCG 20

## RESULT 29

US-10-219-227-11/c  
; Sequence 11, Application US/10219227  
; Patent No. 6891086  
; GENERAL INFORMATION:  
; APPLICANT: Oakes, Janette V.  
; APPLICANT: Chaudhuri, Sumita  
; TITLE OF INVENTION: PLASTID TRANSFORMATION OF BRASSICA  
; FILE REFERENCE: 15398/01/US  
; CURRENT APPLICATION NUMBER: US/10/219,227  
; CURRENT FILING DATE: 2002-08-15  
; PRIOR APPLICATION NUMBER: US/09/465,856  
; PRIOR FILING DATE: 1999-12-17  
; PRIOR APPLICATION NUMBER: 09/220,557  
; PRIOR FILING DATE: 1998-12-23  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 49  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-10-219-227-11

Query Match 56.7%; Score 13.6; DB 3; Length 49;  
Best Local Similarity 80.0%; Pred. No. 5.4e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 CACAGCTGGGGAACAAGACG 24  
||||| ||||| ||||| ||  
Db 39 CACAGCGAGGGAGCAAGTCG 20

## RESULT 30

US-09-396-196G-88421  
; Sequence 88421, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 88421  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: mus musculus  
US-09-396-196G-88421

Query Match 55.8%; Score 13.4; DB 3; Length 25;  
Best Local Similarity 73.9%; Pred. No. 6.1e+03;  
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATGCACAGCTGGGGAACAAGACG 24  
||||| ||||| ||||| ||  
Db 1 ATGGCTCTTTGGGGACAAATCG 23

## RESULT 31

US-09-396-196G-95727  
; Sequence 95727, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 95727  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: mus musculus  
US-09-396-196G-95727

Query Match 55.8%; Score 13.4; DB 3; Length 25;  
Best Local Similarity 93.3%; Pred. No. 6.1e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGCACAGCTGGGGAA 17  
||||| ||||| ||||| ||  
Db 7 TGAACAGCTGGGGAA 21

## RESULT 32

US-09-396-196G-107466/c  
; Sequence 107466, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 107466  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: mus musculus  
US-09-396-196G-107466

Query Match 55.8%; Score 13.4; DB 3; Length 25;  
Best Local Similarity 73.9%; Pred. No. 6.1e+03;  
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATGCACAGCTGGGGAACAAGACG 24  
||||| ||||| ||||| ||  
Db 25 ATTCACAGCTGTTTAAAAAGAGG 3

## RESULT 33

US-09-033-333-17/c  
; Sequence 17, Application US/090333333  
; Patent No. 6137293  
; GENERAL INFORMATION:  
; APPLICANT: Yu, De Chao  
; APPLICANT: Schuur, Eric  
; APPLICANT: Henderson, Daniel

```
;
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC
; TITLE OF INVENTION: FOR CELLS EXPRESSING ANDROGEN RECEPTOR AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,333
; FILING DATE: 02-MAR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine, Polizzi M
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-20007.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-033-333-17

Query Match 55.8%; Score 13.4; DB 3; Length 30;
Best Local Similarity 73.9%; Pred. No. 6.3e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATGCACAGCTGGGGAACAGACG 24
Db 25 AAGCAGAGCGGTGGACAAAGG 3

RESULT 34
US-09-033-428-18/c
; Sequence 19, Application US/09033428
; Patent No. 6254862
; GENERAL INFORMATION:
; APPLICANT: Little, Andrew
; APPLICANT: Lamparski, Henry
; APPLICANT: Schuur, Eric
; APPLICANT: Henderson, Daniel
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
; TITLE OF INVENTION: EXPRESSING ALPHA-FETOPROTEIN AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
```

```
;
; APPLICATION NUMBER: US/09/033,428
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: POLIZZI, CATHERINE M.
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-30004.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141 MRSNFOERS SFO
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-033-428-18

Query Match 55.8%; Score 13.4; DB 3; Length 30;
Best Local Similarity 73.9%; Pred. No. 6.3e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATGCACAGCTGGGGAACAGACG 24
Db 25 AAGCAGAGCGGTGGACAAAGG 3

RESULT 35
US-09-033-556-40/c
; Sequence 40, Application US/09033556
; Patent No. 6432700
; GENERAL INFORMATION:
; APPLICANT: Henderson, Daniel R.
; APPLICANT: Yu, De Chao
; TITLE OF INVENTION: ADENOVIRUS VECTORS CONTAINING
; TITLE OF INVENTION: HETEROLOGOUS TRANSCRIPTION REGULATORY ELEMENTS AND METHODS
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,556
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine, Polizzi M
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-20010.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-033-556-40
```

```
Query Match          55.8%; Score 13.4; DB 3; Length 30;
Best Local Similarity 73.9%; Pred. No. 6.3e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATGCACAGCTGGGGAACAAGC 24
   ||||| ||||| ||||| ||||| |||||
Db 25 AAGCAGAGCGGTGGAACAAAGG 3

RESULT 36
US-09-614-495-17/c
; Sequence 17, Application US/09614495
; Patent No. 6436394
; GENERAL INFORMATION:
; APPLICANT: Yu, De Chao
; Schuur, Eric
; Henderson, Daniel
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC
; FOR CELLS EXPRESSING ANDROGEN RECEPTOR AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/614,495
; FILING DATE: 11-Jul-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/033,333
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine, Polizzi M
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-20007.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-614-495-17

Query Match          55.8%; Score 13.4; DB 3; Length 30;
Best Local Similarity 73.9%; Pred. No. 6.3e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATGCACAGCTGGGGAACAAGC 24
   ||||| ||||| ||||| ||||| |||||
Db 25 AAGCAGAGCGGTGGAACAAAGG 3

RESULT 37
US-09-898-883-18/c
; Sequence 18, Application US/09898883
; Patent No. 6585968
; GENERAL INFORMATION:
; APPLICANT: Little, Andrew
; Lamparski, Henry
; Schuur, Eric
; Henderson, Daniel
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
; EXPRESSING ALPHA-FETOPROTEIN AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/898,883
; FILING DATE: 02-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,428
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: POLIZZI, CATHERINE M.
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-30004.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141 MRSNFOERS SFO
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-898-883-18

Query Match          55.8%; Score 13.4; DB 3; Length 30;
Best Local Similarity 73.9%; Pred. No. 6.3e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATGCACAGCTGGGGAACAAGC 24
   ||||| ||||| ||||| ||||| |||||
Db 25 AAGCAGAGCGGTGGAACAAAGG 3

RESULT 38
US-08-462-159B-6/c
; Sequence 6, Application US/08462159B
; Patent No. 6787640
; GENERAL INFORMATION:
; APPLICANT: Greene Ph.D., John M.
; Dillon Ph.D., Patrick J.
; TITLE OF INVENTION: Fibroblast Growth Factor 14
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSES: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
```

;  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/462,159B  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/207,412  
; FILING DATE: 08-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MULLINS, J.G.  
; REGISTRATION NUMBER: 33,073  
; REFERENCE/DOCKET NUMBER: 325800-440  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 30 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-462-159B-6

Query Match 55.8%; Score 13.4; DB 3; Length 30;  
Best Local Similarity 73.9%; Pred. No. 6.3e+03;  
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATGCACAGCTGGGACAAAGACG 24  
Db 23 ACGCGCCGCTGGGGATCCAGTCG 1

RESULT 39

US-09-814-292-38/c  
; Sequence 38, Application US/09814292  
; Patent No. 6852528  
; GENERAL INFORMATION:

; APPLICANT: Yu, De-Chao  
; APPLICANT: Zhang, Hong  
; APPLICANT: Henderson, Daniel R.  
; TITLE OF INVENTION: HUMAN UROTHELIAL CELL SPECIFIC UROPLAKIN  
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATORY SEQUENCES, VECTORS COMPRISING  
; TITLE OF INVENTION: UROPLAKIN-SPECIFIC TRANSCRIPTIONAL REGULATORY SEQUENCES, AND  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 348022001500  
; CURRENT APPLICATION NUMBER: US/09/814,292  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: 60/191,861  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 38  
; LENGTH: 30  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR Primer 37,124.3  
US-09-814-292-38

Query Match 55.8%; Score 13.4; DB 3; Length 30;  
Best Local Similarity 73.9%; Pred. No. 6.3e+03;  
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATGCACAGCTGGGACAAAGACG 24  
Db 25 AAGCAGAGCGGTGGAAACAAAAGG 3

RESULT 40

US-09-875-228-24/c  
; Sequence 24, Application US/09875228  
; Patent No. 6916918  
; GENERAL INFORMATION:

; APPLICANT: Yu, D.  
; APPLICANT: Henderson, D.R.  
; APPLICANT: Schuur, E.R.  
; TITLE OF INVENTION: A HUMAN GLANDULAR KALLIKREIN ENHANCER, VECTORS COMPRISING THE  
; TITLE OF INVENTION: ENHANCER AND METHODS OF USE THEREOF  
; FILE REFERENCE: 348022000900  
; CURRENT APPLICATION NUMBER: US/09/875,228  
; CURRENT FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: 09/127,834  
; PRIOR FILING DATE: 1998-08-03  
; PRIOR APPLICATION NUMBER: 60/076,545  
; PRIOR FILING DATE: 1998-03-02  
; PRIOR APPLICATION NUMBER: 60/054,523  
; PRIOR FILING DATE: 1997-08-04  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 30  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Sequence is  
; OTHER INFORMATION: produced synthetically.  
US-09-875-228-24

Query Match 55.8%; Score 13.4; DB 3; Length 30;  
Best Local Similarity 73.9%; Pred. No. 6.3e+03;  
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATGCACAGCTGGGACAAAGACG 24  
Db 25 AAGCAGAGCGGTGGAAACAAAAGG 3

Search completed: December 13, 2005, 15:55:00  
Job time : 105.5 secs

**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 12:51:49 ; Search time 2984 Seconds  
(without alignments)  
376.304 Million cell updates/sec

Title: US-10-713-137-3  
Perfect score: 24  
Sequence: 1 gatcacagctgggggaacaagacg 24

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 179606

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_hic:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gss1:\*  
10: gb\_gss2:\*  
11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	15	62.5	38	10	CL214453	CL214453 W255E01 G
C 2	14.6	60.8	37	9	AZ832358	AZ832358 2M0112P10
C 3	14.6	60.8	46	11	CR396399	CR396399 Arabidops
C 4	14	58.3	38	10	AL945338	AL945338 Arabidops
C 5	14	58.3	50	1	AU103763	AU103763 AU103763
C 6	13.6	56.7	39	9	AZ769231	AZ769231 IM0569G07
7	13.2	55.0	31	1	AI156750	AI156750 ue54b07.r
C 8	13	54.2	38	10	CL844510	CL844510 EY12606-5
C 9	13	54.2	41	9	AZ470528	AZ470528 IM0284H11
C 10	13	54.2	43	1	AI185696	AI185696 ge60g07.x
C 11	13	54.2	43	10	CS803673	CS803673 1118044H1
C 12	13	54.2	50	1	AU103768	AU103768 AU103768
C 13	13	54.2	50	1	AU104109	AU104109 AU104109
C 14	13	54.2	50	9	AZ565607	AZ565607 211PVA09
C 15	12.8	53.3	42	9	BH865278	BH865278 SALK 0980
C 16	12.8	53.3	47	1	AV832547	AV832547 AV832547
C 17	12.6	52.5	30	10	AG200388	AG200388 Pan trogl
C 18	12.6	52.5	43	10	CZ472331	CZ472331 d01604-3p
C 19	12.6	52.5	47	10	AG217348	AG217348 Drosophil
C 20	12.6	52.5	49	1	AI527771	AI527771 uJ28H01.Y
C 21	12.4	51.7	25	9	AZ511249	AZ511249 IM0356N10
C 22	12.4	51.7	28	1	AA958372	AA958372 uall1a03.r

23	12.4	51.7	38	10	CW986355	CW986355 KBRH012L0
24	12.4	51.7	42	9	AZ814914	AZ814914 2M0082C24
25	12.4	51.7	45	9	BH855497	BH855497 SALK 0850
26	12.4	51.7	48	9	BH626386	BH626386 1007113H0
C 27	12.4	51.7	49	9	BH640991	BH640991 1008039E0
28	12.4	51.7	49	10	CZ469449	CZ469449 c04702-3p
C 29	12.2	50.8	18	3	BM395302	BM395302 50072-2-8
C 30	12.2	50.8	36	1	AA776443	AA776443 zj50h10.s
C 31	12.2	50.8	37	1	AJ239879	AJ239879 AJ239879
C 32	12.2	50.8	41	1	AA287473	AA287473 zs50a12.x
C 33	12.2	50.8	42	1	AV957763	AV957763 AV957763
C 34	12.2	50.8	44	1	AU255694	AU255694 AU255694
C 35	12.2	50.8	45	1	AJ792767	AJ792767 AJ792767
C 36	12.2	50.8	49	1	AI254367	AI254367 qv33a10.x
C 37	12.2	50.8	50	1	AU105506	AU105506 AU105506
C 38	12.2	50.8	50	1	AU105507	AU105507 AU105507
C 39	12	50.0	30	10	CZ909855	CZ909855 4018011H1
C 40	12	50.0	33	8	DN955268	DN955268 it84h05.g
C 41	12	50.0	38	8	R10392	R10392 Yf37e03.81
C 42	12	50.0	38	9	CC798667	CC798667 SALK 1472
C 43	12	50.0	38	9	CC798676	CC798676 SALK 1472
C 44	12	50.0	39	9	AZ501408	AZ501408 IM0340813
C 45	12	50.0	40	10	AG199766	AG199766 Pan trogl

ALIGNMENTS

RESULT 1  
CL214453  
LOCUS W255E01, mRNA sequence.  
DEFINITION CL214453.2 GI:49489711  
ACCESSION GSS.  
VERSION CL214453.2  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Hansen, J., Flose, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F.,  
Arnold, H.H., Schnutgen, F., Wurst, W., Von Melchner, H. and Ruiz, P.  
TITLE A large-scale, gene-driven mutagenesis approach for the functional  
analysis of the mouse genome  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)  
PUBMED 12904583  
COMMENT On Jan 27, 2005 this sequence version replaced gi:40731354.  
Contact: GGTC  
German Genetrap Consortium (GGTC)  
Email: info@genetrap.de  
ROSAbetageo+1 gene trap. Sequence tag generated by 5'RACE.  
Additional sequence information can be found at:  
'http://genetrap.gsf.de/project/web\_new/database/result\_clone.html?clone\_id=W255E01' ES cell line harboring insertion mutation of target gene is available at:  
'http://genetrap.gsf.de/project/web\_new/order\_clones/howtoorder.htm' 1' Inhouse Sequence Identifier: 12462  
Class: Gene Trap.

FEATURES

source  
1..38  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129 Sv"  
/db\_xref="taxon:10090"  
/clone="W255E01"  
/sex="Male"  
/cell\_type="Embryonic stem cell"  
/cell\_line="ES cells 129S2 (formerly 129/SvPas)"  
/clone\_lib="GGTC Gene Trap Library GV04C04"  
/note="Vector: ROSAbetageo"

ORIGIN



## ORIGIN

Query Match 60.8%; Score 14.6; DB 11; Length 46;  
 Best Local Similarity 81.0%; Pred. No. 8e+04; 4; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATGCACAGCTGGGGAACAAGA 22  
 |||||  
 Db 45 ACGCACAGCTGGGGAAGA 25

## RESULT 4

AL945338/c  
 LOCUS AL945338 38 bp DNA linear GSS 01-APR-2004  
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-288F04-015346,  
 genomic survey sequence.

ACCESSION AL945338  
 VERSION AL945338.1 GI:24401960  
 KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

## ORGANISM

Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

## REFERENCE

1 Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P., and Weissshaar, B.  
 GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for  
 the identification of T-DNA insertion mutants in Arabidopsis  
 thaliana

JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)  
 PUBMED 12874060

## REFERENCE

2 Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and  
 Weissshaar, B.

High-throughput generation of sequence indexes from T-DNA  
 mutagenized Arabidopsis thaliana lines  
 Biotechniques 35 (6), 1164-1168 (2003)  
 14682050

## REFERENCE

3 Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and  
 Weissshaar, B.

High-throughput generation of sequence indexes from T-DNA  
 mutagenized Arabidopsis thaliana lines  
 Biotechniques 35 (6), 1164-1168 (2003)  
 14682050

## REFERENCE

4 Li, Y., Rosso, M.G., Strizhov, N. and Weissshaar, B.  
 Direct Submission

4 (bases 1 to 38)

## TITLE

Submitted (31-MAR-2004) Weissshaar B., Max-Planck-Institut fuer  
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 This sequence has been recovered from the left border of the T-DNA.  
 It indicates an insertion within the locus defined by BAC clone  
 F5D14. Details on the protocols used for generation of the sequence  
 are described in References 1-3. The sequences are generated at the  
 MPI for Plant Breeding Research in the context of the GABI-Kat  
 project. GABI-Kat is part of the German Plant Genomics program  
 designated 'GABI'. Information on line availability can be found  
 at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

## FEATURES

source

1. 38  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:3702"  
 /clone="GK-288F04-015346"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 /ecotype="Col-0"  
 /note="PCR was performed on DNA from Arabidopsis thaliana  
 plants (T1) which were transformed with the T-DNA from  
 vector pAC161 (GenBank accession number: AJ537514). The  
 lines contain one or more T-DNA insertions. The DNA  
 fragment(s) resulting from the PCR were directly sequenced  
 to determine the genomic sequence flanking the insertion.  
 T-DNA derived sequences were removed."

## ORIGIN

Query Match 58.3%; Score 14; DB 10; Length 38;  
 Best Local Similarity 77.3%; Pred. No. 1.5e+05;  
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GATGCACAGCTGGGGAACAAGA 22  
 |||||  
 Db 33 GATGCACAACAGCGCATCAGA 12

## RESULT 5

AL945338/c  
 LOCUS AU103763 50 bp mRNA linear EST 28-JAN-2004  
 DEFINITION AU103763 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
 HEP10745, mRNA sequence.

ACCESSION AU103763  
 VERSION AU103763.1 GI:13553284  
 KEYWORDS EST.

SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.

## REFERENCE

1 (bases 1 to 50)  
 AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,  
 Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,  
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale  
 mapping of mRNA start sites

JOURNAL EMBO Rep. 2 (5), 388-393 (2001)  
 PUBMED 11375929

## COMMENT

Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: [ysuzuki@ims.u-tokyo.ac.jp](mailto:ysuzuki@ims.u-tokyo.ac.jp)  
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and  
 Sugano, S. Construction and characterization of a full  
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),  
 149-156 (1997).

## FEATURES

source

1. 50  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="HEP10745"  
 /clone\_lib="Sugano Homo sapiens cDNA library"

## ORIGIN

Query Match 58.3%; Score 14; DB 1; Length 50;  
 Best Local Similarity 77.3%; Pred. No. 1.5e+05;  
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGCACAGCTGGGGAACAAGAC 23  
 |||||

Db 25 AGGCTAGCTGGCGAACAACAC 4

## RESULT 6

AZ769231/c  
 LOCUS AZ769231 39 bp DNA linear GSS 16-FEB-2001  
 DEFINITION 1M0569G07R Mouse 10Kb plasmid UUC1M library Mus musculus genomic  
 clone UUC1M0569G07 R, genomic survey sequence.

ACCESSION AZ769231  
 VERSION AZ769231.1 GI:12889151

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 39)

**AUTHORS** Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, S., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

**JOURNAL** Unpublished (2000)

**COMMENT** Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0569 row: G column: 07  
Seq primer: CACACGAGAACACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 39.

## FEATURES

```

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0569G07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|342114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

## ORIGIN

Query Match	56.7%	Score 13.6;	DB 9;	Length 39;
Best Local Similarity	80.0%	Pred. No. 2.3e+05;		
Matches 16:	Conservative	0;	Mismatches 4;	Indels 0; Gaps 0;

5 CACAGCTGGGGAA CAAGACG 24

33 CACAGTTAGGTAACAAGATG 14

RESULT 7	AI156750	31 bp	mRNA	linear	EST 30-SEP-1998
OCUS	ue54b07.r1	Soares_mammary_gland	NLMG	Mus musculus	cDNA clone
DEFINITION	IMAGE:1494901.5	similar to TR:Q99942	Q99942	HYPOTHETICAL	19.9 KD
		PROTEIN. <i>i</i> .	mRNA	sequence.	

ACCESSION	AI156750	GI:3685219
VERSION	AI156750.1	
KEYWORDS	EST.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;	

REFERENCE  
AUTHORS

TITLE	JOURNAL	COMMENT
1. The Role of the Teacher in the Classroom	Journal of Educational Research	1980, Vol. 83, No. 1, pp. 1-10
2. The Impact of Technology on Education	Journal of Educational Research	1980, Vol. 83, No. 2, pp. 11-20
3. The Importance of Parental Involvement	Journal of Educational Research	1980, Vol. 83, No. 3, pp. 21-30
4. The Effect of Teacher Expectations on Student Achievement	Journal of Educational Research	1980, Vol. 83, No. 4, pp. 31-40
5. The Role of the School in the Community	Journal of Educational Research	1980, Vol. 83, No. 5, pp. 41-50
6. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	1980, Vol. 83, No. 6, pp. 51-60
7. The Importance of Teacher Professionalism	Journal of Educational Research	1980, Vol. 83, No. 7, pp. 61-70
8. The Effect of Teacher Salary on Student Achievement	Journal of Educational Research	1980, Vol. 83, No. 8, pp. 71-80
9. The Role of the School in the Community	Journal of Educational Research	1980, Vol. 83, No. 9, pp. 81-90
10. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	1980, Vol. 83, No. 10, pp. 91-100

FEATURES source

## ORIGIN

7 CAGCTGGGGAAACAAGACG 24

**Df**

CAGCAGGGAAGAAGACG 23  
|||||  
CAGCAGGGAAGAAGACG 23

DEC 11 1968

RESOLUTION 8  
CT.844510/C

LOCUS

## DEFINITION

# SECRET

**ACCESSION**

**VERSION**

## KEYWORDS

**SOURCE**

## ORGANISM

[illegible]

## REFERENCE

## AUTHORS

D  
E  
B  
T

**TITLE**  
**JOURNAL**

**JOURNAL  
COMMENT**

COMMENT

University of California, Berkeley  
LSA Building, Berkeley, CA 94720-3200, USA  
Fax: 5106433947  
Email: gerry@fruitfly.berkeley.edu  
Sequence recovery method was inverse PCR.  
Sequence orientation is forward strand relative to 5' end of P element

The P element insertion position is base 31 in the 38 bases. This insertion position refers to the first base of the 8 base target recognition sequence.

Class: transposon-tagged.

Location/Qualifiers

## FEATURES

source

1. .38  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone\_lib="Drosophila melanogaster P{EPgy2} P element insertion lines"  
/note="Inverse PCR was performed on Drosophila melanogaster strains each of which contains one or more P{EPgy2} P-element transposon insertion. The resultant fragment for each strain was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at <http://www.fruitfly.org/about/methods/inverse.pcr.html>."

## ORIGIN

Query Match 54.2%; Score 13; DB 10; Length 38;  
Best Local Similarity 76.2%; Pred. No. 4.3e+05;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ATGCACAGCTGGGACAAAGA 22

Db 29 ATGAAGAAGCTGCATAACAAGA 9

## RESULT 9

AZ470528/c  
LOCUS 41 bp DNA linear GSS 04-OCT-2000  
DEFINITION IM0284H1R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0284H1 R, genomic survey sequence.

## ACCESSION

AZ470528

## VERSION

AZ470528.1 GI:10628653

## KEYWORDS

GSS.

## SOURCE

Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

## AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

## TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

## JOURNAL

## COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0284 row: H column: 11

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 41.

Location/Qualifiers

1. .41

/organism="Mus musculus"

## FEATURES

source

1. .41

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0284H1"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 54.2%; Score 13; DB 9; Length 41;  
Best Local Similarity 76.2%; Pred. No. 4.3e+05;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 GCACAGCTGGGACACAGACG 24

Db 40 GCACAGCGGGGGCCAGGATG 20

## RESULT 10

## LOCUS

## DEFINITION

Q66097.x1 Soares fetal lung NBHL19W Homo sapiens cDNA clone IMAGE:1743420 3' similar to SW:PRPM HUMAN P10161 SALIVARY PROLINE-RICH PROTEIN PO ;, mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

This clone is available royalty-free through LNL ; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.

Trace considered overall poor quality

Insert Length: 612 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1. .43

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1743420"

/dev stage="19 weeks"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares\_fetal\_lung\_NBHL19W"

## FEATURES

source

1. .43

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1743420"

/dev stage="19 weeks"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares\_fetal\_lung\_NBHL19W"

/note="Organ: lung; Vector: pTT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-GTGACCAATCTGAAGTGGAGCGCGCAATTTTTTTTTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NBHH19W."

## ORIGIN

Query Match 54.2%; Score 13; DB 1; Length 43;  
Best Local Similarity 76.2%; Pred. No. 4.3e+05;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GATGCACAGCTGGGGNACAAG 21  
||||| | | | | | | | | | | | | | | | | | | | |  
Db 23 GATGCCCCCGGGGGNAAAAG 3

## RESULT 11

CG803673 43 bp DNA linear GSS 10-NOV-2003  
DEFINITION 1118044H12.2EL.Y1 1118 - RescueMu Grid S Zea mays genomic, genomic survey sequence.

ACCESSION CG803673  
VERSION CG803673.1 GI:38239459  
KEYWORDS GSS.

## SOURCE

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

Clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 43)

Walbot.V.

Maize genomic sequences found using engineered RescueMu transposon

Unpublished (2001)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 1118044 row: 14

Class: transposon-tagged.

Location/Qualifiers

1..43

/organism="Zea mays"

/mol\_type="genomic DNA"

/cultivar="mixed background W23/A188/B73"

/db\_xref="taxon:4577"

/tissue\_type="leaf"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="1118 - RescueMu Grid S"

/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid S was grown at San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

## ORIGIN

Query Match 54.2%; Score 13; DB 10; Length 43;  
Best Local Similarity 76.2%; Pred. No. 4.3e+05;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GATGCACAGCTGGGGNACAAG 21  
||||| | | | | | | | | | | | | | | | | | | | |  
Db 11 GATGAACAGATGTGGAGATG 31

## RESULT 12

AU103768/c  
LOCUS AU103768 Sugano Homo sapiens cDNA library EST 28-JAN-2004  
DEFINITION HEPI2651, mRNA sequence.

ACCESSION AU103768

VERSION AU103768.1 GI:13553289

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 50)

Suzuki.Y., Taira.H., Tsunoda.T., Mizushima-Sugano.J., Sese,J.,

Hata,H., Ota,T., Isogai,T., Tanaka,I., Morishita,S., Okubo,K.,

Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.

Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

11375929

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki.Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and

Sugano,S. Construction and characterization of a full

length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),

149-156 (1997).

Location/Qualifiers

1..50

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="HEPI2651"

/clone\_lib="Sugano Homo sapiens cDNA library"

Location/Qualifiers

1..50

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="HEPI2651"

/clone\_lib="Sugano Homo sapiens cDNA library"

Location/Qualifiers

1..50

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="HEPI2651"

/clone\_lib="Sugano Homo sapiens cDNA library"

Location/Qualifiers

1..50

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="HEPI2651"

/clone\_lib="Sugano Homo sapiens cDNA library"

Location/Qualifiers

1..50

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="HEPI2651"

/clone\_lib="Sugano Homo sapiens cDNA library"

**AUTHORS** Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isoqai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S. fine, large-scale mapping of mRNA start sites

**JOURNAL PUBMED** EMBO Rep. 2 (5), 388-393 (2001) 11375929

**COMMENT** Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yezuki@ims.u-tokyo.ac.jp  
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

**FEATURES** source  
1..50  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_lib="HEPI3777"  
/clone\_lib="Sugano Homo sapiens cDNA library"

**ORIGIN**  
Query Match 54.2%; Score 13; DB 1; Length 50;  
Best Local Similarity 76.2%; Pred. No. 4.4e+05;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

**Qy** 1 GATGCACAGCTGGGGAACAAG 21  
|||||  
**Db** 40 GGTGMAAGCTGAGCAACGAG 20  
|||||

**RESULT 14**  
AZ565607/c  
LOCUS 211pvA09 Pv MBN #16 (50 bp DNA linear GSS 07-MAY-2001  
DEFINITION 211pvA09 Pv MBN #16 (amplified twice) Plasmodium vivax genomic 3',  
Genomic survey sequence.  
ACCESSION AZ565607  
VERSION AZ565607.1 GI:13971874  
KEYWORDS GSS.  
SOURCE Plasmodium vivax (malaria parasite P. vivax)  
ORGANISM Plasmodium vivax  
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
1 (bases 1 to 50)  
Carlton, J.M.-R. and Dame, J.B.  
The Plasmodium vivax and P. berghei gene sequence tag projects  
Parasitol. Today 16 (10), 409 (2000)  
11006469  
Contact: Dame JB  
Dept. of Pathobiology, College of Veterinary Medicine  
University of Florida  
2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611, USA  
Tel: 352 392 4700  
Fax: 352 392 9704  
Email: damej@mail.vetmed.ufl.edu  
Seq primer: M13(-20) forward  
Class: shotgun.

**FEATURES** source  
1..50  
Location/Qualifiers  
/organism="Plasmodium vivax"  
/mol\_type="genomic DNA"  
/strain="Belem"  
/db\_xref="taxon:5855"  
/dev\_stage="asexual blood forms"  
/lab\_host="Saimiri boliviensis"  
/clone\_lib="Pv MBN #16 (amplified twice)"  
/note="Vector: Lambda ZAP II (Stratagene); individual clones excised into phagemid pBluescript; Site 1: Ecor I; Site 2: Ecor I; Genomic DNA was prepared from asynchronous blood stage forms of the Belem line of P. vivax grown in squirrel monkeys. Parasitized erythrocytes were purified

from contaminating host leukocytes by filtration of ADP activated blood through acid-washed glass beads and Whatman Cfil cellulose columns by gravity filtration. Purified DNA was digested with mung bean nuclease in the presence of 42.5% formamide at 50°C as described (Galinski, M. et al. 1992. Cell 69,1213-1226; Vernick, K.D. et al.1988. N.A.R. 16, 6883-6896). Eco RI linkers were added and the constructs ligated into Lambda ZAP II. P. vivax Belem was originally isolated from a patient in Belem, Brazil 1980 by Mercia de Arruda, adapted to Saimiri monkeys by Jurg Gysin, and maintained since 1993 in squirrel monkeys."

**ORIGIN**  
Query Match 54.2%; Score 13; DB 9; Length 50;  
Best Local Similarity 76.2%; Pred. No. 4.4e+05;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

**Qy** 1 GATGCACAGCTGGGGAACAAG 21  
|||||  
**Db** 23 GAGGCATCTCTAGGGAACAAG 3  
|||||

**RESULT 15**  
BH865278  
LOCUS 42 bp DNA linear GSS 05-AUG-2002  
DEFINITION SALK\_098078 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK\_098078, genomic survey sequence.  
ACCESSION BH865278  
VERSION BH865278.1 GI:22101176  
KEYWORDS GSS.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 42)  
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.  
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome  
Unpublished (2001)  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At3g23970.  
Class: TDNA tagged.

**FEATURES** source  
1..42  
Location/Qualifiers  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/ecotype="Col-0"  
/db\_xref="taxon:3702"  
/clone\_lib="SALK\_098078"  
/note="PCR was performed on Arabidopsis thaliana TDNA insertion lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

**ORIGIN**  
Query Match 53.3%; Score 12.8; DB 9; Length 42;  
Best Local Similarity 70.8%; Pred. No. 5.3e+05;  
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

QY 1 GATGCACAGCTGGGGAACAGC 24
Db ||||||| ||||| |||||
3 GAGGCACAGCTGTGAGACATGAAG 26

RESULT 16
AV832547/c 47 bp mRNA linear EST 09-MAY-2002
LOCUS AV832547 K. Sato unpublished cDNA library: Hordeum vulgare subsp.
DEFINITION vulgare leaves vegetative stage Hordeum vulgare subsp. vulgare cDNA
cloned baak12a18, mRNA sequence.
ACCESSION AV832547 GI:14524636
VERSION AV832547
KEYWORDS Hordeum vulgare subsp. vulgare
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
1 (bases 1 to 47)
REFERENCE Sato, K.
AUTHORS Barley EST sequencing project in NIG and Okayama Univ
JOURNAL Unpublished (2001)
COMMENT Contact: Kazuhiro Sato
Research Institute for Bioresources
Okayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Email: kzsato@rib.okayama-u.ac.jp,
URL: http://www.rib.okayama-u.ac.jp/barley/
database: http://www.shigen.nig.ac.jp/barley/hcm1.

FEATURES
source
1..47
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Akashinriki"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="baak12a18"
/tissue_type="leaves"
/dev_stage="vegetative stage"
/clone_lib="K. Sato unpublished cDNA library: Hordeum
vulgare subsp. vulgare leaves vegetative stage"

ORIGIN
Query Match 53.3%; Score 12.8; DB 1; Length 47;
Best Local Similarity 77.8%; Pred. NO. 5.4e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATGCACAGCTGGGGAACA 19
Db ||||||| ||||| |||||
31 ATGGACAGCTGGGTANNA 14

RESULT 17
AG200388
LOCUS AG200388 30 bp DNA linear GSS 06-MAR-2004
DEFINITION Pan troglodytes DNA, clone: RP43-082F17.T7, genomic survey
sequence.
ACCESSION AG200388 GI:45232563
VERSION AG200388
KEYWORDS Pan troglodytes (chimpanzee)
SOURCE Pan troglodytes
ORGANISM Pan troglodytes
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Pan.
1
REFERENCE Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
AUTHORS Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
TITLE BAC end sequences of Library RP-43
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 30)
AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,

QY 1 GATGCACAGCTGGGGAACA 19
Db ||||||| ||||| |||||
3 GATGCACAGCTGAGGTACA 21

RESULT 18
CZ472331/c 43 bp DNA linear GSS 29-APR-2005
LOCUS CZ472331 d01604-3prime Exelixis P element XP insertions Drosophila
DEFINITION melanogaster genomic Sequence recovered from 3' end of P element,
genomic survey sequence.
ACCESSION CZ472331 GI:62966344
VERSION CZ472331.1
KEYWORDS Drosophila melanogaster (fruit fly)
SOURCE Drosophila melanogaster
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 43)
REFERENCE Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A.,
AUTHORS Ryner, L., Cheung, L.M., Chong, A., Erickson, C., Fisher, W.W.,
Singh, C.M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H.L.,
Greer, K., Hartouni, S.R., Howie, E., Jakkula, L., Joo, D., Kilpack, K.,
Laufer, A., Mazzotta, J., Smith, R.D., Stevens, L.M., Stuber, C.,
Tan, L.R., Ventura, R., Woo, A., Zakrajsek, I., Zhao, L., Chen, F.,
Swimmer, C., Kopczyński, C., Duyk, G., Winberg, M.L. and Margolis, J.
TITLE A complementary transposon tool kit for Drosophila melanogaster
using P and piggyBac
JOURNAL Nat. Genet. 36 (3), 283-287 (2004)
PUBMED 14981521
COMMENT Contact: Roger A Hoskins
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
Email: RHoskins@lbl.gov
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of P
element.
The P element insertion position is 1 in the 43 bases. This

```

Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.  
 Direct Submission  
 Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of  
 Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC);  
 52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea  
 (E-mail: redstone@mail.kribb.re.kr, URL: http://phs.grc.kribb.re.kr/,  
 Tel: 82-42-866-7181, Fax: 82-42-860-4409)  
 Clones are derived from the chimpanzee BAC library RP-43 This BAC  
 end was generated during the R&D process and may have higher chance  
 of clone tracking errors.

Sequencing: T7  
 LIBRARY  
 Vector : pBACe3.6  
 R.Site 1 : EcoRI  
 R.Site 2 : EcoRI.  
 Location/Qualifiers  
 1..30  
 /organism="Pan troglodytes"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9598"  
 /clones="RP43-082F17.T7"  
 /sex="male"  
 /cell\_type="lymphocytes"  
 /clone\_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN  
 Query Match 52.5%; Score 12.6; DB 10; Length 30;  
 Best Local Similarity 78.9%; Pred. NO. 6.4e+05;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GATGCACAGCTGGGGAACA 19  
 Db ||||||| ||||| |||||

RESULT 18  
 CZ472331/c 43 bp DNA linear GSS 29-APR-2005  
 LOCUS CZ472331 d01604-3prime Exelixis P element XP insertions Drosophila  
 DEFINITION melanogaster genomic Sequence recovered from 3' end of P element,  
 genomic survey sequence.  
 ACCESSION CZ472331 GI:62966344  
 VERSION CZ472331.1  
 KEYWORDS Drosophila melanogaster (fruit fly)  
 SOURCE Drosophila melanogaster  
 ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 43)  
 REFERENCE Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A.,  
 AUTHORS Ryner, L., Cheung, L.M., Chong, A., Erickson, C., Fisher, W.W.,  
 Singh, C.M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H.L.,  
 Greer, K., Hartouni, S.R., Howie, E., Jakkula, L., Joo, D., Kilpack, K.,  
 Laufer, A., Mazzotta, J., Smith, R.D., Stevens, L.M., Stuber, C.,  
 Tan, L.R., Ventura, R., Woo, A., Zakrajsek, I., Zhao, L., Chen, F.,  
 Swimmer, C., Kopczyński, C., Duyk, G., Winberg, M.L. and Margolis, J.  
 TITLE A complementary transposon tool kit for Drosophila melanogaster  
 using P and piggyBac  
 JOURNAL Nat. Genet. 36 (3), 283-287 (2004)  
 PUBMED 14981521

COMMENT Contact: Roger A Hoskins  
 Berkeley Drosophila Genome Project  
 Lawrence Berkeley National Laboratory  
 Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA  
 Tel: 510 486 4015  
 Fax: 510 486 6798  
 Email: RHoskins@lbl.gov  
 Sequence recovery method was inverse PCR.  
 Sequence orientation is forward strand relative to 5' end of P  
 element.  
 The P element insertion position is 1 in the 43 bases. This



insertion position refers to the first base of the 8 base target recognition sequence.  
 Class: transposon insertion site.  
 Location/Qualifiers  
 1. .43  
 /organism="Drosophila melanogaster"  
 /mol\_type="genomic DNA"  
 /strain="isogenic w- strain"  
 /db\_xref="taxon:7227"  
 /clone\_lib="Exelixis P element XP insertions"  
 /note="Vector: P element XP (GenBank accession number AY1515149); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. For the P element XP, we selected an easily mobilized ammunition element among inserts hopped onto the Binsincy balancer. New insertions were collected in vials from dysgenic females using the standard chromosomal source of transposase, delta2-3. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability and used for recovery of flanking genomic sequence by inverse PCR."

#### FEATURES

source

#### ORIGIN

Query Match 52.5%; Score 12.6; DB 10; Length 43;  
 Best Local Similarity 78.9%; Pred. No. 6.6e+05;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Qy 6 ACAGCTGGGGAACAAGCG 24  
 ||||| ||||| ||||| |||||  
 Db 22 ACAGCTGACAAACAAGCCG 4

RESULT 19  
 AG217348/c  
 LOCUS  
 DEFINITION  
 Drosophila melanogaster DNA, clone:NP335-5-1, flanking P[GawB] transposon insertion, genomic survey sequence.

ACCESSION  
 AG217348.1 GI:22764348  
 GSS.  
 Drosophila melanogaster (fruit fly)  
 Drosophila melanogaster  
 Eukaryota; Metazoa; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Ephydroidea; Drosophilidae; Drosophila.

#### REFERENCE

1

Hayashi,S., Ito,K., Sado,Y., Taniguchi,M., Akimoto,A., Takeuchi,H., Aigaki,T., Matsuzaki,F., Nakagoshi,H., Tanimura,T., Ueda,R., Uemura,T., Yoshihara,M. and Goto,S.

#### TITLE

GETDB, a database compiling expression patterns and molecular locations of a collection of Gal4 enhancer traps

#### JOURNAL

Genesis (2002) In press

#### REFERENCE

2 (bases 1 to 47)

#### AUTHORS

Hayashi,S.

#### TITLE

Direct Submission

#### JOURNAL

Submitted (27-AUG-2002) Shigeo Hayashi, RIKEN Center for Developmental Biology, Laboratory for Morphogenetic Signaling; Chuo-ku, Minatojima-minamimachi 2-2-3, Kobe, Hyogo 650-0047, Japan (E-mail:shayashi@cdb.riken.go.jp, Tel:81-78-301-3184, Fax:81-78-301-3183)

#### COMMENT

This clone was isolated from genomic DNA flanking an insertion of the P element vector P[GawB] of a Drosophila strain.

#### FEATURES

source

1. .47  
 /organism="Drosophila melanogaster"  
 /mol\_type="genomic DNA"  
 /strain="NP335"  
 /db\_xref="taxon:7227"  
 /chromosome="2"  
 /map="57B5"  
 /clone="NP335-5-1"  
 /note="flanking P[GawB] transposon insertion"

#### ORIGIN

Query Match 52.5%; Score 12.6; DB 10; Length 47;  
 Best Local Similarity 78.9%; Pred. No. 6.6e+05;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GCACAGCTGGGAACAAGA 22

||||| ||||| ||||| |||||

Db 26 GAACAGCTGGCGCAGAAGA 8

RESULT 20  
 A1527771/c  
 LOCUS  
 DEFINITION  
 U128h01.y1 Sugano mouse kidney mKia Mus musculus cDNA clone IMAGE:191297 5' similar to TR:Q61314 Q61314 APOLIPOPROTEIN B ; mRNA sequence.

ACCESSION  
 A1527771.1 GI:441897  
 VERSION  
 EST.  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE  
 1 (bases 1 to 49)  
 AUTHORS  
 Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999  
 Unpublished (1999)  
 CONTACT: Marra M/WashU-NCI Mouse EST Project 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.edu

This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:977589

Trace considered overall poor quality  
 Possible reversed clone: similarity on wrong strand

Seq primer: custom primer used

High quality sequence stop: 1.

FEATURES

Location/Qualifiers

source

1. .49  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:191297"  
 /sex="female"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="Sugano mouse kidney mKia"  
 /note="Organ: kidney; Vector: pME18S-FL3; Site 1: Draili (CAGCTGTGG); Site 2: Draili (CAGCATGTG); 1st strand cDNA was primed with an oligo(dT) primer (ATGTGGCTTTTCTTTTCTTTT); double-stranded cDNA was ligated to a Draili adaptor (TGTGGCTACTGG), digested and cloned into distinct Draili sites of the pME18S-FL3 vector (5' site CAGCTGTGG, 3' site CAGCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCGTCTCTAAAGCTGCG and 3' end primer CGACCTGCAGCTCAGACACA."

#### ORIGIN

Query Match 52.5%; Score 12.6; DB 1; Length 49;  
 Best Local Similarity 78.9%; Pred. No. 6.6e+05;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATGCACAGCTGGGGACAA 20  
 ||||| ||||| |||||  
 Db 39 ATACACAGAGGGGCAACAA 21

RESULT 21  
 AZ511249/c  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridea; Muridae; Murinae; Mus.  
 1 (bases 1 to 25)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausen, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0356 row: N column: 10  
 Seq primer: CGTTGTAAACAGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 25.

## FEATURES

source

1..25  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0356N10"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

## ORIGIN

Query Match 51.7%; Score 12.4; DB 9; Length 25;

Best Local Similarity 72.7%; Pred. No. 7.7e+05;  
 Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATGCACAGCTGGGGACAAAGAC 23  
 ||||| ||||| ||||| |||||  
 Db 22 ACGAGCAGCGGGGAACACAAAC 1

RESULT 22  
 AA958372  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridea; Muridae; Murinae; Mus.  
 1 (bases 1 to 28)  
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
 Waterston, R.  
 The WashU-HHMI Mouse EST Project  
 Unpublished (1996)  
 Contact: Marra M/Mouse EST Project  
 WashU-HHMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:695172

## FEATURES

source

1..28  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:1346380"  
 /sex="male"  
 /tissue\_type="mammary gland"  
 /dev\_stage="4 weeks"  
 /lab\_host="DH10B"  
 /clone\_lib="Soares mammary gland NbMMG"  
 /note="Organ: mammary gland; Vector: p7T3D-Pac  
 (Pharmacia) with a modified polylinker; Site: 1; Not I;  
 Site 2; Eco RI; 1st strand cDNA was primed with a Not I -  
 oligo(dT) primer [5,  
 TGTTACCAATCTGAAGTGGAGCGCGCGGAATGTTTTTTTTTTTTTTTTTTT  
 T 3']; double-stranded cDNA was ligated to Eco RI  
 adaptors (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of the modified p7T3 vector.  
 RNA provided by Dr. Minoru Ko, Wayne State Univ. Library  
 constructed and normalized by Bento Soares and M. Fatima  
 Bonaldo."

## ORIGIN

Query Match 51.7%; Score 12.4; DB 1; Length 28;  
 Best Local Similarity 92.9%; Pred. No. 7.8e+05;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy 1 GATGCACAGCTGGG 14
Db 2 GATGCAGCTGCTGGG 15

RESULT 23
LOCUS CW986355
DEFINITION KBrH012L05R KBrH, Brassica rapa HindIII BAC library linear GSS 29-DEC-2004
subseq. pekinensis genomic clone KBrH012L05, genomic survey
sequence.
ACCESSION CW986355
VERSION CW986355.1 GI:56852379
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 38)
AUTHORS Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Lim, Y.P. and Park, B.S.
TITLE End sequence of Brassica rapa HindIII BAC library (KBrH)
JOURNAL Unpublished (2004)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis HindIII BAC clone
KBrH012L05
Seq primer: M13 Reverse
Class: BAC ends.
FEATURES
source
Location/Qualifiers
1..38
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrH012L05"
/tissue_type="young leaves"
/lab_host="E.coli DH10B"
/clone_lib="KBrH, Brassica rapa HindIII BAC library"
/note="Vector: pCUGIBacI; Site 1: HindIII; Brassica rapa
ssp. pekinensis inbred line Chiifu BAC library (KBrH BAC)
is provided by Yong-Pyo Lim."

ORIGIN
Query Match 51.7%; Score 12.4; DB 10; Length 38;
Best Local Similarity 92.9%; Pred. No. 8e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TGGGGAACAGAGC 24
Db 4 TGGGGAACAGAGG 17

RESULT 24
A2814914
LOCUS 2M0082C24R Mouse 10kb plasmid UUGC1M library linear GSS 20-FEB-2001
DEFINITION clone UUGC2M0082C24 R, genomic survey sequence.
ACCESSION A2814914
VERSION A2814914.1 GI:12984822
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

Qy 1 (bases 1 to 42)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0082 row: C column: 24
Seq primer: CACACGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 42.
FEATURES
source
Location/Qualifiers
1..42
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0082C24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 51.7%; Score 12.4; DB 9; Length 42;
Best Local Similarity 72.7%; Pred. No. 8.1e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATGCACAGCTGGGACAGAC 23
Db 18 ATGCACAGGTGTGCAGGAAGCC 39

RESULT 25
BH855497
LOCUS SALK_085040.16.20.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_085040.16.20.x, genomic
survey sequence.
ACCESSION BH855497
VERSION BH855497.1 GI:21705087
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 45)  
Alonso,J.M., Leishe,T.J., Barajas,P., Chen,H., Cheuk,R.,  
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

## JOURNAL

Unpublished (2001)

## COMMENT

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within an annotated exon of At4g09190.

Class: TDNA tagged.

## FEATURES

source

Location/Qualifiers

1..45

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/ecotype="Col-0"

/db\_xref="taxon:3702"

/clone="SALK\_085040.16.20.x"

/clone\_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

## ORIGIN

Query Match

Best Local Similarity 51.7%; Score 12.4; DB 9; Length 45;

Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY

2 ATGCACAGCTGGGGAAACAGAC 23

||||| | | | | | | | | |

12 ATGCATACCTAGAGACGAGAC 33

RESULT 26

BH626386

LOCUS

DEFINITION 1007113406.1EL\_x1 1007 - RescueMu Grid H Zea mays genomic, genomic

survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 48)

Walbot.V.

Maize genomic sequences found using engineered RescueMu transposon

Unpublished (2001)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Very probable ligation site of ends cut by single endonuclease.

Reverse complemented post-ligation sequence from source sequence.

Plate: 1007113 column: 24

Class: transposon-tagged

Location/Qualifiers

1..49

/organism="Zea mays"

/mol\_type="genomic DNA"

/cultivar="mixed background W23/A188/B73"

/db\_xref="taxon:4577"

/tissue\_type="leaf"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="1008 - RescueMu Grid I"

/note="Organ: leaf; Vector: RescueMu (engineered from

pBlueScript backbone); Site 1: BamHI; Site 2: BglII;

RescueMu is a 4.9 kb, modified maize Mu transposon

source

1..48

/organism="Zea mays"

/mol\_type="genomic DNA"

/cultivar="mixed background W23/A188/B73"

/db\_xref="taxon:4577"

/tissue\_type="leaf"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="1007 - RescueMu Grid H"

/note="Organ: leaf; Vector: RescueMu (engineered from

pBlueScript backbone); Site 1: BamHI; Site 2: BglII;

RescueMu is a 4.9 kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription

units. For more information on RescueMu, go to the web

site 'www.zmdb.iastate.edu' and follow the links for

'RescueMu.' Grid H was grown at Berkeley in 2001. DNA

was extracted from leaf punches, double digested using

BamHI and BglII, and ligated to form circular plasmids.

DH10B cells were transformed and then screened on LB

plates with ampicillin."

## ORIGIN

Query Match

Best Local Similarity 51.7%; Score 12.4; DB 9; Length 48;

Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY

1 GATCACAGCTGGGGAAACAAGA 22

||||| | | | | | | | | |

25 GAAGGACAGCTGGAGGATAGGA 46

RESULT 27

BH640991/c

LOCUS

DEFINITION 1008039E08.1EL\_x1 1008 - RescueMu Grid I Zea mays genomic, genomic

survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 49)

Walbot.V.

Maize genomic sequences found using engineered RescueMu transposon

Unpublished (2001)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Very probable ligation site of ends cut by single endonuclease.

Reverse complemented post-ligation sequence from source sequence.

Plate: 1008039 row: 29

Class: transposon-tagged.

Location/Qualifiers

1..49

/organism="Zea mays"

/mol\_type="genomic DNA"

/cultivar="mixed background W23/A188/B73"

/db\_xref="taxon:4577"

/tissue\_type="leaf"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="1008 - RescueMu Grid I"

/note="Organ: leaf; Vector: RescueMu (engineered from

pBlueScript backbone); Site 1: BamHI; Site 2: BglII;

RescueMu is a 4.9 kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site [www.zmdb.iastate.edu](http://www.zmdb.iastate.edu) and follow the links for 'RescueMu.' Grid 1 was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

## ORIGIN

Query Match 51.7%; Score 12.4; DB 9; Length 49;  
Best Local Similarity 72.7%; Pred. NO. 8.2e+05;  
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TGCACAGCTGGGACACG 24  
||||| ||| ||| ||| |||  
Db 42 TGCACAACTTGACACCAAG 21

## RESULT 28

LOCUS CZ469449 49 bp DNA linear GSS 29-APR-2005  
DEFINITION c04702-3prime Exelixis piggyBac PB insertions Drosophila melanogaster genomic Sequence recovered from 3' end of piggyBac, genomic survey sequence.

ACCESSION CZ469449 GI:62963462

VERSION GSS.

KEYWORDS Drosophila melanogaster (fruit fly)

## SOURCE

ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 49)

AUTHORS Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A., Singh, C.M., Buchholz, R., Demsky, M., Pawcett, R., Francis-Lang, H.L., Ryner, L., Cheung, L.M., Chong, A., Erickson, C., Fisher, W.W., Graer, K., Hantouni, S.R., Howie, E., Jakkula, L., Joo, D., Killpack, K., Laufer, A., Mazzotta, J., Smith, R.D., Stevens, L.M., Stubek, C., Tan, L.R., Ventura, R., Woo, A., Zakrajsek, I., Zhao, L., Chen, F., Swimmer, C., Kopczyński, C., Duyk, G., Winberg, M.L. and Margolis, J.  
A complementary transposon tool kit for Drosophila melanogaster using P and piggyBac  
Nat. Genet. 36 (3), 283-287 (2004)

## TITLE

JOURNAL 14981521

## PUBMED

COMMENT Contact: Roger A Hoskins  
Berkeley Drosophila Genome Project  
Lawrence Berkeley National Laboratory  
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA  
Tel: 510 486 4015  
Fax: 510 486 6798

Email: [RHoskins@lbl.gov](mailto:RHoskins@lbl.gov)

Sequence recovery method was inverse PCR.

Sequence orientation is forward strand relative to 5' end of piggyBac element.

The piggyBac insertion position is 1 in the 49 bases. This insertion position refers to the first base of the 4 base TTA target recognition sequence.

Class: transposon insertion site.

## FEATURES

## source

1..49  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/strains="isogenic w- strain"  
/db\_xref="taxon:7227"  
/clone\_lib="Exelixis piggyBac PB insertions"  
/note="Vector: An isogenic w- Drosophila melanogaster strain AF15146; An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. We remobilized the PB element using Hsp70:piggyBac transposase from a single ammunition element on either the X or third chromosome. We induced

transposase expression by immersing bottles in a circulating 370C water bath for a daily (days 3-10 after egg-laying) 1-h heat shock. We outcrossed the resulting dygenic males to an isogenic w- strain. New insertions were identified on the basis of a change in eye color (third chromosome ammunition) or the appearance of w+ male progeny (X chromosome ammunition). All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking genomic sequence by inverse PCR."

## ORIGIN

Query Match 51.7%; Score 12.4; DB 10; Length 49;  
Best Local Similarity 92.9%; Pred. NO. 8.2e+05;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGCACAGCTGGGGA 16  
||||| ||| ||| ||| |||  
Db 11 TGCACACCTGGGGA 24

## RESULT 29

LOCUS BM395302 18 bp mRNA linear EST 17-JAN-2002  
DEFINITION 50072-2-8-E01.r.1 Chilcoat/Turkewitz cDNA (large fraction) Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM395302 GI:18195355

VERSION EST.

KEYWORDS Tetrahymena thermophila

## SOURCE

ORGANISM Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.

REFERENCE 1 (bases 1 to 18)

AUTHORS Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,

Frankel, J. and Klobutcher, L.

EST from Tetrahymena thermophila, strain CU428.1, growing cells

## TITLE

JOURNAL Unpublished (2002)

## COMMENT

Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: [apturkew@midway.uchicago.edu](mailto:apturkew@midway.uchicago.edu)

Seq primer: T3

## FEATURES

## source

1..18  
/location/Qualifiers  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

## ORIGIN

Query Match 50.8%; Score 12.2; DB 3; Length 18;  
Best Local Similarity 82.4%; Pred. NO. 9.3e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 ACAGCTGGGGAACAAGA 22

||||| ||| ||| ||| |||

Db 17 ACAGCTGGGGGCCCAAG 1

## RESULT 30

LOCUS AA776443 36 bp mRNA linear EST 05-FEB-1998  
DEFINITION zj50h10.s1 Soares fetal liver spleen INFLS.S1 Homo sapiens CDNA clone IMAGE:453763.3, similar to gb|L28107|TRRRRH Trichoderma reesei 25S ribosomal (rRNA);, mRNA sequence.

```

ACCESSION      AA776443
VERSION        AA776443.1  GI:2835777
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE      1 (bases 1 to 36)
AUTHORS        Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
                Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
                Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
                Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
TITLE          WashU-NCI human EST Project
JOURNAL        Unpublished (1997)
COMMENT        Contact: Wilton RK
                Washington University School of Medicine
                4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                Tel: 314 286 1800
                Fax: 314 286 1810
                Email: est@wustl.edu
                This clone is available royalty-free through LNLML ; contact the
                IMAGE Consortium (info@image.llnl.gov) for further information.
                Seq primer: -40ml3 fwd. ET from Amersham
                High quality sequence stop: 1.
FEATURES       Location/Qualifiers
                1..36
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:1390119"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:453763"
                     /sex="male"
                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares fetal liver spleen INFLS S1"
                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
                     This is a subtracted version of the original Soares fetal
                     liver spleen INFLS library. 1st strand cDNA was primed
                     with a Pac I - oligo(dT) primer [5',
                     AACTGGAAGATTATTAAGATCTTTTCTTTTCTTTT 3'].
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M. Patricia Bonaldo."
ORIGIN
Query Match      50.8%; Score 12.2; DB 1; Length 36;
Best Local Similarity 82.4%; Pred. NO. 9.9e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 CAGCTGGGACAGAC 23
    |||||
Db 17 CAGCGGGGAAGAAGAC 1

RESULT 31
AJ239879
LOCUS          AJ239879          37 bp      mRNA      linear      EST 10-AUG-1999
DEFINITION    AJ239879 Aspergillus niger ATCC6275 Aspergillus niger cDNA clone
              AN05D11, mRNA sequence.
ACCESSION     AJ239879
VERSION       AJ239879.1  GI:5443870
KEYWORDS      EST.
SOURCE        Aspergillus niger
ORGANISM      Aspergillus niger
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE     1 (bases 1 to 37)
AUTHORS       Choi, J.Y., Lee, D.W., Koh, J.S., Kim, J.H., Yang, M.S. and Chae, K.S.
TITLE         Identification of expressed sequence tags (ESTs) of the highly

```

```

transcribed genes in Aspergillus niger
Biotechnol. Lett. 21, 381-384 (1999)
Contact: Chae KS
Faculty of Biological Sciences
Chonbuk National University
Chonju 561-756, Republic of Korea.
Location/Qualifiers
1..37
   /organism="Aspergillus niger"
   /mol_type="mRNA"
   /strain="ATCC6275"
   /db_xref="taxon:5061"
   /clone="AN05D11"
   /clone_lib="Aspergillus niger ATCC6275"
ORIGIN
Query Match      50.8%; Score 12.2; DB 1; Length 37;
Best Local Similarity 77.8%; Pred. NO. 9.9e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 TGCACAGCTGGGACAA 20
    |||
Db 20 TGCCCAACTGGGNAAAA 37

RESULT 32
AA287473
LOCUS          AA287473          41 bp      mRNA      linear      EST 13-AUG-1997
DEFINITION    zs50a12.r1 NCI CGAP GCBI Homo sapiens cDNA clone IMAGE:700894 5.
              similar to dbj|D16558|SCJRDNA Scytosiphon lomentaria rDNA for 18S,
              5.8S and 25S (rRNA);, mRNA sequence.
ACCESSION     AA287473
VERSION       AA287473.1  GI:1933172
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE     1 (bases 1 to 41)
AUTHORS       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
              National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
              Unpublished (1997)
              Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              This clone is available royalty-free through LNLML ; contact the
              IMAGE Consortium (info@image.llnl.gov) for further information.
              Trace considered overall poor quality
              Insert Length: 1111 Std Error: 0.00
              Seq primer: -28ml3 rev2 ET from Amersham
              High quality sequence stop: 1.
FEATURES       Location/Qualifiers
                1..41
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:5740328"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:700894"
                     /tissue_type="germinal center B cell"
                     /lab_host="DH10B"
                     /clone_lib="NCI CGAP GCBI"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
                     was prepared from human tonsillar cells enriched for
                     germinal center B cells by flow sorting (CD20+, IgD-,
                     provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                     (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
                     primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGAGCGCCGCTCATTTTCTTTTCTTTT-3'
                     ]. Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library

```

went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

```

ORIGIN
Query Match      50.8%; Score 12.2; DB 1; Length 41;
Best Local Similarity 82.4%; Pred. No. 1e+06;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 CAGCTGGGGAACAGAC 23
    ||||| ||||| ||||| |||||
Db 3 CAGCAGGGAAGAGAC 19

RESULT 33
AV957763      42 bp mRNA linear EST 14-MAR-2002
LOCUS AV957763 Nori Satoh unpublished cDNA library, egg Ciona
DEFINITION intestinalis cDNA clone cieg05k15 5', mRNA sequence.
ACCESSION AV957763
VERSION AV957763.1 GI:19446062
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
REFERENCE 1 (bases 1 to 42)
AUTHORS Satoh.N., Satou.Y., Kohara.Y. and Shin-i.T.
TITLE Expressed genes in Ciona intestinalis
JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES
source
1..42
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="cieg05k15"
/tissue_type="whole animal"
/dev_stage="egg"
/clone_lib="Nori Satoh unpublished cDNA library, egg"

ORIGIN
Query Match      50.8%; Score 12.2; DB 1; Length 42;
Best Local Similarity 82.4%; Pred. No. 1e+06;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 AGCTGGGGAACAGACG 24
    ||||| ||||| ||||| |||||
Db 16 AGCTGTGGAAGAGATG 32

RESULT 34
AU255694/c
LOCUS AU255694 44 bp mRNA linear EST 25-APR-2002
DEFINITION BE00006185 3'-directed mouse cDNA library Mus musculus cDNA clone
ACCESSION AU255694
VERSION AU255694.1 GI:20318679
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 44)
AUTHORS Kato,K. and Matoba,R.
TITLE Generation of expressed sequence tags from mouse brain
JOURNAL Unpublished (2002)

```

```

COMMENT Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5589
Email: kkatob@bs.aist-nara.ac.jp,
URL:http://love2.aist-nara.ac.jp/BED/index.html.

FEATURES
source
1..44
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="BED0006185"
/tissue_type="brain"
/clone_lib="3'-directed mouse cDNA library"

ORIGIN
Query Match      50.8%; Score 12.2; DB 1; Length 44;
Best Local Similarity 82.4%; Pred. No. 1e+06;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 CAGCTGGGGAACAGAC 23
    ||||| ||||| ||||| |||||
Db 38 CAATTGGGGAACAGGAC 22

RESULT 35
AJ792767
LOCUS AJ792767 45 bp mRNA linear EST 08-DEC-2004
DEFINITION AJ792767 Antirrhinum majus whole plant Antirrhinum majus cDNA clone
018.2.12.i08, mRNA sequence.
ACCESSION AJ792767
VERSION AJ792767.1 GI:51108095
KEYWORDS EST.
SOURCE Antirrhinum majus (snapdragon)
ORGANISM Antirrhinum majus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Lamiales; Plantaginaceae; Antirrhineae;
Antirrhinum.
REFERENCE 1 (bases 1 to 45)
AUTHORS Bey,M., Stueber,K., Fellenberg,K., Schwarz-Sommer,Z., Sommer,H.,
Saedler,H. and Zachgo,S.
TITLE Characterization of Antirrhinum Petal Development and
Identification of Target Genes of the Class B MADS Box Gene
DEFICIENS
JOURNAL Plant Cell 16 (12), 3197-3215 (2004)
PUBMED 15539471
COMMENT Contact: Schwarz-Sommer Z
Molekulare Pflanzen-genetik
MPI fuer Zuechtungs-forschung
Carl-von-Linne Weg 10, D-50829, Germany.

FEATURES
source
1..45
/organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:4151"
/clone="018.2.12.i08"
/tissue_type="whole plant"
/clone_lib="Antirrhinum majus whole plant"

ORIGIN
Query Match      50.8%; Score 12.2; DB 1; Length 45;
Best Local Similarity 82.4%; Pred. No. 1e+06;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 AGCTGGGGAACAGACG 24
    ||||| ||||| ||||| |||||
Db 21 AGCTGCCGGAACAGAG 37

RESULT 36

```

AI254367 LOCUS 49 bp mRNA linear EST 03-FEB-1999  
 qv33a10.x1 NCI\_CGAP\_Ov31 Homo sapiens cDNA clone IMAGE:1983354 3'  
 similar to gb:U21696 cdai PROTHYMOSIN ALPHA (HUMAN); contains  
 TARI.ti TARI repetitive element ;, mRNA sequence.  
 AI254367 JOURNAL  
 AI254367.1 GI:3861892  
 EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 REFERENCE 1 (bases 1 to 49)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: c9apbs-r@mail.nih.gov  
 Tissue Procurement: W. Marston Linehan, M.D., Rodrigo F. Chuauqui,  
 M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: David B. Krizman, Ph.D.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium, LLNL  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
 Trace considered overall poor quality  
 Insert Length: 307 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1..49  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1983354"  
 /sex="female"  
 /tissue type="papillary serous carcinoma"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Ov31"  
 /notes="Organ: ovary; Vector: pAMP1; mRNA made from ovarian  
 carcinoma, cDNA made by oligo-dT priming.  
 Non-directionally cloned. Size-selected on agarose gel,  
 average insert size 500 bp. Non-amplified library."

Query Match 50.8%; Score 12.2; DB 1; Length 49;  
 Best Local Similarity 82.4%; Pred. No. 1e+06; Indels 0; Gaps 0;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 AGCTGGGGACACAGACG 24  
 |||||  
 DB 10 AGGTGGGGAGGAAGACG 26

RESULT 37  
 AI25506/c LOCUS 50 bp mRNA linear EST 28-JAN-2004  
 DEFINITION HRC12806, mRNA sequence.  
 ACCESSION AI25506  
 VERSION AI25506.1 GI:13555027  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 REFERENCE 1 (bases 1 to 50)  
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,  
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
 Diverse transcriptional initiation revealed by fine, large-scale  
 mapping of mRNA start sites  
 EMBO Rep. 2 (5), 388-393 (2001)  
 11375929  
 CONTACT: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: ysuzuki@ims.u-tokyo.ac.jp  
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and  
 Sugano, S. Construction and characterization of a full  
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),  
 149-156 (1997).  
 Location/Qualifiers  
 1..50  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="HRC12806"  
 /clone\_lib="Sugano Homo sapiens cDNA library"

ORIGIN  
 Query Match 50.8%; Score 12.2; DB 1; Length 50;  
 Best Local Similarity 82.4%; Pred. No. 1e+06; Indels 0; Gaps 0;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GATCACAGCTGGGGAA 17  
 |||||  
 DB 46 GCTGCTCACCCTGGGAA 30

RESULT 38  
 AI25507/c LOCUS 50 bp mRNA linear EST 28-JAN-2004  
 DEFINITION HRC12884, mRNA sequence.  
 ACCESSION AI25507  
 VERSION AI25507.1 GI:13555028  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 REFERENCE 1 (bases 1 to 50)  
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,  
 Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,  
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
 Diverse transcriptional initiation revealed by fine, large-scale  
 mapping of mRNA start sites  
 EMBO Rep. 2 (5), 388-393 (2001)  
 11375929  
 CONTACT: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: ysuzuki@ims.u-tokyo.ac.jp  
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and  
 Sugano, S. Construction and characterization of a full  
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),  
 149-156 (1997).  
 Location/Qualifiers  
 1..50  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="HRC12884"  
 /clone\_lib="Sugano Homo sapiens cDNA library"

ORIGIN  
 Query Match 50.8%; Score 12.2; DB 1; Length 50;



Best Local Similarity 82.4%; Pred. No. 1e+06; 3; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 3;

Qy 1 GATGCACAGCTGGGAA 17  
Db 46 GCTGCTCACCTGGGAA 30

RESULT 39  
CZ909855 30 bp DNA linear GSS 08-AUG-2005  
LOCUS 4018011H10.1BL x1 4018 - RescueMu Grid x Zea mays genomic, genomic  
DEFINITION survey sequence.

ACCESSION CZ909855  
VERSION CZ909855  
KEYWORDS GSS.  
SOURCE GSS.

ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 30)

REFERENCE Walbot, V.  
AUTHORS Maize genomic sequences found using engineered RescueMu transposon  
TITLE Unpublished (2001)  
JOURNAL  
COMMENT

Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221

Email: walbot@stanford.edu  
Very probable ligation site of ends cut by single endonuclease.  
Reverse complemented post-ligation sequence from source sequence.  
Plate: 4018011 row: H column: 10  
Class: transposon-tagged.

FEATURES  
source  
1..30  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/culturvar="mixed background W23/A188/B73/K55"  
/db\_xref="taxon:4577"  
/tissue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="4018 - RescueMu Grid x"

/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid x was grown at UCSD in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

## ORIGIN

Query Match 50.0%; Score 12; DB 10; Length 30;  
Best Local Similarity 75.0%; Pred. No. 1.2e+06;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 GCACAGCTGGGAAACAGAC 23  
Db 5 GCACAGATGGCGGCGAAAC 24

RESULT 40  
DN955268 33 bp mRNA linear EST 04-MAY-2005  
LOCUS it84h05.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA  
DEFINITION sequence.

ACCESSION DN955268  
VERSION DN955268.1  
KEYWORDS GI:63027406  
SOURCE EST.  
ORGANISM Gnetum gnemon

REFERENCE 1 (bases 1 to 33)  
AUTHORS Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N., O'Shaughnessy, A.L., Bali, V., Martienssen, R.A., McCombie, R.W., Benfey, P., Coruzzi, G. and Stevenson, D.

TITLE Expressed tag sequences from Gnetum female cone (NYBG)  
JOURNAL Unpublished (2003)  
COMMENT

Contact: W. Richard McCombie  
Lita Annenberg Hazen Genome Sequencing Center  
Cold Spring Harbor Laboratory  
PO Box 100, Cold Spring Harbor, NY 11724, USA  
Tel: 516 367 8884  
Fax: 516 367 8874  
Email: mcombie@cshl.org  
Seq primer: -21M13UnivRev.

FEATURES  
source  
1..33  
/organism="Gnetum gnemon"  
/mol\_type="mRNA"  
/db\_xref="taxon:3382"  
/sex="female"  
/clone\_lib="Gnetum female cone (NYBG)"  
/note="Organ: mature, unfertilized reproductive strobili; Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date: Completed 02/11/02, submitted for sequencing 02/12/02. Library: Stratagene ZAP Express cDNA Synthesis Kit. The library was size-fractionated to enrich for large inserts. Sample: NYBG accession number #436/84"

## ORIGIN

Query Match 50.0%; Score 12; DB 8; Length 33;  
Best Local Similarity 75.0%; Pred. No. 1.2e+06;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ATGCACAGCTGGGAAACAAG 21  
Db 10 AAGCAAAGCTCGGCGAGAAG 29

Search completed: December 13, 2005, 15:51:25  
Job time : 2988 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 11:03:03 ; Search time 368.5 Seconds  
(without alignments)  
434.064 Million cell updates/sec

Title: US-10-713-137-3  
Perfect score: 24  
Sequence: 1 gatgcacagctggggaacaagacg 24

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 4879314

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq\_21:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2002bs:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*
- 14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	ADZ75766	Adz75766 Human ind
2	15.6	65.0	26	ADW69302	Adw69302 Forward p
C 3	15	62.5	38	ADQ74734	Aaq74734 KHCV enve
C 4	14.4	60.0	19	ADT77767	Adt77767 Livin RNA
C 5	14.4	60.0	20	AAD05966	Aad05966 Human dia
C 6	14.4	60.0	30	ABV76929	Abv76929 Blocking
C 7	14.4	60.0	42	ADF72069	Adf72069 Human XPC
8	14.2	59.2	21	ADS74065	Ads74065 Tumour su
9	14.2	59.2	22	ABZ30347	Abz30347 Candida a
C 10	14.2	59.2	23	AAx77148	Aax77148 Nerve mut
11	14.2	59.2	37	AAQ55126	Aaq55126 Primer fo
12	14.2	59.2	50	ABZ06705	Abz06705 Human leu
C 13	14.2	59.2	50	ABZ07095	Abz07095 Human leu
14	14	58.3	37	AAI47160	Aai47160 S pneumon
15	14	58.3	47	AAZ67650	Aaz67650 Human map
16	14	58.3	50	ABZ06403	Abz06403 Human leu
C 17	14	58.3	50	ABZ06793	Abz06793 Human leu
18	13.8	57.5	17	ABN08477	Abn08477 Human GDM
C 19	13.8	57.5	17	ACC52706	Acc52706 Human tum

20	13.8	57.5	17	13	ACN71567	Acn71567 Human GDM
21	13.8	57.5	20	2	AAQ53128	Aaq53128 Gene dete
C 22	13.8	57.5	20	2	AAT48684	Aat48684 Probe for
C 23	13.8	57.5	20	2	AAV20056	Aav20056 N-ras pro
24	13.8	57.5	20	2	AAV73038	Aav73038 Human ras
C 25	13.8	57.5	20	2	AAV73141	Aav73141 Human ras
26	13.8	57.5	20	6	ABL43554	Abi43554 Human chr
27	13.8	57.5	20	12	ADJ22962	Adj22962 Human end
28	13.8	57.5	20	12	ADJ23298	Adj23298 Human end
29	13.8	57.5	20	12	ADJ22961	Adj22961 Human end
30	13.8	57.5	20	12	ADJ23531	Adj23531 Human end
31	13.8	57.5	25	6	ABN13371	Abn13371 Human GDM
32	13.8	57.5	25	6	ABN13372	Abn13372 Human GDM
33	13.8	57.5	25	6	ABN13376	Abn13376 Human GDM
34	13.8	57.5	25	6	ABN13373	Abn13373 Human GDM
35	13.8	57.5	25	6	ABN13370	Abn13370 Human GDM
36	13.8	57.5	25	6	ABN13377	Abn13377 Human GDM
37	13.8	57.5	25	6	ABN13369	Abn13369 Human GDM
38	13.8	57.5	25	6	ABN13374	Abn13374 Human GDM
39	13.8	57.5	25	6	ABN13375	Abn13375 Human GDM
C 40	13.8	57.5	25	12	ADQ80648	Adq80648 Binding d
41	13.8	57.5	25	13	ACN76465	Acn76465 Human GDM
42	13.8	57.5	25	13	ACN76461	Acn76461 Human GDM
43	13.8	57.5	25	13	ACN76463	Acn76463 Human GDM
44	13.8	57.5	25	13	ACN76459	Acn76459 Human GDM
45	13.8	57.5	25	13	ACN76467	Acn76467 Human GDM

## ALIGNMENTS

## RESULT 1

ADZ75766  
ID ADZ75766 standard; DNA; 24 BP.

AC ADZ75766;

DT 28-JUL-2005 (first entry)

DE Human inducible nitric oxide synthase gene exon 7 reverse PCR primer.

ss; PCR; high altitude pulmonary edema; pulmonary edema;

respiratory-gen.; respiratory disease; SNP detection; allelic variation;

KW primer; exon.

XX Homo sapiens.

OS US2005106573-A1.

XX 19-MAY-2005.

PD 13-NOV-2003; 2003US-00713137.

PF 13-NOV-2003; 2003US-00713137.

PR 13-NOV-2003; 2003US-00713137.

XX (COUN-) COUNCIL SCI & IND RES INDIA.

XX Pasha AQM, Ahsan A;

XX WPI; 2005-384299/39.

XX Detecting predisposition to high altitude pulmonary edema (HAPE) by

amplifying intron 7 of human inducible nitric oxide synthase gene, and

predicting and analyzing differences in the distribution of allelic

variants.

XX Claim 6; SEQ ID NO 3; 13pp; English.

XX The invention relates to a novel method for detecting predisposition to

high altitude pulmonary edema (HAPE). The method comprises amplifying

intron 7 of the human inducible nitric oxide synthase (iNOS) gene

(ADZ75764) by designing and synthesizing forward and reverse

oligonucleotide primers (ADZ75765+ADZ75766), and predicting and

CC statistically analyzing differences in the distribution of the allelic  
 CC variants in the populations, where GG genotype at 19480 position are at  
 CC low risk of HAPe, and AA genotype at 19480 position are at high risk of  
 CC HAPe. The present sequence represents the forward oligonucleotide primer  
 CC of the invention.

XX Sequence 24 BP; 8 A; 5 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 14; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 0.21;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGCACAGCTGGGAACAGACG 24  
 |||||  
 DB 1 GATGCACAGCTGGGAACAGACG 24

RESULT 2  
 ADW69302  
 ID ADW69302 standard; DNA; 26 BP.  
 XX  
 AC ADW69302;  
 XX  
 DT 24-MAR-2005 (first entry)  
 XX  
 DE Forward primer for PCR of chinese hamster beta-actin promoter.  
 XX  
 KW Primer; ss; DNA amplification; PCR; beta-actin promoter.  
 XX  
 OS Cricetulus griseus.  
 XX  
 PN WO2005000888-A2.  
 XX  
 PD 06-JAN-2005.  
 XX  
 PF 24-JUN-2004; 2004WO-US017422.  
 XX  
 PR 24-JUN-2003; 2003US-0480768P.  
 XX  
 PA (GENZ ) GENZYME CORP.  
 XX  
 PI Estees SD, Zhang W;  
 XX  
 WPI; 2005-058125/06.

XX New beta-actin and ribosomal protein S21 (rpS21) promoters, useful as  
 PT enhancers and repressors for expression of heterologous nucleic acids  
 PT encoding therapeutic proteins such as approximately alpha-glucosidase,  
 PT antibodies, and insulin.  
 XX  
 PS Example 2; SEQ ID NO 35; 95pp; English.  
 XX  
 PS The present invention relates to new rodent beta-actin and ribosomal  
 CC protein S21 (rpS21) promoters that have a low level of sequence homology  
 CC to previously known B-actin and rpS21 promoters. The invention is based  
 CC on the discovery that beta-actin promoters have higher promoter activity  
 CC than CMV's promoter activity, and the discovery that the hamster rpS21  
 CC promoter is at least as active as the hamster Beta-actin promoter when  
 CC used for expressing certain genes. The nucleotide sequences are useful as  
 CC probes for screening genomic libraries for isolation of genomic sequences  
 CC that hybridize to one or more of the promoter sequences or their  
 CC variants. The promoters are useful as enhancers and repressors, and in a  
 CC vector for expression of heterologous nucleic acids encoding therapeutic  
 CC proteins, such as alpha-glucosidase, acid sphingomyelinase, insulin,  
 CC tissue plasminogen activator, thyrogen stimulating hormone,  
 CC erythropoietin, glucocorticoidase, alpha-galactosidase and various  
 CC antibodies. The present sequence is a forward primer for PCR detection of  
 CC the chinese hamster beta-actin promoter containing intron 1.

XX Sequence 26 BP; 9 A; 7 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 65.0%; Score 15.6; DB 14; Length 26;  
 Best Local Similarity 81.8%; Pred. No. 2e+03;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 ATGCACAGCTGGGAACAGAC 23  
 |||||  
 DB 1 AGGCCACAGCTGGGAACAGAC 22

RESULT 3  
 AAQ74734/c  
 ID AAQ74734 standard; cDNA; 38 BP.

XX  
 AC AAQ74734;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 26-MAY-1995 (first entry)  
 XX  
 DE KHCV envelope primer PE1EGT2.

XX Korean-type hepatitis C virus; KHCV; HCV; envelope protein; E1G; E2A;  
 KW E2E; epitope; diagnosis; primer; polymerase chain reaction; PCR;  
 KW amplification; ss.

XX Synthetic.

XX WO9425486-A1.

XX 10-NOV-1994.

XX 29-APR-1994; 94WO-KR000040.

XX 30-APR-1993; 93KR-00007440.

XX (LUCK-) LUCKY CO LTD.

XX Cho JM, Choi DY, Kim CH, So HS, Yang JY, Kim IS, Kim JH;  
 WPI; 1994-358190/44.

XX New Korean hepatitis C virus antigenic proteins - comprising epitopes of  
 PT core protein, non-structural proteins or envelope protein, used for  
 PT diagnosis.

XX Disclosure; Page 27; 91pp; English.

XX The primers given in AAQ74732-47 were used to amplify KHCV envelope gene  
 CC fragments and to clone each fragment into a vector comprising the  
 CC ubiquitin gene under control of the trp promoter, for expression in  
 CC Escherichia coli W3110 (ATCC 37339), allowing identification of epitopes  
 CC E1G (AAR62512), E2A (AAR62513) and E2E (AAR62514). Primer PE1EGT2  
 CC comprises an Sali recognition site and nucleotides 1201-1221 of KHCV-  
 CC LBC1. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 38 BP; 4 A; 12 C; 10 G; 12 T; 0 U; 0 Other;

Query Match 62.5%; Score 15; DB 2; Length 38;  
 Best Local Similarity 78.3%; Pred. No. 3.9e+03;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GATGCACAGCTGGGAACAGAC 23  
 |||||  
 DB 35 GGTGACAGCTGGGAACAGAC 13

RESULT 4  
 ADT77767/c  
 ID ADT77767 standard; RNA; 19 BP.

XX ADT77767;

XX 30-DEC-2004 (first entry)

XX Livin RNA used to prepare siRNA for therapy-resistant tumour therapy.

KW Livin; inhibitor of apoptosis protein; short interfering RNA; siRNA;  
KW RNAi; gene silencing; cytostatic; gene therapy; ss.  
XX Homo sapiens.  
XX  
XX EP1469070-A1.  
XX  
XX 20-OCT-2004.  
XX  
XX 15-APR-2003; 2003EP-00008081.  
XX  
XX 15-APR-2003; 2003EP-00008081.  
XX  
XX (DEKR-) DEUT KRBSFORSCHUNGSZENTRUM.  
XX  
XX Butz K, Crnkovic-Mertens I, Hoppe-Seyler F;  
XX WPI; 2004-730758/72.  
XX  
XX Use of a nucleic acid, or its fragment or derivative, for preparing Livin  
PT -specific siRNAs as an apoptosis inhibitor for the treatment of therapy-  
PT resistant tumors.  
XX  
XX Claim 1; SEQ ID NO 1; 22pp; English.  
XX  
XX The present sequence corresponds to nucleotides 611-629 of the coding  
CC sequence of the livin (inhibitor of apoptosis protein) gene. Use of a  
CC nucleic acid containing this sequence, or its fragment of derivative, to  
CC prepare siRNA which sensitises therapy-resistant tumour cells for  
CC apoptosis is claimed. The siRNA is preferably delivered into a therapy-  
CC resistant tumour cell by using liposomes or hydrodynamic injection.  
CC Another claimed nucleic acid ADT7769 comprises DNA corresponding to the  
CC present sequence joined, via a linker, to a complementary DNA strand.  
CC This is also used to prepare siRNA which sensitises therapy-resistant  
CC tumour cells for apoptosis, and is inserted into an expression vector  
CC such as pSUPPER for production of double-stranded RNA. The siRNAs of the  
CC invention are preferably used in combination with radiation therapy or  
CC with a cytostatic compound, death receptor ligand, death receptor  
CC antibody or negative regulator of anti-apoptotic proteins. The therapy  
CC resistant tumour is neuroblastoma, intestinal carcinoma preferably  
CC rectal, colon, familial adenomatous polyposis, hereditary non-polyposis  
CC colorectal, oesophageal, labial, laryngeal, hypopharynx, salivary and  
CC gastric carcinoma, adenocarcinoma, medullary thyroid carcinoma, papillary  
CC thyroid carcinoma, follicular thyroid carcinoma, anaplastic thyroid  
CC carcinoma, renal carcinoma, kidney parenchyma carcinoma, ovarian  
CC carcinoma, cervical carcinoma, uterine carcinoma, endometrial carcinoma,  
CC chorion carcinoma, pancreatic carcinoma, prostate carcinoma, testicular  
CC carcinoma, breast carcinoma, urinary carcinoma, melanoma, brain tumours  
CC preferably glioblastoma, astrocytoma, meningioma, medulloblastoma and  
CC peripheral neuroectodermal tumours, Hodgkin's lymphoma, non-Hodgkin's  
CC lymphoma, Burkitt's lymphoma, acute lymphatic leukaemia (ALL), chronic  
CC lymphatic leukaemia (CLL), acute myeloid leukaemia (AML), chronic myeloid  
CC leukaemia (CML), adult T-cell leukaemia lymphoma, hepatocellular  
CC carcinoma, gall bladder carcinoma, bronchial carcinoma, small cell lung  
CC carcinoma, non-small cell lung carcinoma, multiple myeloma, basaloma,  
CC teratoma, retinoblastoma, choroida melanoma, seminoma, rhabdomyosarcoma,  
CC craniopharyngioma, osteosarcoma, chondrosarcoma, myosarcoma, liposarcoma,  
CC fibrosarcoma, Ewing sarcoma and plasmocytoma, and preferably cervical  
CC carcinoma or melanoma (all claimed).  
XX  
XX Sequence 19 BP; 2 A; 7 C; 5 G; 0 T; 5 U; 0 Other;  
SQ  
Query Match 60.0%; Score 14.4; DB 13; Length 19;  
Best Local Similarity 93.8%; Pred. No. 6.9e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 6 ACAGCTGGGGGAACAG 21  
DB 16 ACAGCTGGGGGAACAG 1  
RESULT 5  
AAD05966/c

ID AAD05966 standard; DNA; 20 BP.  
XX  
XX AAD05966;  
XX  
XX 31-JUL-2001 (first entry)  
XX  
XX Human diacylglycerol kinase-zeta intron 22/exon 23 junction sequence.  
DE  
XX Human; catalyst; diacylglycerol; DAG; phosphatidic acid; DAG modulator;  
KW diacylglycerol kinase zeta; DGK; ds.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH intron 1..10  
FT /\*tag= a  
FT /number= 22  
FT /partial  
FT 11..20  
FT /\*tag= b  
FT /number= 23  
FT /partial  
XX  
XX US6221658-B1.  
XX  
XX 24-APR-2001.  
XX  
XX 25-AUG-1999; 99US-00382911.  
XX  
XX 22-APR-1996; 96US-0016210P.  
XX 22-APR-1997; 97US-00841483.  
XX (UTAH ) UNIV UTAH RES FOUND.  
XX  
XX Prescott SM, Bunting M, Tang W, Topham M;  
PI WPI; 2001-327248/34.  
XX  
XX New DNAs of the human diacylglycerol kinase, useful for modulating the  
PT levels of diacylglycerol kinase in cells to catalyze the conversion of  
PT diacylglycerol to phosphatidic acid, therefore increasing phosphatidic  
PT acid levels.  
XX  
XX Disclosure; Col 17-18; 74pp; English.  
XX  
XX The patent discloses novel human diacylglycerol kinase (DGK) isoforms  
CC namely diacylglycerol kinase epsilon, diacylglycerol kinase zeta,  
CC diacylglycerol kinase zeta-2 and their corresponding cDNAs. Human  
CC diacylglycerol kinase DNA is useful for coding human diacylglycerol  
CC kinase, which is useful for catalysing the conversion of diacylglycerol  
CC to phosphatidic acid. In particular, the human diacylglycerol kinase and  
CC its DNA are useful for decreasing intracellular levels of diacyl-  
CC glycerol (DAG) and for increasing intracellular levels of phosphatidic  
CC acid in cells. The present DNA sequence is the exon/intron junction  
CC sequence of human diacylglycerol kinase (DGK) zeta gene  
XX  
XX Sequence 20 BP; 1 A; 7 C; 5 G; 7 T; 0 U; 0 Other;  
SQ  
Query Match 60.0%; Score 14.4; DB 5; Length 20;  
Best Local Similarity 93.8%; Pred. No. 6.9e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 4 GCACAGCTGGGGAACA 19  
DB 16 GCACAGCTGGGGAACA 1  
RESULT 6  
ABV76929  
ID ABV76929 standard; DNA; 30 BP.  
XX  
XX AC ABV76929;  
XX

```

DT 03-MAR-2003 (first entry)
XX
DE Blocking oligonucleotide #5 for chymotrypsin B precursor.
XX
KW Nucleic acid synthesis; blocking agent; polymerase; DNA library;
KW chymotrypsin B precursor; ss.
XX
OS Synthetic.
XX
XX EP1253205-A1.
XX
XX 30-OCT-2002.
XX
PF 24-APR-2001; 2001EP-00109971.
XX
XX 24-APR-2001; 2001EP-00109971.
XX
XX (LION-) LION BIOSCIENCE AG.
XX
XX Hoefler M, Kranz H, Klink M;
XX
XX WPI; 2003-077619/08.
XX
XX Preferential nucleic acid synthesis reaction of selected regions of
PT target nucleic acids, by using a blocking agent which preferentially
PT binds templates which are not desirable when amplifying the nucleic
PT acids.
XX
XX Example 1; Page 6; 20pp; English.
XX
XX The specification describes a nucleic acid synthesis reaction of selected
CC regions of target nucleic acids from a group of two different target
CC nucleic acids. The method comprises combining in a reaction mixture, two
CC different target nucleic acids, polymerase, additionally combining a
CC blocking agent capable of binding a nucleic acid template molecule so
CC that the polymerase is not able to utilize bound target nucleic acids as
CC a template, and exposing the reaction mixture to a temperature at which
CC nucleic acids are synthesized by the polymerase. The method is useful for
CC nucleic acid synthesis reactions, and is especially useful for creating
CC DNA libraries. ABV76929-30 represent blocking oligonucleotides, which are
CC used in the method of the invention to block amplification of the
CC chymotrypsin B precursor. The oligonucleotides are used to demonstrate
CC the method of the invention
XX
XX Sequence 30 BP; 9 A; 2 C; 15 G; 4 T; 0 U; 0 Other;
SQ
Query Match 60.0%; Score 14.4; DB 8; Length 30;
Best Local Similarity 75.0%; Pred. No. 7.3e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 GATGCACAGCTGGGGAACAAGACG 24
Db 6 GATGCACGGAGGGGGAGGAAGAGG 29
RESULT 7
ADF72069/c
ID ADF72069 standard; DNA; 42 BP.
XX
XX ADF72069;
XX
XX 12-FEB-2004 (first entry)
XX
XX Human XPC gene PCR primer SEQ ID NO:36.
XX
XX proliferation; cancer; cancer cell growth inhibition; human; PCR primer;
XX ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO2003082078-A2.
XX

```

```

PD 09-OCT-2003.
XX
XX 27-MAR-2003; 2003WO-US009428.
XX
XX 28-MAR-2002; 2002US-0368288P.
PR
XX 28-MAR-2002; 2002US-0368409P.
XX
XX (MEDI-) MEDICAL COLLEGE OHIO.
XX
XX Willey JC, Weaver DA, Warner KA, Graves TG, Demuth JP;
PI Crawford EL;
XX
XX WPI; 2003-902899/82.
XX
XX Determining whether an agent can be used to reduce the proliferation,
PT cause the death or inhibit the growth of cancer cell population by
PT obtaining a sample of cancer cells and quantifying the level of
PT expression of a marker in the cells.
XX
XX Example 1; SEQ ID NO 36; 106pp; English.
XX
XX The present invention describes a method for determining whether an agent
CC can be used to reduce the proliferation and/or cause the death of cancer
CC cells or inhibit the growth of a cancer cell population. The method is
CC useful in determining whether an agent can be used to reduce the
CC proliferation and/or cause the death of cancer cells or inhibit the
CC growth of a cancer cell population. The present sequence represents a PCR
CC primer which is used in the exemplification of the present invention.
XX
XX Sequence 42 BP; 4 A; 14 C; 6 G; 18 T; 0 U; 0 Other;
SQ
Query Match 60.0%; Score 14.4; DB 10; Length 42;
Best Local Similarity 75.0%; Pred. No. 7.7e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 GATGCACAGCTGGGGAACAAGACG 24
Db 37 GATGAGAGGAGGGGACCAAG 14
RESULT 8
ADS74065
ID ADS74065 standard; DNA; 21 BP.
XX
XX ADS74065;
XX
XX 16-DEC-2004 (first entry)
XX
XX Tumour suppressor p53 RT-PCR primer E11R.
XX
XX Tumour; suppressor; p53; splice variant; cytostatic; gene therapy;
KW diagnosis; RT-PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX EP1462521-A1.
XX
XX 29-SEP-2004.
XX
XX 27-MAR-2003; 2003EP-00007000.
XX
XX 27-MAR-2003; 2003EP-00007000.
XX
XX (DEPP/) DEPERT W W.
XX
XX Deppert WW, Dornreiter I;
XX
XX WPI; 2004-663615/65.
XX
XX New nucleic acid encoding a p53 variant that can transactivate p21- and
PT 14-3-3 sigma-promoter but not e.g. the p13-promoter, for obtaining
PT complementary sequences capable of inhibiting expression of p53 variant
PT and treating tumor.

```

XX Example 1; SEQ ID NO 17; 29pp; English.  
 PS The present sequence is that of RT-PCR primer E11R for the p53 tumour  
 CC suppressor gene. RT-PCR was used to detect possible alternative splicing  
 CC of p53 in different primate cell lines. A novel isoform of p53 (deltap53)  
 CC was identified that is generated by alternative exon splicing. RT-PCR  
 CC showed that deltap53 lacks 198 nucleotides from exons 7, 8 and 9. The  
 CC deletion junction contains a donor site-like splicing-cassette within the  
 CC coding exon 7 (nucleotide 767) and an acceptor site-like splicing-  
 CC cassette within the coding exon 9 (nucleotide 965). The resulting  
 CC transcript contains a unique junction of exon 7 with 9, which does not  
 CC alter the open reading frame. Thus, the novel p53-isoform lacks 66 amino  
 CC acid residues from the central portion and hinge region of the protein  
 CC but includes the functionally important C-terminal domain. The 984 bp  
 CC transcript of deltap53 is found in human, African green monkey and Rhesus  
 CC monkey. Unlike full-length p53, the p53 splice variant is capable of  
 CC transactivating the endogenous p21- and 14-3-3sigma promoter but not the  
 CC mdm2-, bax- or p1G3 promoter. The invention provides means for inhibiting  
 CC the activity of the p53 variant, using antisense RNA or a ribozyme, for  
 CC cancer therapy. Diagnostic compositions comprising a probe for detection  
 CC of the splice variant are also claimed.

XX SQ Sequence 21 BP; 7 A; 4 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 59.2%; Score 14.2; DB 13; Length 21;  
 Best Local Similarity 84.2%; Pred. No. 8.7e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCACAGCTGGGGAACAAGA 22  
 ||||| ||||| |||||  
 Db 1 GCTCAGTGGGGGAACAAGA 19

## RESULT 9

ABZ30347  
 ID ABZ30347 standard; DNA; 22 BP.

XX AC ABZ30347;

XX DT 30-JAN-2003 (first entry)

XX DE Candida albicans GRACE strain PCR primer SEQ ID NO 4498.

XX KW Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;  
 KW signal transduction; DNA replication; cell division; growth;  
 KW proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.

XX OS Candida albicans.

XX PN WO200253728-A2.

XX PD 11-JUL-2002.

XX PF 26-DEC-2001; 2001WO-US049486.

XX PR 29-DEC-2000; 2000US-0259128P.

XX PR 20-FEB-2001; 2001US-00792024.

XX PR 22-AUG-2001; 2001US-0314050P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;

XX DR WPI; 2002-566694/60.

XX PT Constructing strains for identifying gene products as effective targets  
 PT for therapeutic intervention, by inactivating in the strain one allele of  
 PT a gene and placing other allele of the gene under conditional expression.

XX PS Claim 36; SEQ ID NO 4498; 167pp + Sequence Listing; English.

XX CC The invention relates to constructing (M1) a strain of diploid fungal

CC cells in which both alleles of a gene are modified, comprising modifying  
 CC one allele by insertion or replacement by a cassette having an  
 CC expressible selectable marker and modifying other allele by  
 CC recombination, of a promoter replacement fragment with a heterologous  
 CC promoter, so that expression of the second allele is regulated by the  
 CC promoter. (M1) is useful for constructing a strain of diploid fungal  
 CC cells in which both alleles of a gene are modified. The diploid fungal  
 CC cells having both alleles modified are useful for identifying a gene that  
 CC is essential to the survival or growth of a fungus, a gene that  
 CC contributes to the virulence and/or pathogenicity of a fungus, a gene  
 CC that contributes to the resistance of a diploid fungus to an antifungal  
 CC agent, an antifungal agent that inhibits the growth of a diploid fungus  
 CC and for identifying a therapeutic agent for treatment of a mammalian  
 CC disease. (M1) is useful for identifying a compound which modulates the  
 CC activity of a gene product, preferably enzymatic activity, carbon  
 CC compound catabolism, biosynthetic, transporter, transcriptional,  
 CC translational, signal transduction, DNA replication and cell division  
 CC activity. The method is useful for identifying a compound having the  
 CC ability to inhibit growth or proliferation of C. albicans cells and for  
 CC treating infection by C. albicans. The present sequence is that of a PCR  
 CC primer used in the method of the invention. Note: The sequence data for  
 CC this patent is not represented in the printed specification but is based  
 CC on sequence information supplied to Derwent by the European Patent Office

XX SQ Sequence 22 BP; 6 A; 2 C; 9 G; 5 T; 0 U; 0 Other;

Query Match 59.2%; Score 14.2; DB 6; Length 22;

Best Local Similarity 84.2%; Pred. No. 8.7e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GATGCACAGCTGGGGAACA 19  
 ||||| ||||| |||||  
 Db 4 GATGGAGAGCTGGTGAACA 22

## RESULT 10

AAAX77148/c

ID AAAX77148 standard; DNA; 23 BP.

XX AC AAAX77148;

XX DT 03-AUG-1999 (first entry)

XX DE Nerve mutation factor DNA amplifying primer.

XX KW Nerve mutation factor; chromosome 10; glioma; tumour suppressor;  
 KW brain tumour; astrocytoma; gene therapy; human; mouse; PCR primer; ss.

XX OS Synthetic.

XX PN WO9925827-A1.

XX PD 27-MAY-1999.

XX PF 24-AUG-1998; 98WO-JP003737.

XX PR 14-NOV-1997; 97JP-00313211.

XX PA (SUME) SUMITOMO ELECTRIC IND CO.

XX PI Nakata M, Nakamura H, Yoshida M, Saya H;

XX DR WPI; 1999-347474/29.

XX PT Human gene on chromosome 10 homologous to Drosophila neuralized gene,  
 PT useful in the diagnosis and gene therapy of brain tumors.

XX PS Example; Page 25; 78pp; Japanese.

XX CC The invention relates to a protein which is a nerve mutation factor and  
 CC is the expression product of a gene located on chromosome 10. The gene is  
 CC in a region frequently deleted in highly malignant gliomas. Sequences  
 CC (AAAX77135 and AAAX77136) encoding human and mouse nerve mutation factors

DBb 11 GCGCAGCTGGGACTAAGA 29

Human leukocyte gene expression profiling probe SEQ ID NO 7

XX  
DE Human leukocyte gene expression profiling probe SEQ ID NO 7086.



KW T7; leukocyte; gene expression profiling; allograft rejection;  
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;  
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;  
KW ss.  
XX Homo sapiens.  
XX WO200257414-A2.  
XX PD 25-JUL-2002.  
XX XX  
XX PF 22-OCT-2001; 2001WO-US047856.  
XX XX  
XX PR 20-OCT-2000; 2000US-0241994P.  
XX PR 08-JUN-2001; 2001US-0296764P.  
XX XX  
XX PA (BIOC-) BIOCARDIA INC.  
XX XX

PI Wohlgenuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;  
PI Ly N, Woodward R, Quattermous T, Johnson F;  
XX WPI; 2002-636525/68.  
XX DR  
XX XX  
XX New system for leukocyte expression profiling, diagnosing a disease, or  
PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis  
PT or congestive heart failure, comprises diagnostic oligonucleotides.  
XX  
XX Claim 1; Page 556; Opp; English.  
XX  
XX The invention relates to a system for detecting gene expression, which  
CC comprises one or two isolated DNA molecules that detect expression of a  
CC gene, where the gene corresponds to any of 8143 oligonucleotides  
CC (ABZ0010-ABZ08152) each having 50 base pairs (bp). The system is useful  
CC for leukocyte expression profiling. It is particularly useful for  
CC diagnosing a disease, monitoring (rate of) progression of a disease,  
CC predicting therapeutic outcome, determining prognosis for a patient,  
CC predicting disease complications in an individual or monitoring response  
CC to treatment in an individual. The diseases include cardiac allograft  
CC rejection, kidney allograft rejection, liver allograft rejection,  
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,  
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection  
XX  
SQ Sequence 50 BP; 10 A; 15 C; 9 G; 16 T; 0 U; 0 Other;

Query Match 59.2%; Score 14.2; DB 6; Length 50;  
Best Local Similarity 84.2%; Pred. No. 9.8e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 6 ACAGCTGGGGACACAGACG 24  
DB 49 ACAGCTGAGAACACAGAG 31  
||||| |||||||  
||||| |||||||

RESULT 14  
AAL47160  
ID AAL47160 standard; DNA; 37 BP.  
XX  
XX AAL47160;  
XX  
XX 30-AUG-2002 (first entry)  
XX  
XX S pneumoniae SpA gene PCR primer SH24.  
XX  
XX SpA; pneumococcal; surface protein; secretory IgA; vaccine; infection;  
KW PCR; primer; ss.  
XX  
XX Streptococcus pneumoniae.  
OS  
XX DE19708537-A1.  
XX  
XX 10-SEP-1998.  
XX  
XX 03-MAR-1997; 97DE-01008537.

Query Match 59.2%; Score 14.2; DB 6; Length 50;  
Best Local Similarity 84.2%; Pred. No. 9.8e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 6 ACAGCTGGGGACACAGACG 24  
DB 49 ACAGCTGAGAACACAGAG 31  
||||| |||||||  
||||| |||||||

RESULT 14  
AAL47160  
ID AAL47160 standard; DNA; 37 BP.  
XX  
XX AAL47160;  
XX  
XX 30-AUG-2002 (first entry)  
XX  
XX S pneumoniae SpA gene PCR primer SH24.  
XX  
XX SpA; pneumococcal; surface protein; secretory IgA; vaccine; infection;  
KW PCR; primer; ss.  
XX  
XX Streptococcus pneumoniae.  
OS  
XX DE19708537-A1.  
XX  
XX 10-SEP-1998.  
XX  
XX 03-MAR-1997; 97DE-01008537.

XX 03-MAR-1997; 97DE-01008537.  
PR (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
PA  
XX Chhatwal GS, Hammerschmidt S;  
XX WPI; 1998-481924/42.  
XX DR  
XX Pneumococcal surface protein SpA - for use in producing vaccines.  
PT  
XX Example 6; Page 5-6; 12pp; German.  
PS  
XX The present invention provides the protein and coding sequences of a  
CC Streptococcus pneumoniae surface protein, called SpA, that binds to  
CC secretory IgA. The sequences can be used in vaccines for treating  
CC pneumococcal infections. The present sequence is a PCR primer used to  
CC isolate the coding sequences of the invention  
XX  
SQ Sequence 37 BP; 12 A; 10 C; 13 G; 2 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 2; Length 37;  
Best Local Similarity 77.3%; Pred. No. 1.2e+04;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 GATGCACAGCTGGGGAAACAAGA 22  
DB 12 GATCCACAGCTGGAAACAAGA 33  
||||| |||||||  
||||| |||||||

RESULT 15  
AAZ67650  
ID AAZ67650 standard; DNA; 47 BP.  
XX  
XX AAZ67650;  
XX  
XX 10-SEP-2001 (first entry)  
XX  
XX Human map-related biallelic marker SEQ ID NO:1997.  
XX  
XX Human genome; biallelic marker; high density disequilibrium map;  
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;  
KW haplotyping; hybridisation; identification; characterisation; diagnosis;  
KW single nucleotide polymorphism; SNP; ds.

XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH variation replace(24,G)  
FT /\*tag= a  
FT /standard\_name= "single nucleotide polymorphism"  
XX  
XX WO9954500-A2.  
XX  
XX 28-OCT-1999.  
XX  
XX 21-APR-1999; 99WO-IB000822.  
XX  
XX 21-APR-1998; 98US-0082614P.  
XX 23-NOV-1998; 98US-0109732P.  
XX  
XX (GEST ) GENSET.  
XX  
XX Cohen D, Blumenfeld M, Chumakov I;  
PI WPI; 2000-013267/01.  
XX  
XX Novel biallelic markers used to construct a high density disequilibrium  
PT map of the human genome.  
PT  
XX Claim 1; Page 656; 2745pp; English.  
XX  
XX AAZ65654 to AAZ69578 represent human biallelic markers from the present

CC invention, which contain a polymorphic base at position 24 of their  
 CC nucleotide sequences. AA269579 to AA277440 represent amplification  
 CC primers for the biallelic markers. The biallelic markers of the invention  
 CC have a variety of uses: they can be used for high density mapping of the  
 CC human genome, and in complex association studies and haplotyping studies  
 CC which are useful in determining the genetic basis for disease states.  
 CC Compositions and methods of the invention can also be useful for the  
 CC identification of the targets for the development of pharmaceutical  
 CC agents and diagnostic methods, as well as the characterisation of the  
 CC differential efficacious responses to and side effects from  
 CC pharmaceutical agents acting on a disease as well as other treatment.  
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and  
 CC 3367, are not actually given a sequence in the Sequence Listing from the  
 CC present invention

XX Sequence 47 BP; 16 A; 13 C; 6 G; 12 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 3; Length 47;  
 Best Local Similarity 77.3%; Pred. No. 1.2e+04;  
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATGCACAGCTGGGGAACAAGAC 23  
 ||||| |||||  
 Db 25 ATGCACACCTGTTTCAAGAC 46

RESULT 16  
 ABZ06403  
 ID ABZ06403 standard; DNA; 50 BP.  
 XX  
 AC ABZ06403;  
 XX  
 DT 09-JAN-2003 (first entry)  
 XX  
 DE Human leukocyte gene expression profiling probe SEQ ID NO 6394.  
 XX  
 KW T7; leukocyte; gene expression profiling; allograft rejection;  
 KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;  
 KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;  
 KW ss.

OS Homo sapiens.  
 XX  
 PN WO200257414-A2.  
 XX  
 PD 25-JUL-2002.  
 XX  
 PF 22-OCT-2001; 2001WO-US047856.  
 XX  
 PR 20-OCT-2000; 2000US-0241994P.  
 PR 08-JUN-2001; 2001US-0296764P.  
 XX  
 PA (BIOC-) BIOCARDIA INC.  
 XX  
 PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;  
 PI Ly N, Woodward R, Quertermous T, Johnson F;  
 XX  
 WP1; 2002-636525/68.

XX New system for leukocyte expression profiling, diagnosing a disease, or  
 PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis  
 PT or congestive heart failure, comprises diagnostic oligonucleotides.  
 XX  
 PS Claim 1; Page 536; Opp; English.

XX The invention relates to a system for detecting gene expression, which  
 CC comprises one or two isolated DNA molecules that detect expression of a  
 CC gene, where the gene corresponds to any of 8143 oligonucleotides  
 CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful  
 CC for leukocyte expression profiling. It is particularly useful for  
 CC diagnosing a disease, monitoring (rate of) progression of a disease,  
 CC predicting therapeutic outcome, determining prognosis for a patient,  
 CC predicting disease complications in an individual or monitoring response

CC to treatment in an individual. The diseases include cardiac allograft  
 CC rejection, kidney allograft rejection, liver allograft rejection,  
 CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,  
 CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection  
 XX  
 SQ Sequence 50 BP; 16 A; 8 C; 19 G; 7 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 6; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 GCTGGGGAACAAGA 22  
 ||||| |||||  
 Db 31 GCTGGGGAACAAGA 44

RESULT 17  
 ABZ06793/c  
 ID ABZ06793 standard; DNA; 50 BP.  
 XX  
 AC ABZ06793;  
 XX  
 DT 09-JAN-2003 (first entry)  
 XX  
 DE Human leukocyte gene expression profiling probe SEQ ID NO 6784.  
 XX  
 KW T7; leukocyte; gene expression profiling; allograft rejection;  
 KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;  
 KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;  
 KW ss.

OS Homo sapiens.  
 XX  
 PN WO200257414-A2.  
 XX  
 PD 25-JUL-2002.  
 XX  
 PF 22-OCT-2001; 2001WO-US047856.  
 XX  
 PR 20-OCT-2000; 2000US-0241994P.  
 PR 08-JUN-2001; 2001US-0296764P.  
 XX  
 PA (BIOC-) BIOCARDIA INC.  
 XX  
 PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;  
 PI Ly N, Woodward R, Quertermous T, Johnson F;  
 XX  
 WP1; 2002-636525/68.

XX New system for leukocyte expression profiling, diagnosing a disease, or  
 PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis  
 PT or congestive heart failure, comprises diagnostic oligonucleotides.  
 XX  
 PS Claim 1; Page 547; Opp; English.

XX The invention relates to a system for detecting gene expression, which  
 CC comprises one or two isolated DNA molecules that detect expression of a  
 CC gene, where the gene corresponds to any of 8143 oligonucleotides  
 CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful  
 CC for leukocyte expression profiling. It is particularly useful for  
 CC diagnosing a disease, monitoring (rate of) progression of a disease,  
 CC predicting therapeutic outcome, determining prognosis for a patient,  
 CC predicting disease complications in an individual or monitoring response  
 CC to treatment in an individual. The diseases include cardiac allograft  
 CC rejection, kidney allograft rejection, liver allograft rejection,  
 CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,  
 CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection  
 XX

SQ Sequence 50 BP; 7 A; 19 C; 8 G; 16 T; 0 U; 0 Other;

Query Match 58.3%; Score 14; DB 6; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 9 GCTGGGGAACAAGA 22  
Db 20 GCTGGGGAACAAGA 7

RESULT 18  
ABN08477  
ID ABN08477 standard; DNA; 17 BP.  
AC ABN08477;  
XX  
XX 29-MAY-2002 (first entry)  
XX  
XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8469.  
XX  
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200192524-A2.  
XX  
XX 06-DEC-2001.  
XX  
XX 25-MAY-2001; 2001WO-US016981.  
XX  
XX 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
XX  
XX (AEOM-) AEOMICA INC.  
XX  
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX WPI; 2002-179446/23.  
XX  
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
XX  
XX Disclosure; SEQ ID NO 8469; 214pp; English.  
XX  
XX The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
CC nucleic acids can be used as probes to detect, characterise and quantify  
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption/ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMPLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.

CC The present sequence represents an oligomer used in the screening of the  
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence  
XX  
XX Sequence 17 BP; 6 A; 3 C; 6 G; 2 T; 0 U; 0 Other;  
SQ

Query Match 57.5%; Score 13.8; DB 6; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.3e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 8 AGCTGGGGAACAAGACG 24  
Db 1 AGCTGGGGAACAAGACG 17

RESULT 19  
ACC52706/c  
ID ACC52706 standard; DNA; 17 BP.  
XX  
XX ACC52706;  
XX  
XX 27-JUN-2003 (first entry)  
XX  
XX Human tumour suppressor sequence #1473.  
XX  
XX ss: tumour suppressor; antitumour; cytostatic; tumour suppression;  
KW tumour regression; apoptosis; virus resistance; diagnosis;  
KW cellular degeneration.  
XX  
XX Homo sapiens.  
XX  
XX FR2826373-A1.  
XX  
XX 27-DEC-2002.  
XX  
XX 20-JUN-2001; 2001FR-00008139.  
XX  
XX 20-JUN-2001; 2001FR-00008139.  
PR (MOLE-) MOLECULAR ENGINES LAB SA.  
XX  
XX Tuijnder M, Telerman A, Amson R;  
XX  
XX WPI; 2003-250498/25.  
XX  
XX New nucleic acid sequences associated with tumor suppression, regression,  
PT apoptosis or virus resistance are useful to diagnose and treat viral  
PT disease, development of tumor cells and cell degeneration.  
XX  
XX Claim 1; Page 380; 798pp; French.  
XX  
XX This sequence represents an isolated nucleic acid sequence associated  
CC with tumour suppression or regression, apoptosis or virus resistance. The  
CC invention relates to these sequences or sequences having at least 80%  
CC identity to them, and polypeptides encoded by the sequences or  
CC polypeptides having 80% identity to the polypeptide sequences. The  
CC invention is used to diagnose or treat viral disease or disease  
CC characterized by development of tumour cells or cellular degeneration  
XX  
XX Sequence 17 BP; 3 A; 6 C; 3 G; 5 T; 0 U; 0 Other;  
SQ

Query Match 57.5%; Score 13.8; DB 10; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.3e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 ATGCACAGCTGGGGAAC 18  
Db 17 ATGCACAGCTGGGGAAC 1

RESULT 20

ACN71567  
 ID ACN71567 standard; DNA; 17 BP.  
 XX  
 AC ACN71567;  
 XX  
 XX 02-DEC-2004 (first entry)  
 XX  
 XX Human GDMPLP-1 probe SEQ ID NO:8469.  
 DE  
 XX Human; ss; probe; myosin-like protein-1; hGDMPLP-1;  
 KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;  
 KW skeletal muscle function.  
 XX  
 XX Homo sapiens.  
 OS  
 XX US2004137589-A1.  
 PN  
 XX 15-JUL-2004.  
 PD  
 XX 26-NOV-2003; 2003US-00723361.  
 PF  
 XX 26-MAY-2000; 2000US-0207456P.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US000661.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 30-JAN-2001; 2001WO-US000670.  
 PR 05-FEB-2001; 2001US-0266860P.  
 PR 25-MAY-2001; 2001US-00866108.  
 XX  
 XX (GUYX/) GU Y.  
 PA (JIYY/) JI Y.  
 PA (PENN/) PENN S G.  
 PA (HANZ/) HANZEL D K.  
 PA (RANK/) RANK D.  
 PA (CHEN/) CHEN W.  
 PA (SHAN/) SHANNON M E.  
 XX  
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;  
 XX WPI; 2004-533378/51.  
 DR  
 XX  
 XX Novel myosin-like protein-1, useful for treating or preventing disorder  
 PT associated with decreased expression or activity of human genome-derived  
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle  
 PT function.  
 PT  
 XX  
 PS Disclosure; SEQ ID NO 8469; 0pp; English.  
 XX  
 XX The invention relates to a novel polypeptide (I) comprising a sequence  
 CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully  
 CC defined in the specification, a fragment of at least 8 amino acids of  
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and  
 CC 65% identity to (S1). A polypeptide of the invention acts as a agonist or  
 CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A  
 CC pharmaceutical composition of the invention is useful for treating or  
 CC preventing a disorder associated with decreased expression or activity of  
 CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.  
 CC The present sequence represents a 17-mer nucleotide, used in the  
 CC invention for scanning the sequence represented in ACN63103  
 XX  
 SQ Sequence 17 BP; 6 A; 3 C; 6 G; 2 T; 0 U; 0 Other;  
 Query Match 57.5%; Score 13.8; DB 13; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 1.3e+04;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 XX

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 8 AGCTGGGGAACAAGACG 24  
 ||||| ||||| |||||  
 Db 1 AGCTGGAGACATGACG 17  
 RESULT 21  
 AAQ53128  
 ID AAQ53128 standard; DNA; 20 BP.  
 XX  
 AC AAQ53128;  
 XX  
 XX 03-JUN-1994 (first entry)  
 DT  
 XX Gene detection sequence 52.  
 DE  
 XX Gene detection; radio-isotopes; target gene; electrode; detection;  
 KW optical fibre; hybridise; hybridisation; electrochemical; photochemical;  
 KW electrolysis; probe; ss.  
 KW  
 XX Synthetic.  
 OS  
 XX JP05285000-A.  
 PN  
 XX 02-NOV-1993.  
 PD  
 XX 10-SEP-1992; 92JP-00242397.  
 PF  
 XX 13-FEB-1992; 92JP-00025621.  
 PR  
 XX (TOKE ) TOSHIBA KK.  
 PA  
 XX WPI; 1993-382240/48.  
 DR  
 XX Detection method of gene without using radio-isotope - by hybridisation  
 PT of nucleic acid probe which is single strand having complementary  
 PT sequence of gene and single strand denatured sample DNA.  
 PT  
 XX Disclosure; Page 23; 26pp; Japanese.  
 PS  
 XX The sequences (AAQ53077-Q53136) are used in the invention to detect  
 CC specific genes without the use of radio-isotopes. Detection is carried  
 CC out by hybridisation of denatured (ss) sample DNA with a (ss) nucleic  
 CC acid probe, complementary to the target sequence. Hybridisation occurs on  
 CC the surface of an electrode or optical fibre and detection is visualised  
 CC by the addition of an entity that recognises (ds) hybridised DNA and is  
 CC electrochemically / photochemically active  
 CC  
 XX Sequence 20 BP; 9 A; 2 C; 7 G; 2 T; 0 U; 0 Other;  
 SQ  
 Query Match 57.5%; Score 13.8; DB 2; Length 20;  
 Best Local Similarity 88.2%; Pred. No. 1.3e+04;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 6 ACAGCTGGGGAACAAGA 22  
 ||||| ||||| |||||  
 Db 1 ACAGCTGGGGAACAAGA 17  
 RESULT 22  
 AAT48684/c  
 ID AAT48684 standard; DNA; 20 BP.  
 XX  
 AC AAT48684;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT  
 XX 02-OCT-1997 (first entry)  
 DE  
 XX Probe for detecting N-ras gene mutations in the codon at position 61.  
 KW Mutated codon; single base mutation; human; acute myeloid leukaemia;  
 KW tumour; activated ras gene; N-ras; H-ras; K-ras; ss.

```

XX OS Synthetic.
XX PN US5591582-A.
XX PD 07-JAN-1997.
XX PF 23-JUN-1994; 9AUS-00264425.
XX PR 23-JUL-1985; 85US-00758104.
XX PR 04-AUG-1987; 87US-00081490.
XX PR 21-APR-1992; 92US-00873352.
XX XX (UYLE-) RIJKSUNIV LEIDEN.
XX PI Van Der Eb AJ, Bos JL;
XX XX WPI; 1997-086629/08.
XX DR
XX PT Detection of activated ras gene - using oligo:nucleotide probes to detect
XX PT mutated codon.
XX PS Claim 25; Col 29; 20pp; English.
XX CC A new method has been produced for the detection of an activated ras gene
XX CC containing a mutated codon. The method involves: either cleaving a human
XX CC subject's genomic DNA with a restriction enzyme to produce DNA fragments
XX CC and treating the fragments to obtain single-stranded DNA molecules or
XX CC isolating the subject's polyA+ mRNA; contacting the single-stranded DNA
XX CC molecules or polyA+ mRNA under hybridising conditions with a labelled
XX CC synthetic DNA molecule, optionally bound to a solid support, comprising
XX CC 12-20 nucleotides, where the synthetic DNA molecule is 5'-B-Q-D-3', in the
XX CC case of single-stranded DNA or is complementary to 5'-B-Q-D-3', in the
XX CC case of polyA+ mRNA, B = 0-9 nucleotides having a sequence complementary
XX CC to a sequence in the activated ras gene 5' of the mutated codon, D = 0-12
XX CC nucleotides having a sequence complementary to a sequence in the
XX CC activated ras gene 3' of the mutated codon, provided that B and D contain
XX CC a total of at least 9 nucleotides, and Q is complementary to the mutated
XX CC codon; treating the resulting hybridised molecules under conditions
XX CC permitting only fully complementary molecules to remain hybridised; and
XX CC detecting the presence of the labelled synthetic DNA molecule in the
XX CC hybridised molecules. The present sequence represents the synthetic DNA
XX CC probe used for detecting the activated N-ras gene when the mutated codon
XX CC is at position 61 and has a single base substitution in the first or
XX CC second nucleotide position so that it encodes an amino acid other than
XX CC Glu. The method can be used for the diagnosis of acute myeloid leukaemia
XX CC and other tumours. (Updated on 25-MAR-2003 to correct PF field.)
XX XX
XX SQ Sequence 20 BP; 2 A; 7 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 57.5%; Score 13.8; DB 2; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.3e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 ACAGCTGGGACACAGA 22
Db 20 ACAGCTGGAGAGAAGA 4

RESULT 23
AAV20056/c
ID AAV20056 standard; DNA; 20 BP.
XX AC AAV20056;
XX DT 06-JUL-1998 (first entry)
XX DE N-ras probe 665T.
XX PR Probe; N-ras; mutation detection; mismatch binding protein;
XX KW cancer diagnosis; single strand binding protein; ss.
XX OS Synthetic.

```

```

XX WO9745555-A1.
XX PN 04-DEC-1997.
XX PD
XX PF 22-MAY-1997; 97WO-SB000839.
XX PR 29-MAY-1996; 96SE-00002062.
XX XX (PHAA ) PHARMACIA BIOTECH AB.
XX PI Hasebe M, Goto M, Tosu M;
XX XX WPI; 1998-130209/12.
XX DR
XX PT Method for detecting mutation(s) by mismatch binding protein - useful for
XX PT separating mutation from non-mutated target polynucleotide in sample,
XX PT used in early diagnosis of cancer.
XX PS Disclosure; Page 9; 24pp; English.
XX CC This sequence represents a probe for the N-ras gene, that can be used in
XX CC the method of the invention. The method is for detecting a mutation
XX CC from a non-mutated sequence of a target polynucleotide (TP) in a sample,
XX CC by using a mismatch binding protein (MBP), comprises: (a) providing a non
XX CC -mutated and mutated TP; (b) forming duplex of the non-mutated and
XX CC mutated single strands of TP in (a); (c) adding a single strand binding
XX CC protein to the polynucleotide from (b); (d) incubating MBP with an
XX CC activating agent; (e) adding the incubated MBP from (d) to the
XX CC polynucleotide from (c), so that MBP binds to the duplex formed by one
XX CC non-mutated and one mutated single strand of TP; and (f) detecting the
XX CC presence of any MBP bound to TP. The method may be used for early
XX CC diagnosis of cancer. Binding of MBP to single strands is inhibited by the
XX CC single strand binding protein. By activating MBP with an activator,
XX CC before addition to the sample, binding to double strands lacking
XX CC mismatches does not take place
XX SQ Sequence 20 BP; 2 A; 7 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 57.5%; Score 13.8; DB 2; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.3e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 ACAGCTGGGACACAGA 22
Db 20 ACAGCTGGAGAGAAGA 4

RESULT 24
AAV73038
ID AAV73038 standard; DNA; 20 BP.
XX AC AAV73038;
XX DT 09-FEB-1999 (first entry)
XX DE Human ras oncogene probe #13.
XX KW Ras oncogene; probe; point mutation; detection; cancer; ss.
XX OS Synthetic.
XX PN US5847095-A.
XX XX 08-DEC-1998.
XX PD
XX PF 03-JAN-1997; 97US-00778543.
XX PR 23-JUL-1985; 85US-00758104.
XX PR 04-AUG-1987; 87US-00081490.
XX PR 21-APR-1992; 92US-00873352.
XX PR 23-JUN-1994; 94US-00264425.
XX OS

```

PA (UYLB-) RIJKSUNIV LEIDEN.  
XX Bos JL, Van Der Eb AJ;  
XX WPI; 1999-059149/05.  
XX Probes for detecting ras oncogene point mutations - useful for the  
PT diagnosis of cancer associated with single base mutations.  
XX  
XX Claim 6; Col 5; 18pp; English.  
XX  
XX AAV73026-V73071 are probes used to detect a single-base mutation in a  
CC human ras oncogene. These probes comprise 12-43 nucleotides of formula 5'  
CC -B-Q-D-3', Q = 3 nucleotides complementary to the mutated codon, and B  
CC and D each = 0-20 nucleotides complementary to the ras sequences flanking  
CC the mutated codon. The probes are useful for detecting cancers associated  
CC with point mutations  
XX  
XX Sequence 20 BP; 9 A; 2 C; 7 G; 2 T; 0 U; 0 Other;  
SQ

Query Match 57.5%; Score 13.8; DB 2; Length 20;  
Best Local Similarity 88.2%; Pred. No. 1.3e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX

Qy 6 ACAGCTGGGGAACAAGA 22  
|||||  
Db 1 ACAGCTGGGGAAGAAGA 17

RESULT 25  
AAV73141/c  
ID AAV73141 standard; DNA; 20 BP.  
XX  
XX AAV73141;  
AC  
XX 09-FEB-1999 (first entry)  
DT  
XX Human ras oncogene mutant detecting oligomer N-61a.  
DE  
XX Ras oncogene; probe; point mutation; detection; cancer; ss.  
KW  
XX Synthetic.  
OS  
XX US5847095-A.  
PN  
XX 08-DEC-1998.  
PD  
XX 03-JAN-1997; 97US-00778543.  
PF  
XX 23-JUL-1985; 85US-00758104.  
PR  
XX 04-AUG-1987; 87US-00081490.  
PR  
XX 21-APR-1992; 92US-00873352.  
PR  
XX 23-JUN-1994; 94US-00264425.  
XX  
XX (UYLB-) RIJKSUNIV LEIDEN.  
PA  
XX Bos JL, Van Der Eb AJ;  
PI  
XX WPI; 1999-059149/05.  
XX  
XX Probes for detecting ras oncogene point mutations - useful for the  
PT diagnosis of cancer associated with single base mutations.  
PT  
XX Disclosure; Col 19-20; 18pp; English.  
PS  
XX AAV73084-V73145 are oligomers used in a method to detect a single-base  
CC mutation in a human ras oncogene. These probes comprise 12-43 nucleotides  
CC of formula 5'-B-Q-D-3', Q = 3 nucleotides complementary to the mutated  
CC codon, and B and D each = 0-20 nucleotides complementary to the ras  
CC sequences flanking the mutated codon. The probes are useful for detecting  
CC cancers associated with point mutations  
XX  
XX Sequence 20 BP; 2 A; 7 C; 2 G; 9 T; 0 U; 0 Other;  
SQ

Query Match 57.5%; Score 13.8; DB 2; Length 20;  
Best Local Similarity 88.2%; Pred. No. 1.3e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX

Qy 6 ACAGCTGGGGAACAAGA 22  
|||||  
Db 20 ACAGCTGGGGAAGAAGA 4

RESULT 26  
ABL43554  
ID ABL43554 standard; DNA; 20 BP.  
XX  
XX ABL43554;  
AC  
XX 11-APR-2002 (first entry)  
DT  
XX Human chromosome 1p36-35 PCR primer SEQ ID NO:598.  
DE  
XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;  
KW PCR primer; ss.  
XX  
XX Homo sapiens.  
OS  
XX JP2001321190-A.  
PN  
XX 20-NOV-2001.  
PD  
XX 12-MAR-2001; 2001JP-00068285.  
PF  
XX 10-MAR-2000; 2000JP-00066716.  
PR  
XX (RIKA) RIKAGAKU KENKYUSHO.  
PA (GENO-) GENOTEX YG.  
PA  
XX WPI; 2002-144136/19.  
DR  
XX Arraying genome clones.  
XX  
XX Claim 4; Page 16; 528pp; Japanese.  
PS  
XX The present invention describes a method of arraying genome clones. The  
CC method comprises: (a) clones of the genomic libraries contained in  
CC multiwell plates numbered for discrimination are mixed in each of the  
CC multiwell plates; (b) a primer designed based on the chromosome marker  
CC sequence is added to the mixture to carry out an amplification reaction;  
CC (c) a signal corresponding to the marker is detected from the resultant  
CC amplified product to specify the discrimination Nos. of the multiwell  
CC plates containing the clones having said marker sequence; (d) the order  
CC of the markers is changed so that the same discrimination Nos. succeed to  
CC the maximum in the specified discrimination Nos. to array the multiwell  
CC plates; (e) the clones in the multiwell plates of the specified  
CC discrimination Nos. are mixed respectively in each wells of longitudinal  
CC and lateral directions; (f) the mixed clones are cultured and the  
CC resultant cultures are amplified by using the above primer; (g) signals  
CC are detected from the amplified products; (h) the clones in the multiwell  
CC plates are specified from the detected result; and (i) the clones are  
CC reconstituted as the positions on the chromosome and arrayed. The  
CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent  
CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634  
CC represent PCR primers for human chromosome 21q22.1, which are  
CC specifically claimed for use in the present invention  
XX  
XX Sequence 20 BP; 7 A; 2 C; 9 G; 2 T; 0 U; 0 Other;  
SQ

Query Match 57.5%; Score 13.8; DB 6; Length 20;  
Best Local Similarity 88.2%; Pred. No. 1.3e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX

Qy 8 AGCTGGGGAACAAGACG 24  
|||||  
Db 4 AGCTGGTGAAGAAGACG 20



KW Antilipaeamic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;  
 KW Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;  
 KW cardiovascular disorder; metabolic syndrome X; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..20  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "This oligonucleotide has a phosphorothioate  
 FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'  
 FT and 3' ends, which are 4 nucleotides in length. Also all  
 FT cytidine residues are 5-methylcytidines"  
 XX  
 PN WO2004009541-A2.  
 XX  
 XX 29-JAN-2004.  
 PD  
 XX 18-JUL-2003; 2003WO-US022410.  
 PF  
 XX 19-JUL-2002; 2002US-0397106P.  
 PR  
 XX (PHAA ) PHARMACIA CORP.  
 PA  
 XX Bhat BG;  
 PI  
 XX WPI; 2004-132912/13.  
 DR  
 XX New antisense oligonucleotide for modulating endothelial lipase  
 PT expression, for diagnosing, preventing or treating e.g. dyslipidemia, low  
 PT high density lipoprotein or cardiovascular disorders.  
 PT  
 XX Claim 3; SEQ ID NO 1359; 1007pp; English.  
 PS  
 XX The present invention relates to antisense oligonucleotides (ADJ21603-  
 CC ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence  
 CC (ADJ25517), where the antisense oligonucleotide specifically hybridises  
 CC with and inhibits the expression of EL. The antisense oligonucleotides  
 CC are useful for modulating the expression of endothelial lipase in cells  
 CC or tissues to treat diseases associated with EL expression, such as  
 CC dyslipidaemia, low high density lipoprotein (HDL), cardiovascular  
 CC disorder or metabolic syndrome X. In addition, the oligonucleotides are  
 CC used for diagnostics, prophylaxis, or as research reagents or kits.  
 CC  
 XX Sequence 20 BP; 4 A; 3 C; 11 G; 2 T; 0 U; 0 Other;  
 SQ  
 Query Match 57.5%; Score 13.8; DB 12; Length 20;  
 Best Local Similarity 88.2%; Pred. No. 1.3e+04;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 8 AGCTGGGGAACAGACG 24  
 Db ||||| ||||| ||||| ||||| |||||  
 3 AGCTGGGGAACAGACG 19  
 RESULT 30  
 ADJ23531  
 ID ADJ23531 standard; DNA; 20 BP.  
 AC  
 XX ADJ23531;  
 AC  
 XX 20-MAY-2004 (first entry)  
 DT  
 XX Human endothelial lipase antisense oligonucleotide, SEQ ID 1929.  
 DE  
 XX Antilipaeamic; Cardiovascular; Analgesic; Antianginal; Antisense therapy;  
 KW Human; Endothelial Lipase; dyslipidaemia; high density lipoprotein; HDL;  
 KW cardiovascular disorder; metabolic syndrome X; ss.  
 KW  
 XX Homo sapiens.  
 OS  
 OS Synthetic.

XX Key Location/Qualifiers  
 FH modified\_base 1..20  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "This oligonucleotide has a phosphorothioate  
 FT backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'  
 FT and 3' ends, which are 4 nucleotides in length. Also all  
 FT cytidine residues are 5-methylcytidines"  
 XX  
 PN WO2004009541-A2.  
 XX  
 XX 29-JAN-2004.  
 PD  
 XX 18-JUL-2003; 2003WO-US022410.  
 PF  
 XX 19-JUL-2002; 2002US-0397106P.  
 PR  
 XX (PHAA ) PHARMACIA CORP.  
 PA  
 XX Bhat BG;  
 PI  
 XX WPI; 2004-132912/13.  
 DR  
 XX New antisense oligonucleotide for modulating endothelial lipase  
 PT expression, for diagnosing, preventing or treating e.g. dyslipidemia, low  
 PT high density lipoprotein or cardiovascular disorders.  
 PT  
 XX Claim 3; SEQ ID NO 1929; 1007pp; English.  
 PS  
 XX The present invention relates to antisense oligonucleotides (ADJ21603-  
 CC ADJ25510) targeted to human Endothelial Lipase (EL) coding sequence  
 CC (ADJ25517), where the antisense oligonucleotide specifically hybridises  
 CC with and inhibits the expression of EL. The antisense oligonucleotides  
 CC are useful for modulating the expression of endothelial lipase in cells  
 CC or tissues to treat diseases associated with EL expression, such as  
 CC dyslipidaemia, low high density lipoprotein (HDL), cardiovascular  
 CC disorder or metabolic syndrome X. In addition, the oligonucleotides are  
 CC used for diagnostics, prophylaxis, or as research reagents or kits.  
 CC  
 XX Sequence 20 BP; 5 A; 3 C; 11 G; 1 T; 0 U; 0 Other;  
 SQ  
 Query Match 57.5%; Score 13.8; DB 12; Length 20;  
 Best Local Similarity 88.2%; Pred. No. 1.3e+04;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 8 AGCTGGGGAACAGACG 24  
 Db ||||| ||||| ||||| ||||| |||||  
 2 AGCTGGGGAACAGACG 18  
 RESULT 31  
 ABN13371  
 ID ABN13371 standard; DNA; 25 BP.  
 XX  
 AC ABN13371;  
 XX  
 XX 29-MAY-2002 (first entry)  
 DT  
 XX Human GDMPLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13363.  
 DE  
 XX Human; genome-derived myosin-like protein 1; GDMPLP-1; heart;  
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KW skeletal muscle disorder; amplicon; screening; ss.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200192524-A2.  
 PN  
 XX 06-DEC-2001.  
 PD  
 XX 25-MAY-2001; 2001WO-US016981.  
 PF  
 XX



PR 26-MAY-2000; 2000US-0207456P.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US000661.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 05-FEB-2001; 2001US-0266860P.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
 XX  
 XX WPI; 2002-179446/23.  
 DR  
 XX  
 XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,  
 PT or as specific biomolecule capture probes for surface-enhanced laser  
 PT desorption ionization, comprises human myosin-like protein hGDMLP-1.  
 PT  
 XX  
 XX Disclosure; SEQ ID NO 13363; 214pp; English.  
 PS  
 XX  
 CC The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1  
 CC nucleic acids can be used as probes to detect, characterise and quantify  
 CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMLP  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption/ionisation, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence  
 XX  
 SQ Sequence 25 BP; 8 A; 6 C; 9 G; 2 T; 0 U; 0 Other;  
 Query Match 57.5%; Score 13.8; DB 6; Length 25;  
 Best Local Similarity 88.2%; Pred No. 1.4e+04;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 8 AGCTGGGGAACAAGACG 24  
 DB 7 AGCTGGAGAACATGACG 23  
 RESULT 32  
 ABN13372  
 ID ABN13372 standard; DNA; 25 BP.  
 XX  
 AC ABN13372;  
 XX  
 DT 29-MAY-2002 (first entry)  
 XX  
 DE Human GDMLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13364.  
 XX  
 KW Human; genome-derived myosin-like protein 1; hGDMLP-1; heart;

KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KW skeletal muscle disorder; amplicon; screening; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200192524-A2.  
 XX  
 XX 06-DEC-2001.  
 XX  
 XX 25-MAY-2001; 2001WO-US016981.  
 XX  
 XX 26-MAY-2000; 2000US-0207456P.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US000661.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 05-FEB-2001; 2001US-0266860P.  
 XX  
 XX (AEOM-) AEOMICA INC.  
 XX  
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
 XX  
 XX WPI; 2002-179446/23.  
 DR  
 XX  
 XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,  
 PT or as specific biomolecule capture probes for surface-enhanced laser  
 PT desorption ionization, comprises human myosin-like protein hGDMLP-1.  
 PT  
 XX  
 XX Disclosure; SEQ ID NO 13364; 214pp; English.  
 PS  
 XX  
 CC The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1  
 CC nucleic acids can be used as probes to detect, characterise and quantify  
 CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMLP  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption/ionisation, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence  
 XX  
 SQ Sequence 25 BP; 7 A; 6 C; 10 G; 2 T; 0 U; 0 Other;  
 Query Match 57.5%; Score 13.8; DB 6; Length 25;  
 Best Local Similarity 88.2%; Pred No. 1.4e+04;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 8 AGCTGGGGAACAAGACG 24  
 DB 6 AGCTGGAGAACATGACG 22  
 RESULT 32  
 ABN13372  
 ID ABN13372 standard; DNA; 25 BP.  
 XX  
 AC ABN13372;  
 XX  
 DT 29-MAY-2002 (first entry)  
 XX  
 DE Human GDMLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13364.  
 XX  
 KW Human; genome-derived myosin-like protein 1; hGDMLP-1; heart;

RESULT 33  
ABN13376  
ID ABN13376 standard; DNA; 25 BP.  
XX  
AC ABN13376;  
XX  
DT 29-MAY-2002 (first entry)  
XX  
DE Human GDMPLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13368.  
XX  
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200192524-A2.  
XX  
PD 06-DEC-2001.  
XX  
PF 25-MAY-2001; 2001WO-US016981.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
XX  
PA (AEOM-) AEOMICA INC.  
XX  
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon MB;  
XX  
DR WPI; 2002-179446/23.  
XX  
PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
XX  
PS Disclosure; SEQ ID NO 13368; 214pp; English.  
XX  
CC The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
CC nucleic acids can be used as probes to detect, characterise and quantify  
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption/ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMPLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pat\_sequence

SQ Sequence 25 BP; 9 A; 5 C; 9 G; 2 T; 0 U; 0 Other;  
Query Match 57.5%; Score 13.8; DB 6; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.4e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 8 AGCTGGGGAACAAGACG 24  
DB 2 AGCTGGGGAACATGACG 18  
RESULT 34  
ABN13373  
ID ABN13373 standard; DNA; 25 BP.  
XX  
AC ABN13373;  
XX  
DT 29-MAY-2002 (first entry)  
XX  
DE Human GDMPLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13365.  
XX  
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200192524-A2.  
XX  
PD 06-DEC-2001.  
XX  
PF 25-MAY-2001; 2001WO-US016981.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
XX  
XX (AEOM-) AEOMICA INC.  
XX  
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon MB;  
XX  
DR WPI; 2002-179446/23.  
XX  
PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
XX  
PS Disclosure; SEQ ID NO 13365; 214pp; English.  
XX  
CC The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
CC nucleic acids can be used as probes to detect, characterise and quantify  
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption/ionisation, as

CC therapeutic supplement in patients having specific deficiency in hGDMLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence

XX Sequence 25 BP; 8 A; 5 C; 10 G; 2 T; 0 U; 0 Other;

Query Match 57.5%; Score 13.8; DB 6; Length 25;  
 Best Local Similarity 88.2%; Pred. No. 1.4e+04;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 AGCTGGGGAACAGACG 24

Db 5 AGCTGGGGAACATGACG 21

RESULT 35

ABN13370  
 ID ABN13370 standard; DNA; 25 BP.

XX AC ABN13370;

XX 29-MAY-2002 (first entry)

XX Human GDMLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13362.

XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;  
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KW skeletal muscle disorder; amplicon; screening; ss.

XX OS Homo sapiens.

XX PN WO200192524-A2.

XX PD 06-DEC-2001.

XX PF 25-MAY-2001; 2001WO-US016981.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PR 30-JAN-2001; 2001WO-US000661.

XX PR 30-JAN-2001; 2001WO-US000662.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 30-JAN-2001; 2001WO-US000668.

XX PR 30-JAN-2001; 2001WO-US000669.

XX PR 30-JAN-2001; 2001WO-US000670.

XX PR 05-FEB-2001; 2001US-0266860P.

XX (AEOM-) AEOMICA INC.

XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX WPI; 2002-179446/23.

XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,  
 PT or as specific biomolecule capture probes for surface-enhanced laser  
 PT desorption ionization, comprises human myosin-like protein hGDMLP-1.  
 XX Disclosure; SEQ ID NO 13362; 214pp; English.  
 XX The present invention describes a human genome-derived myosin-like

CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1  
 CC nucleic acids can be used as probes to detect, characterise and quantify  
 CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMLP  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption ionisation, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence

XX Sequence 25 BP; 8 A; 7 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 57.5%; Score 13.8; DB 6; Length 25;

Best Local Similarity 88.2%; Pred. No. 1.4e+04;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 AGCTGGGGAACAGACG 24

Db 8 AGCTGGGGAACATGACG 24

RESULT 36

ABN13377  
 ID ABN13377 standard; DNA; 25 BP.

XX AC ABN13377;

XX 29-MAY-2002 (first entry)

XX Human GDMLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13369.

XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;  
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KW skeletal muscle disorder; amplicon; screening; ss.

XX OS Homo sapiens.

XX PN WO200192524-A2.

XX PD 06-DEC-2001.

XX PF 25-MAY-2001; 2001WO-US016981.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PR 30-JAN-2001; 2001WO-US000661.

XX PR 30-JAN-2001; 2001WO-US000662.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 30-JAN-2001; 2001WO-US000668.

XX PR 30-JAN-2001; 2001WO-US000669.

XX PR 30-JAN-2001; 2001WO-US000670.

XX 05-FEB-2001; 2001US-0266860P.

XX (AEOM-) AEOMICA INC.

PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
 XX WPI; 2002-179446/23.  
 XX  
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
 PT or as specific biomolecule capture probes for surface-enhanced laser  
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
 XX  
 XX Disclosure; SEQ ID NO 13369; 214pp; English.  
 XX  
 CC The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
 CC nucleic acids can be used as probes to detect, characterise and quantify  
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption/ionisation, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMPLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence  
 XX  
 SQ Sequence 25 BP; 10 A; 5 C; 8 G; 2 T; 0 U; 0 Other;  
 Query Match 57.5%; Score 13.8; DB 6; Length 25;  
 Best Local Similarity 88.2%; Pred. No. 1.4e+04;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 8 AGCTGGGGACACAGACG 24  
 DB 1 AGCTGGAGAACATGACG 17  
 RESULT 37  
 ABN13369  
 ID ABN13369 standard; DNA; 25 BP.  
 AC ABN13369;  
 XX  
 XX 29-MAY-2002 (first entry)  
 DT  
 XX Human GDMPLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13361.  
 DE  
 XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
 KW muscle; myosin; chromosome 22; Gene therapy; vaccine; heart disease;  
 KW skeletal muscle disorder; amplicon; screening; ss.  
 XX Homo sapiens.  
 OS  
 XX WO200192524-A2.  
 PN  
 XX 06-DEC-2001.  
 PD  
 XX  
 XX 25-MAY-2001; 2001WO-US016981.  
 PF  
 XX 26-MAY-2000; 2000US-0207456P.  
 PR  
 XX 21-SEP-2000; 2000US-0234687P.  
 PR  
 XX 27-SEP-2000; 2000US-0236359P.  
 PR  
 XX 04-OCT-2000; 2000GB-00024263.  
 PR  
 XX 30-JAN-2001; 2001WO-US000661.  
 PR  
 XX 30-JAN-2001; 2001WO-US000662.  
 PR  
 XX 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 30-JAN-2001; 2001WO-US000670.  
 PR 05-FEB-2001; 2001US-0266860P.  
 XX  
 XX (AEOM-) AEOMICA INC.  
 XX  
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
 PI WPI; 2002-179446/23.  
 XX  
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
 PT or as specific biomolecule capture probes for surface-enhanced laser  
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
 XX  
 XX Disclosure; SEQ ID NO 13361; 214pp; English.  
 PS  
 XX The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
 CC nucleic acids can be used as probes to detect, characterise and quantify  
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption/ionisation, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMPLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence  
 XX  
 SQ Sequence 25 BP; 8 A; 6 C; 9 G; 2 T; 0 U; 0 Other;  
 Query Match 57.5%; Score 13.8; DB 6; Length 25;  
 Best Local Similarity 88.2%; Pred. No. 1.4e+04;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 8 AGCTGGGGACACAGACG 24  
 DB 9 AGCTGGAGAACATGACG 25  
 RESULT 38  
 ABN13374  
 ID ABN13374 standard; DNA; 25 BP.  
 AC ABN13374;  
 XX  
 XX 29-MAY-2002 (first entry)  
 DT  
 XX Human GDMPLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13366.  
 DE  
 XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
 KW muscle; myosin; chromosome 22; Gene therapy; vaccine; heart disease;  
 KW skeletal muscle disorder; amplicon; screening; ss.  
 XX Homo sapiens.  
 OS  
 XX WO200192524-A2.  
 PN  
 XX

PD 06-DEC-2001.  
XX 25-MAY-2001; 2001WO-US016981.  
XX 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
XX (AEOM-) AEOMICA INC.  
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX WPI; 2002-179446/23.  
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
XX Disclosure; SEQ ID NO 13366; 214pp; English.  
XX The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
CC nucleic acids can be used as probes to detect, characterise and quantify  
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption/ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMPLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequence  
SQ Sequence 25 BP; 8 A; 5 C; 10 G; 2 T; 0 U; 0 Other;  
Query Match 57.5%; Score 13.8; DB 6; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.4e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 8 AGCTGGGGAACAAGACG 24  
DB ||||| ||||| |||||  
4 AGCTGGGGAACAATGACG 20  
RESULT 39  
ABN13375  
ID ABN13375 standard; DNA; 25 BP.  
XX  
AC ABN13375;  
XX  
DT 29-MAY-2002 (first entry)

XX Human GDMPLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13367.  
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.  
XX Homo sapiens.  
XX WO200192524-A2.  
XX 06-DEC-2001.  
XX 25-MAY-2001; 2001WO-US016981.  
XX 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
XX (AEOM-) AEOMICA INC.  
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX WPI; 2002-179446/23.  
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
XX Disclosure; SEQ ID NO 13367; 214pp; English.  
XX The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
CC nucleic acids can be used as probes to detect, characterise and quantify  
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption/ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMPLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequence  
SQ Sequence 25 BP; 8 A; 6 C; 9 G; 2 T; 0 U; 0 Other;  
Query Match 57.5%; Score 13.8; DB 6; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.4e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 8 AGCTGGGGAACAAGACG 24

```
Db          ||||| ||||| |||||
3 ACCTGGAGAACATGACG 19

RESULT 40
ADQ80648/c
ID ADQ80648 standard; DNA; 25 BP.
XX
AC ADQ80648;
XX
DT 09-SEP-2004 (first entry)
XX
DE Binding domain-functional group fusion related pRK primer.
XX
KW dimer; chimeric recombinant binding domain-functional group fusion;
KW steric hindrance; PCR; primer; ss.
XX
OS Unidentified.
XX
PN KR2004004095-A.
XX
PD 13-JAN-2004.
XX
PF 30-JUN-2003; 2003KR-00043599.
XX
PR 29-JUN-2002; 2002KR-00037770.
XX
PA (CHOE/) CHO E M H.
XX
PI Choe MH, Choi SH, Kim YJ, Kwon HW, Lee YC, Song JH, Won JS;
PI Yoo MH;
XX
DR WPI; 2004-370653/35.
XX
PT Dimer of chimeric recombinant binding domain-functional group fusion
PT formed via disulfide-bond-bridge and production process thereof.
XX
PS Example 3; Page 25; 65pp; Korean.
XX
CC The invention describes a dimer of a chimeric recombinant binding domain-
CC functional group fusion formed via disulfide-bond-bridge and a production
CC process thereof. The dimer has two times-improved adhesion, and
CC excellently functions on a target. A dimer of chimeric recombinant
CC binding domain-functional group fusion is provided, wherein an extended
CC amino acid sequence (Ext) which is extended from the binding domain (B)
CC to the function group (F) fuses the binding domain (B) and the functional
CC group (F); the extended amino acid sequence (Ext) contains cysteine
CC without an inner chain pair and forms disulfide-bond-bridge when the
CC cysteine is oxidised; and a flexible amino acid sequence (Flx) is
CC contained between the last cysteine and the functional group (F), and
CC consists of flexible amino acid sequences of GASQEND, so that it can
CC decrease steric hindrance between the functional group when the chimeric
CC recombinant binding domain(B)-functional group (F) fusion forms the
CC dimer. This sequence represents a primer associated with the chimeric
CC recombinant binding domain-functional group fusion of the invention.
XX
SQ Sequence 25 BP; 1 A; 10 C; 9 G; 5 T; 0 U; 0 Other;

Query Match          57.5%; Score 13.8; DB 12; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.4e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 GCACAGCTGGGGAACAA 20
        ||| ||||| |||||
Db      17 GCGCGGCTGGGGAACAA 1
```

Search completed: December 13, 2005, 13:34:17  
Job time : 371.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 12:48:14 ; Search time 1116.5 Seconds  
(without alignments)  
1221.892 Million cell updates/sec

Title: US-10-713-137-3

Perfect score: 24

Sequence: 1 gatgcacagctggggaacaagacg 24

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 2097806

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_in.\*

3: gb\_env.\*

4: gb\_on.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pr.\*

9: gb\_ro.\*

10: gb\_ats.\*

11: gb\_sy.\*

12: gb\_un.\*

13: gb\_vi.\*

14: gb\_htg.\*

15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	24	100.0	24	6	CS101223	Sequence
2	15.6	65.0	26	6	CQ979281	Sequence
C 3	15	62.5	38	6	AR071012	Sequence
4	14.6	60.8	47	6	AR290262	Sequence
C 5	14.4	60.0	19	6	CQ890345	Sequence
C 6	14.4	60.0	19	6	CQ896981	Sequence
7	14.4	60.0	30	6	AX588101	Sequence
8	14.4	60.0	30	6	AX642888	Sequence
9	14.2	59.2	21	6	CQ878645	Sequence
10	14.2	59.2	21	6	CQ890107	Sequence
11	14.2	59.2	22	6	AX487198	Sequence
C 12	14.2	59.2	23	6	E26387	Neuralized
13	14	58.3	37	6	A86551	Sequence 13
14	14	58.3	37	6	BD082235	Surface p
15	14	58.3	47	6	AR290163	Sequence
16	13.8	57.5	17	6	CQ623729	Sequence
17	13.8	57.5	17	6	AR464792	Sequence
C 18	13.8	57.5	17	6	AX673028	Sequence

C	19	13.8	57.5	20	6	AR167144	Sequence
	20	13.8	57.5	20	6	BD088354	A method
	21	13.8	57.5	20	6	I02471	Sequence 3
	22	13.8	57.5	20	11	AB067911	Synthetic
	23	13.8	57.5	25	6	CQ628621	Sequence
	24	13.8	57.5	25	6	CQ628622	Sequence
	25	13.8	57.5	25	6	CQ628623	Sequence
	26	13.8	57.5	25	6	CQ628624	Sequence
	27	13.8	57.5	25	6	CQ628625	Sequence
	28	13.8	57.5	25	6	CQ628626	Sequence
	29	13.8	57.5	25	6	CQ628627	Sequence
	30	13.8	57.5	25	6	CQ628628	Sequence
	31	13.8	57.5	25	6	CQ628629	Sequence
	32	13.8	57.5	25	6	AR469684	Sequence
	33	13.8	57.5	25	6	AR469685	Sequence
	34	13.8	57.5	25	6	AR469686	Sequence
	35	13.8	57.5	25	6	AR469687	Sequence
	36	13.8	57.5	25	6	AR469688	Sequence
	37	13.8	57.5	25	6	AR469689	Sequence
	38	13.8	57.5	25	6	AR469690	Sequence
	39	13.8	57.5	25	6	AR469691	Sequence
	40	13.8	57.5	25	6	AR469692	Sequence
	41	13.8	57.5	29	6	BD082096	Reagents
C	42	13.8	57.5	42	6	AX734289	Sequence
C	43	13.8	57.5	47	6	AR292118	Sequence
C	44	13.6	56.7	24	6	AX052659	Sequence
C	45	13.6	56.7	24	6	AX445211	Sequence

#### ALIGNMENTS

RESULT 1  
CS101223 LOCUS CS101223 24 bp DNA linear PAT 10-JUN-2005  
DEFINITION Sequence 3 from Patent WO2005047540.  
ACCESSION CS101223  
VERSION CS101223.1 GI:67509720

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE 1

AUTHORS Pasha, A.O. and Ahsan, A.

TITLE Method of detecting predisposition to high altitude pulmonary edema

JOURNAL Patent: WO 2005047540-A 3 26-MAY-2005;

Council of Scientific and Industrial Research (IN)

Location/Qualifiers

FEATURES

source

1..24

/organism="synthetic construct"

/mol\_type="unassigned DNA"

/db\_xref="taxon:32630"

/note="Synthetic Oligonucleotide"

ORIGIN  
Query Match 100.0%; Score 24; DB 6; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGCACAGCTGGGGAACAAGACG 24

|||||

Db 1 GATGCACAGCTGGGGAACAAGACG 24

RESULT 2

CQ979281 LOCUS CQ979281 26 bp DNA linear PAT 19-JAN-2005

DEFINITION Sequence 35 from Patent WO2005000888.

ACCESSION CQ979281

VERSION CQ979281.1 GI:57976534

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM synthetic construct

other sequences; artificial sequences.	
1	
REFERENCE	
AUTHORS	Estes,S.D. and Zhang,W.
TITLE	Novel Beta-actin and RPS21 promoters and uses thereof
JOURNAL	Patent: WO 2005000888-A 35 06-JAN-2005;
Genzyme Corporation (US)	
FEATURES	
source	Location/Qualifiers
1..26	
/organism="synthetic construct"	
/mol_type="unassigned DNA"	
/db_xref="taxon:32630"	
/note="forward primer for amplifying beta-actin promoter containing intron 1"	
ORIGIN	
Query Match	65.0%; Score 15.6; DB 6; Length 26;
Best Local Similarity	81.8%; Pred. No. 1.9e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
QY	2 ATGCACAGCTGGGGAAACAAGAC 23
Db	1 AGGCCACAGCTTGGGACCAAGAC 22
RESULT 3	
LOCUS	AR071012/c
DEFINITION	Sequence 13 from patent US 5910405.
ACCESSION	AR071012
VERSION	AR071012.1 GI:7221900
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	Cho,J.Myoung., Choi,D.Young., Kim,C.Hyung., So,H.Seob., Yang,J.Young., Kim,I.Soo. and Kim,J.Ho.
TITLE	HCV diagnostic agents
JOURNAL	Patent: US 5910405-A 13 08-JUN-1999;
FEATURES	Location/Qualifiers
source	1..38
/organism="unknown"	
/mol_type="unassigned DNA"	
ORIGIN	
Query Match	62.5%; Score 15; DB 6; Length 38;
Best Local Similarity	78.3%; Pred. No. 3.7e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
QY	1 GATGCACAGCTGGGGAAACAAGAC 23
Db	35 GGTGAACAGCTGGGAACACCAC 13
RESULT 4	
LOCUS	AR290262
DEFINITION	Sequence 1997 from patent US 6537751.
ACCESSION	AR290262
VERSION	AR290262.1 GI:31677546
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE	Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL	Patent: US 6537751-A 1997 25-MAR-2003;
Genset S.A.;;	
FEATURES	Location/Qualifiers
source	1..47
/organism="unknown"	
/mol_type="genomic DNA"	
ORIGIN	
Query Match	60.0%; Score 14.6; DB 6; Length 47;
Best Local Similarity	73.9%; Pred. No. 5.8e+04;
Matches 17; Conservative 1; Mismatches 5; Indels 0; Gaps 0;	
QY	1 GATGCACAGCTGGGGAAACAAGAC 23
Db	24 RATGCACACCTGTTTTCACAAGAC 46
RESULT 5	
LOCUS	CQ890345/c
DEFINITION	Sequence 1 from Patent EP1469070.
ACCESSION	CQ890345
VERSION	CQ890345.1 GI:55163328
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Butz,K., Crnkovic-Mertens,I. and Hoppe-Seyler,F.D.
TITLE	Livin-specific siRNAs for the treatment of therapy-resistant tumors
JOURNAL	Patent: EP 1469070-A 1 20-OCT-2004;
Deutsches Krebsforschungszentrum Stiftung des oeffentlichen n Rechts (DE)	
FEATURES	Location/Qualifiers
source	1..19
/organism="Homo sapiens"	
/mol_type="unassigned RNA"	
/db_xref="taxon:9606"	
ORIGIN	
Query Match	60.0%; Score 14.4; DB 6; Length 19;
Best Local Similarity	93.8%; Pred. No. 7.7e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	6 ACAGCTGGGGAAACAAG 21
Db	16 ACAGCTGGGGAAACCAG 1
RESULT 6	
LOCUS	CQ896981/c
DEFINITION	Sequence 1 from Patent WO2004091388.
ACCESSION	CQ896981
VERSION	CQ896981.1 GI:55581823
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Butz,K., Crnkovic-Mertens,I. and Hoppe-Seyler,F.
TITLE	LIVIN-SPECIFIC siRNAs FOR THE TREATMENT OF THERAPY-RESISTANT TUMORS
JOURNAL	Patent: WO 2004091388-A 1 28-OCT-2004;
Deutsches Krebsforschungszentrum Stiftung des oeffentlichen n Rechts (DE)	
FEATURES	Location/Qualifiers
source	1..19
/organism="Homo sapiens"	
/mol_type="unassigned RNA"	
/db_xref="taxon:9606"	
ORIGIN	
Query Match	60.0%; Score 14.4; DB 6; Length 19;



```
Best Local Similarity 93.8%; Pred. No. 7.7e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 ACAGCTGGGAACAAG 21
    |||||
Db 16 ACAGCTGGGAACAAG 1

RESULT 7
LOCUS AX588101 30 bp DNA linear PAT 24-JAN-2003
DEFINITION Sequence 7 from Patent EP1253205.
ACCESSION AX588101
VERSION AX588101.1 GI:27899755
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 Hofer,M., Kranz,H. and Klink,M.
AUTHORS Method of blocking amplification of selected sequences
TITLE Patent: EP 1253205-A 7 30-OCT-2002;
JOURNAL LION Bioscience AG (DE)
FEATURES
source
1. .30
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 60.0%; Score 14.4; DB 6; Length 30;
Best Local Similarity 75.0%; Pred. No. 7.5e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GATGCACAGCTGGGAACAAGC 24
    |||||
Db 6 GATGCACGAGGGGAGGAGAGG 29

RESULT 8
LOCUS AX642888 30 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7 from Patent WO2086155.
ACCESSION AX642888
VERSION AX642888.1 GI:28475108
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Hofer,M., Klink,M. and Kranz,H.
AUTHORS Method for the preferential nucleic acid synthesis reaction of one
TITLE or more selected regions of one or more target nucleic acids
JOURNAL Patent: WO 02086155-A 7 31-OCT-2002;
LION Bioscience AG (DE)
FEATURES
source
1. .30
Location/Qualifiers
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

ORIGIN
Query Match 60.0%; Score 14.4; DB 6; Length 30;
Best Local Similarity 75.0%; Pred. No. 7.5e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GATGCACAGCTGGGAACAAGC 24
    |||||
Db 6 GATGCACGAGGGGAGGAGAGG 29

Best Local Similarity 93.8%; Pred. No. 7.7e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 ACAGCTGGGAACAAG 21
    |||||
Db 16 ACAGCTGGGAACAAG 1

RESULT 9
LOCUS CQ878645 21 bp DNA linear PAT 04-OCT-2004
DEFINITION Sequence 17 from Patent EP1462521.
ACCESSION CQ878645
VERSION CQ878645.1 GI:53791103
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 Deppert,W.W. and Dornreiter,I.
AUTHORS Human p53 splice variant displaying differential transcriptional
TITLE activity
JOURNAL Patent: EP 1462521-A 17 29-SEP-2004;
Deppert, Wolfgang Willi (DE)
FEATURES
source
1. .21
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer E1R"

ORIGIN
Query Match 59.2%; Score 14.2; DB 6; Length 21;
Best Local Similarity 84.2%; Pred. No. 9.6e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCACAGCTGGGAACAAGA 22
    |||||
Db 1 GCTCAGTGGGGGAACAAGA 19

RESULT 10
LOCUS CQ890107 21 bp DNA linear PAT 19-OCT-2004
DEFINITION Sequence 17 from Patent WO2004085468.
ACCESSION CQ890107
VERSION CQ890107.1 GI:54305801
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 Deppert,W.W. and Dornreiter,I.
AUTHORS Novel human p53 splice variant displaying differential
TITLE transcriptional activity
JOURNAL Patent: WO 2004085468-A 17 07-OCT-2004;
Deppert, Wolfgang Willi (DE)
FEATURES
source
1. .21
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer E1R"

ORIGIN
Query Match 59.2%; Score 14.2; DB 6; Length 21;
Best Local Similarity 84.2%; Pred. No. 9.6e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCACAGCTGGGAACAAGA 22
    |||||
Db 1 GCTCAGTGGGGGAACAAGA 19

RESULT 11
LOCUS AX487198 22 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 4498 from Patent WO2053728.
ACCESSION AX487198
VERSION AX487198.1 GI:22321346
KEYWORDS
```

<hr/>					
RESULT 13	A86551	37 bp	DNA	linear	PAT 21-JAN-2000
LOCUS					
DEFINITION	Sequence 13 from Patent WO9839450.				
ACCESSION	A86551				
VERSION	A86551.1 GI:6735149				
KEYWORDS	unidentified				
SOURCE	unclassified sequences.				
ORGANISM	1 (bases 1 to 37)				
REFERENCE	Chhatwal,G.S. and Hammerschmidt,S.				
AUTHORS	SURFACE PROTEIN (SPeA PROTEIN) OF STREPTOCOCCUS PNEUMONIAE, DELETED				
TITLE	DERIVATIVES, EXPRESSION SYSTEM FOR SAID PROTEINS AND VACCINE SYSTEM				
JOURNAL	WITH SAID PROTEINS				
FEATURES	Patent: WO 9839450-A 13 11-SEP-1998;				
source	BIOTECHNOLOG FORSCHUNG GMBH (DE); CHHATWAL GURSHARAN SINGH (DE)				
ORIGIN	Location/Qualifiers				
	1..37				
	/organism="unidentified"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:32644"				
Query Match	58.3%; Score 14; DB 6; Length 37;				
Best Local Similarity	77.3%; Pred. No. 1.2e+05;				
Matches	17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;				
Qy	1 GATGCACAGCTGGGGAACAAGA 22				
Db	12 GATCCACAGCGTGGAAACAAGA 33				
<hr/>					
RESULT 14	BD082235	37 bp	DNA	linear	PAT 27-AUG-2002
LOCUS					
DEFINITION	Surface protein (SPeA protein) of streptococcus pneumoniae, deleted				
	derivatives, expression system for said proteins and vaccine system				
	with said proteins.				
ACCESSION	BD082235				
VERSION	BD082235.1 GI:22627845				
KEYWORDS	JP 2001524073-A/12.				
SOURCE	synthetic construct				
ORGANISM	other sequences; artificial sequences.				
REFERENCE	1 (bases 1 to 37)				
AUTHORS	Chhatwal,G.S. and Hammerschmidt,S.				
TITLE	Surface protein (SPeA protein) of streptococcus pneumoniae, deleted				
	derivatives, expression system for said proteins and vaccine system				
	with said proteins				
JOURNAL	Patent: JP 2001524073-A 12 27-NOV-2001;				
COMMENT	GESELLSCHAFT FÜR BIOTECHNOLOGISCHE FORSCHUNG MBH				
	PN JP 2001524073-A/12				
	PD 27-NOV-2001				
	PF 02-MAR-1998 JP 1998538137				
	PR 03-MAR-1997 DE 19708537.7				
	PI GURSHARAN SINGH CHHATWAL,SVEN HAMMERSCHMIDT				
	PC C12N15/31,C07K14/315,A61K39/09,C12N15/70				
	Strandedness: Single;				
	CC Topology: Linear;				
	CC /description = 'Primer'				
FEATURES	Key Location/Qualifiers.				
source	1..37				
	/organism="synthetic construct"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:32630"				
ORIGIN					
Query Match	59.3%; Score 14; DB 6; Length 37;				
Best Local Similarity	77.3%; Pred. No. 1.2e+05;				
Matches	17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;				



```

SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    Unclassified.
1 (bases 1 to 20)
AUTHORS      Bos, J.L. and Van der Eb, A.J.
TITLE        Probes and methods for detecting activated ras oncogenes
JOURNAL      Patent: US 4871838-A 3 03-OCT-1989;
              The Board of Rijks Universiteit Leiden; Leiden;
              NL;
FEATURES     Location/Qualifiers
              source
              1..20
              /organism="unknown"
              /mol_type="unassigned DNA"
ORIGIN
Query Match      57.5%; Score 13.8; DB 6; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY              6 ACAGCTGGGGAACAAGA 22
              ||||||| |||||
Db              20 ACAGCTGGGGAAGAAGA 4
              ||||||| |||||

RESULT 20
LOCUS      BD088354                20 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION A method of arraying genome clone.
ACCESSION  BD088354
VERSION     BD088354.1 GI:226333964
KEYWORDS   JP 2001321190-A/598.
SOURCE     synthetic construct
ORGANISM   synthetic construct
other sequences; artificial sequences.
REFERENCE  Soeda, E.
AUTHORS    Patent: JP 2001321190-A 598 20-NOV-2001;
JOURNAL    THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
GENOTECHS
COMMENT    OS Artificial Sequence
PN JP 2001321190-A/598
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PI EIICHI SORDA
PC C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N33/53, G01N33/566, PC
C12N15/00,
PC C12N15/00
CC Description of Artificial Sequence: Synthetic DNA FH Key
FT source
FT Location/Qualifiers
           1..20
           /organism="synthetic construct"
           /mol_type="genomic DNA"
           /db_xref="taxon:32630"
FEATURES   Location/Qualifiers
           source
           1..20
           /organism="synthetic construct"
           /mol_type="genomic DNA"
           /db_xref="taxon:32630"
ORIGIN
Query Match      57.5%; Score 13.8; DB 6; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY              8 AGCTGGGGAACAAGACG 24
              ||||||| |||||
Db              4 AGCTGGTGAAGAAGACG 20
              ||||||| |||||

RESULT 21
LOCUS      102471                20 bp      ss-DNA     linear      PAT 21-MAY-1993
DEFINITION Sequence 3 from Patent US 4871838.
ACCESSION  102471
VERSION     102471.1 GI:270472
KEYWORDS

SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    Unclassified.
1 (bases 1 to 20)
AUTHORS      Bos, J.L. and Van der Eb, A.J.
TITLE        Probes and methods for detecting activated ras oncogenes
JOURNAL      Patent: US 4871838-A 3 03-OCT-1989;
              The Board of Rijks Universiteit Leiden; Leiden;
              NL;
FEATURES     Location/Qualifiers
              source
              1..20
              /organism="unknown"
              /mol_type="unassigned DNA"
ORIGIN
Query Match      57.5%; Score 13.8; DB 11; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY              8 AGCTGGGGAACAAGACG 24
              ||||||| |||||
Db              4 AGCTGGTGAAGAAGACG 20
              ||||||| |||||

RESULT 22
LOCUS      AB067911                20 bp      DNA      linear      SYN 21-MAY-2003
DEFINITION Synthetic construct DNA, reverse primer for human STS sts-F19245 at
1p36.
ACCESSION  AB067911
VERSION     AB067911.1 GI:15128715
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
other sequences; artificial sequences.
REFERENCE  Chen, Y. Z., Hayaehi, Y., Wu, J. G., Takaoka, E., Maekawa, K.,
AUTHORS    Watanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H.,
              Morohashi, A., Ohira, M., Nakagawara, A., Liu, S., Hoshi, M., Horii, A.
              and Soeda, E.
              A BAC-based STS-content map spanning a 35-Mb region of human
              chromosome 74 (1), 55-70 (2001)
              Genomics 74 (1), 55-70 (2001)
              11374902
JOURNAL    PUEMED
REFERENCE  2 (bases 1 to 20)
AUTHORS    Horii, A.
TITLE      Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
              Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
              Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,
              Tel: 81-22-717-8042, Fax: 81-22-717-8047)
              Location/Qualifiers
           1..20
           /organism="synthetic construct"
           /mol_type="genomic DNA"
           /db_xref="taxon:32630"
misc_feature
           1..20
           /note="reverse primer for human STS sts-F19245 at 1p36
              sts-F19245 obtained from clones B313L13, B244M15, Human
              BAC library RPCI-11"
ORIGIN
Query Match      57.5%; Score 13.8; DB 11; Length 20;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY              8 AGCTGGGGAACAAGACG 24
              ||||||| |||||
Db              4 AGCTGGTGAAGAAGACG 20
              ||||||| |||||

RESULT 23
LOCUS      CQ628621
DEFINITION
ACCESSION
VERSION
KEYWORDS

```

LOCUS CQ628621 25 bp DNA linear PAT 02-FEB-2004  
DEFINITION Sequence 13361 from Patent WO0192524.  
ACCESSION CQ628621  
VERSION CQ628621.1 GI:41678839  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.  
TITLE Myosin-like gene expressed in human heart and muscle  
JOURNAL Patent: WO 0192524-A 13361 06-DEC-2001;  
Aeomica, Inc. (US)  
FEATURES  
source Location/Qualifiers  
1..25  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 57.5%; Score 13.8; DB 6; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.5e+05;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 8 AGCTGGGGAACAGACG 24  
Db 9 AGCTGGAGAACATGACG 25  
RESULT 24  
CQ628622 25 bp DNA linear PAT 02-FEB-2004  
LOCUS CQ628622  
DEFINITION Sequence 13362 from Patent WO0192524.  
ACCESSION CQ628622  
VERSION CQ628622.1 GI:41678840  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.  
TITLE Myosin-like gene expressed in human heart and muscle  
JOURNAL Patent: WO 0192524-A 13362 06-DEC-2001;  
Aeomica, Inc. (US)  
FEATURES  
source Location/Qualifiers  
1..25  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 57.5%; Score 13.8; DB 6; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.5e+05;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 8 AGCTGGGGAACAGACG 24  
Db 8 AGCTGGAGAACATGACG 24  
RESULT 25  
CQ628623 25 bp DNA linear PAT 02-FEB-2004  
LOCUS CQ628623  
DEFINITION Sequence 13363 from Patent WO0192524.  
ACCESSION CQ628623  
VERSION CQ628623.1 GI:41678841  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.  
TITLE Myosin-like gene expressed in human heart and muscle  
JOURNAL Patent: WO 0192524-A 13363 06-DEC-2001;  
Aeomica, Inc. (US)  
FEATURES  
source Location/Qualifiers  
1..25  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 57.5%; Score 13.8; DB 6; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.5e+05;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 8 AGCTGGGGAACAGACG 24  
Db 7 AGCTGGAGAACATGACG 23  
RESULT 26  
CQ628624 25 bp DNA linear PAT 02-FEB-2004  
LOCUS CQ628624  
DEFINITION Sequence 13364 from Patent WO0192524.  
ACCESSION CQ628624  
VERSION CQ628624.1 GI:41678842  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.  
TITLE Myosin-like gene expressed in human heart and muscle  
JOURNAL Patent: WO 0192524-A 13364 06-DEC-2001;  
Aeomica, Inc. (US)  
FEATURES  
source Location/Qualifiers  
1..25  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 57.5%; Score 13.8; DB 6; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.5e+05;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 8 AGCTGGGGAACAGACG 24  
Db 6 AGCTGGAGAACATGACG 22  
RESULT 27  
CQ628625 25 bp DNA linear PAT 02-FEB-2004  
LOCUS CQ628625  
DEFINITION Sequence 13365 from Patent WO0192524.  
ACCESSION CQ628625  
VERSION CQ628625.1 GI:41678843  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE  
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.  
TITLE Myosin-like gene expressed in human heart and muscle  
JOURNAL Patent: WO 0192524-A 13365 06-DEC-2001;  
Aeomica, Inc. (US)  
FEATURES source  
1. .25  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 57.5%; Score 13.8; DB 6; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.5e+05;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 8 AGCTGGGGAACAAGACG 24  
||||| ||||| |||||  
Db 5 AGCTGGAGAACATGACG 21  
RESULT 28  
LOCUS CQ628626 25 bp DNA linear PAT 02-FEB-2004  
DEFINITION Sequence 13366 from Patent WO0192524.  
ACCESSION CQ628626  
VERSION CQ628626.1 GI:41678844  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.  
REFERENCE  
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.  
TITLE Myosin-like gene expressed in human heart and muscle  
JOURNAL Patent: WO 0192524-A 13366 06-DEC-2001;  
Aeomica, Inc. (US)  
FEATURES source  
1. .25  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 57.5%; Score 13.8; DB 6; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.5e+05;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 8 AGCTGGGGAACAAGACG 24  
||||| ||||| |||||  
Db 4 AGCTGGAGAACATGACG 20  
RESULT 29  
LOCUS CQ628627 25 bp DNA linear PAT 02-FEB-2004  
DEFINITION Sequence 13367 from Patent WO0192524.  
ACCESSION CQ628627  
VERSION CQ628627.1 GI:41678845  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.  
REFERENCE  
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.  
TITLE Myosin-like gene expressed in human heart and muscle  
JOURNAL Patent: WO 0192524-A 13367 06-DEC-2001;

Aeomica, Inc. (US)  
FEATURES source  
1. .25  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 57.5%; Score 13.8; DB 6; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.5e+05;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 8 AGCTGGGGAACAAGACG 24  
||||| ||||| |||||  
Db 3 AGCTGGAGAACATGACG 19  
RESULT 30  
LOCUS CQ628628 25 bp DNA linear PAT 02-FEB-2004  
DEFINITION Sequence 13368 from Patent WO0192524.  
ACCESSION CQ628628  
VERSION CQ628628.1 GI:41678846  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.  
REFERENCE  
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.  
TITLE Myosin-like gene expressed in human heart and muscle  
JOURNAL Patent: WO 0192524-A 13368 06-DEC-2001;  
Aeomica, Inc. (US)  
FEATURES source  
1. .25  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 57.5%; Score 13.8; DB 6; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.5e+05;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 8 AGCTGGGGAACAAGACG 24  
||||| ||||| |||||  
Db 2 AGCTGGAGAACATGACG 18  
RESULT 31  
LOCUS CQ628629 25 bp DNA linear PAT 02-FEB-2004  
DEFINITION Sequence 13369 from Patent WO0192524.  
ACCESSION CQ628629  
VERSION CQ628629.1 GI:41678847  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.  
REFERENCE  
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.  
TITLE Myosin-like gene expressed in human heart and muscle  
JOURNAL Patent: WO 0192524-A 13369 06-DEC-2001;  
Aeomica, Inc. (US)  
FEATURES source  
1. .25  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"

```
/db_xref="taxon:9606"

ORIGIN
Query Match          57.5%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 AGCTGGGGAACAAGACG 24
    ||||| ||||| |||||
Db 1 AGCTGGGGAACAATGACG 17
    ||||| ||||| |||||

RESULT 32
AR469684
LOCUS
DEFINITION
Sequence 13361 from patent US 6686188.
ACCESSION
AR469684
VERSION
AR469684.1 GI:42704741
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE
Polynucleotide encoding a human myosin-like polypeptide expressed
predominantly in heart and muscle
Patent: US 6686188-A 13361 03-FEB-2004;
JOURNAL
Amersham PLC; Buckinghamshire;
GBX;
FEATURES
source
Location/Qualifiers
1..25
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match          57.5%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 AGCTGGGGAACAAGACG 24
    ||||| ||||| |||||
Db 9 AGCTGGGGAACAATGACG 25
    ||||| ||||| |||||

RESULT 33
AR469685
LOCUS
DEFINITION
Sequence 13362 from patent US 6686188.
ACCESSION
AR469685
VERSION
AR469685.1 GI:42704742
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE
Polynucleotide encoding a human myosin-like polypeptide expressed
predominantly in heart and muscle
Patent: US 6686188-A 13362 03-FEB-2004;
JOURNAL
Amersham PLC; Buckinghamshire;
GBX;
FEATURES
source
Location/Qualifiers
1..25
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match          57.5%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 AGCTGGGGAACAAGACG 24
    ||||| ||||| |||||
Db 8 AGCTGGGGAACAATGACG 23
    ||||| ||||| |||||

RESULT 34
AR469686
LOCUS
DEFINITION
Sequence 13363 from patent US 6686188.
ACCESSION
AR469686
VERSION
AR469686.1 GI:42704743
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE
Polynucleotide encoding a human myosin-like polypeptide expressed
predominantly in heart and muscle
Patent: US 6686188-A 13363 03-FEB-2004;
JOURNAL
Amersham PLC; Buckinghamshire;
GBX;
FEATURES
source
Location/Qualifiers
1..25
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match          57.5%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 AGCTGGGGAACAAGACG 24
    ||||| ||||| |||||
Db 8 AGCTGGGGAACAATGACG 24
    ||||| ||||| |||||

RESULT 35
AR469687
LOCUS
DEFINITION
Sequence 13364 from patent US 6686188.
ACCESSION
AR469687
VERSION
AR469687.1 GI:42704744
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE
Polynucleotide encoding a human myosin-like polypeptide expressed
predominantly in heart and muscle
Patent: US 6686188-A 13364 03-FEB-2004;
JOURNAL
Amersham PLC; Buckinghamshire;
GBX;
FEATURES
source
Location/Qualifiers
1..25
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match          57.5%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.5e+05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 AGCTGGGGAACAAGACG 24
    ||||| ||||| |||||
Db 6 AGCTGGGGAACAATGACG 22
    ||||| ||||| |||||

RESULT 36
AR469688
```

LOCUS AR469688 25 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 13365 from patent US 6686188.  
ACCESSION AR469688  
VERSION AR469688.1 GI:42704745  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
JOURNAL Patent: US 6686188-A 13365 03-FEB-2004;  
Amersham PLC; Buckinghamshire;  
GBX;  
FEATURES  
source Location/Qualifiers  
1..25  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
Query Match 57.5%; Score 13.8; DB 6; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.5e+05;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 8 AGCTGGGGAACAAGACG 24  
||||| ||||| |||||  
Db 5 AGCTGGAGAACATGACG 21  
||||| ||||| |||||  
RESULT 37  
AR469689 25 bp DNA linear PAT 20-FEB-2004  
LOCUS  
DEFINITION Sequence 13366 from patent US 6686188.  
ACCESSION AR469689  
VERSION AR469689.1 GI:42704746  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
JOURNAL Patent: US 6686188-A 13366 03-FEB-2004;  
Amersham PLC; Buckinghamshire;  
GBX;  
FEATURES  
source Location/Qualifiers  
1..25  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
Query Match 57.5%; Score 13.8; DB 6; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.5e+05;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 8 AGCTGGGGAACAAGACG 24  
||||| ||||| |||||  
Db 4 AGCTGGAGAACATGACG 20  
||||| ||||| |||||  
RESULT 38  
AR469690 25 bp DNA linear PAT 20-FEB-2004  
LOCUS  
DEFINITION Sequence 13367 from patent US 6686188.  
ACCESSION AR469690  
VERSION AR469690.1 GI:42704747  
KEYWORDS  
SOURCE  
ORGANISM

Unclassified.  
1 (bases 1 to 25)  
Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
JOURNAL Patent: US 6686188-A 13367 03-FEB-2004;  
Amersham PLC; Buckinghamshire;  
GBX;  
FEATURES  
source Location/Qualifiers  
1..25  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
Query Match 57.5%; Score 13.8; DB 6; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.5e+05;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 8 AGCTGGGGAACAAGACG 24  
||||| ||||| |||||  
Db 3 AGCTGGAGAACATGACG 19  
||||| ||||| |||||  
RESULT 39  
AR469691 25 bp DNA linear PAT 20-FEB-2004  
LOCUS  
DEFINITION Sequence 13368 from patent US 6686188.  
ACCESSION AR469691  
VERSION AR469691.1 GI:42704748  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
JOURNAL Patent: US 6686188-A 13368 03-FEB-2004;  
Amersham PLC; Buckinghamshire;  
GBX;  
FEATURES  
source Location/Qualifiers  
1..25  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
Query Match 57.5%; Score 13.8; DB 6; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.5e+05;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 8 AGCTGGGGAACAAGACG 24  
||||| ||||| |||||  
Db 2 AGCTGGAGAACATGACG 18  
||||| ||||| |||||  
RESULT 40  
AR469692 25 bp DNA linear PAT 20-FEB-2004  
LOCUS  
DEFINITION Sequence 13369 from patent US 6686188.  
ACCESSION AR469692  
VERSION AR469692.1 GI:42704749  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.  
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle  
JOURNAL Patent: US 6686188-A 13369 03-FEB-2004;  
Amersham PLC; Buckinghamshire;  
GBX;



Amersham PLC; Buckinghamshire;  
GBX;  
Location/Qualifiers  
1. .25  
/organism="unknown"  
/mol\_type="genomic DNA"

FEATURES

source

ORIGIN

Query Match 57.5%; Score 13.8; DB 6; Length 25;  
Best Local Similarity 88.2%; Pred. No. 1.5e+05;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 AGCTGGGGACACAGACG 24  
||||| ||||| |||||  
Db 1 AGCTGGAGACATGACG 17

Search completed: December 13, 2005, 14:11:40  
Job time : 1118.5 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 13:34:24 ; Search time 214.5 Seconds  
(without alignments)  
41.830 Million cell updates/sec

Title: US-10-713-137-2

Perfect score: 24

Sequence: 1 cagcggatgatggaacgacgac 24

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3392430 seqs, 186927314 residues

Total number of hits satisfying chosen parameters: 6638722

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA New:\*

- 1: /cgn2\_6/ptodata/2/pubna/US09\_NEW\_PUB.seq.\*
- 2: /cgn2\_6/ptodata/2/pubna/US06\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubna/US07\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubna/US08\_NEW\_PUB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubna/PCT\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubna/US10\_NEW\_PUB.seq.\*
- 7: /cgn2\_6/ptodata/2/pubna/US11\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/2/pubna/US11\_NEW\_PUB.seq2.\*
- 9: /cgn2\_6/ptodata/2/pubna/US11\_NEW\_PUB.seq3.\*
- 10: /cgn2\_6/ptodata/2/pubna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	15.8	65.8	19	8	US-11-101-244-947800
2	15.8	65.8	19	9	US-11-083-784-947800
3	14.4	60.0	19	8	US-11-101-244-386342
4	14.4	60.0	19	9	US-11-083-784-386342
5	14.2	59.2	32	6	US-10-939-294A-17050
6	13.8	57.5	19	8	US-11-101-244-647873
7	13.8	57.5	19	9	US-11-083-784-647873
8	13.4	55.8	19	8	US-11-101-244-882569
9	13.4	55.8	19	9	US-11-083-784-882569
10	13.2	55.0	19	8	US-11-101-244-248753
11	13.2	55.0	19	9	US-11-101-244-287598
12	13.2	55.0	19	8	US-11-101-244-341923
13	13.2	55.0	19	9	US-11-101-244-426653
14	13.2	55.0	19	8	US-11-101-244-770754
15	13.2	55.0	19	9	US-11-083-784-248753
16	13.2	55.0	19	9	US-11-083-784-287598
17	13.2	55.0	19	9	US-11-083-784-341923
18	13.2	55.0	19	9	US-11-083-784-426653
19	13.2	55.0	19	9	US-11-083-784-770754
20	13.2	55.0	32	6	US-10-939-294A-17174
21	13	54.2	19	8	US-11-101-244-332886
22	13	54.2	19	9	US-11-083-784-332886
23	13	54.2	21	6	US-10-770-726-27035

24	13	54.2	21	6	US-10-770-726-27036	Sequence 27036, A
25	13	54.2	21	6	US-10-770-726-27533	Sequence 27533, A
26	13	54.2	21	6	US-10-770-726-27534	Sequence 27534, A
27	13	54.2	21	6	US-10-770-726-27536	Sequence 27536, A
28	13	54.2	21	6	US-10-770-726-27537	Sequence 27537, A
29	13	54.2	21	6	US-10-770-726-27539	Sequence 27539, A
30	13	54.2	21	6	US-10-770-726-27989	Sequence 27989, A
31	13	54.2	21	6	US-10-770-726-27990	Sequence 27990, A
32	13	54.2	21	6	US-10-770-726-28073	Sequence 28073, A
33	13	54.2	21	6	US-10-770-726-28074	Sequence 28074, A
34	13	54.2	21	6	US-10-770-726-28076	Sequence 28076, A
35	13	54.2	21	6	US-10-770-726-28077	Sequence 28077, A
36	13	54.2	21	6	US-10-770-726-28079	Sequence 28079, A
37	13	54.2	32	6	US-10-939-294A-17960	Sequence 17960, A
38	12.8	53.3	19	8	US-11-101-244-385942	Sequence 385942, A
39	12.8	53.3	19	8	US-11-101-244-394642	Sequence 394642, A
40	12.8	53.3	19	8	US-11-101-244-394667	Sequence 394667, A
41	12.8	53.3	19	8	US-11-101-244-472467	Sequence 472467, A
42	12.8	53.3	19	8	US-11-101-244-703352	Sequence 703352, A
43	12.8	53.3	19	8	US-11-101-244-834656	Sequence 834656, A
44	12.8	53.3	19	8	US-11-101-244-947795	Sequence 947795, A
45	12.8	53.3	19	8	US-11-101-244-1574497	Sequence 1574497, A

#### ALIGNMENTS

RESULT 1  
US-11-101-244-947800  
; Sequence 947800, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101.244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 947800  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-947800

Query Match 65.8%; Score 15.8; DB 8; Length 19;  
Best Local Similarity 78.9%; Pred No. 1.2e+02;  
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGTGTCGCAAGCAGCA 23  
||| :|||:|||||  
Db 1 GGACUGAUGGCAAGUACGA 19

RESULT 2  
US-11-083-784-947800  
; Sequence 947800, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William

```

; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 947800
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-947800

```

```

Query Match      65.8%; Score 15.8; DB 9; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.2e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      5 GGAGTGATGGCAAGCAGCA 23
      |||..|||:|||||
Db      1 GGACUGAUGGCAAGUACGA 19

```

```

RESULT 3
US-11-101-244-386342
; Sequence 386342, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 386342
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-386342

```

```

Query Match      60.0%; Score 14.4; DB 8; Length 19;
Best Local Similarity 87.5%; Pred. No. 5.2e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      6 GAGTGATGGCAAGCAGC 21
      |||..|||:|||||
Db      1 GAGAGAUGGCAAGCAGC 16

```

```

RESULT 4
US-11-083-784-386342
; Sequence 386342, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin

```

```

; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 386342
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-386342

```

```

Query Match      60.0%; Score 14.4; DB 9; Length 19;
Best Local Similarity 87.5%; Pred. No. 5.2e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      6 GAGTGATGGCAAGCAGC 21
      |||..|||:|||||
Db      1 GAGAGAUGGCAAGCAGC 16

```

```

RESULT 5
US-10-939-294A-17050
; Sequence 17050, Application US/10939294A
; Publication No. US20050266417A1
; GENERAL INFORMATION:
; APPLICANT: Barany, Francis
; APPLICANT: Turner, Daniel
; APPLICANT: Pingle, Maneesh
; APPLICANT: Pincas, Hanna
; TITLE OF INVENTION: Methods for identifying target nucleic acid molecules
; FILE REFERENCE: 19603/4121 (CRF D-2995-02)
; CURRENT APPLICATION NUMBER: US/10/939,294A
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US 60/502/731
; PRIOR FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 38895
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 17050
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide probe
US-10-939-294A-17050

```

```

Query Match      59.2%; Score 14.2; DB 6; Length 32;
Best Local Similarity 84.2%; Pred. No. 6.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      1 CAGCGGAGTGATGGCAAGC 19
      |||..|||:|||||
Db      4 CAGCGGGGTGACGGGAAGC 22

```

```

RESULT 6
US-11-101-244-647873
; Sequence 647873, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William

```

```
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 647873
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-647873
```

```
Query Match 57.5%; Score 13.8; DB 8; Length 19;
Best Local Similarity 82.4%; Pred. No. 9.7e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 CAGCGGAGTGATGGCAA 17
      ||||| :|| ||||
Db 2 CAGCGGACUGAAGGCAA 18
```

## RESULT 7

```
US-11-083-784-647873
; Sequence 647873, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 647873
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-647873
```

```
Query Match 57.5%; Score 13.8; DB 9; Length 19;
Best Local Similarity 82.4%; Pred. No. 9.7e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 CAGCGGAGTGATGGCAA 17
      ||||| :|| ||||
Db 2 CAGCGGACUGAAGGCAA 18
```

## RESULT 8

```
US-11-101-244-882569/c
; Sequence 882569, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
```

```
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 882569
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-882569
```

```
Query Match 55.8%; Score 13.4; DB 8; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 7 AGTCATGGCAAGCAC 21
      ||| ||||| |||||
Db 19 AGTAATGGCAAGCAC 5
```

## RESULT 9

```
US-11-083-784-882569/c
; Sequence 882569, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 882569
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-882569
```

```
Query Match 55.8%; Score 13.4; DB 9; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 7 AGTCATGGCAAGCAC 21
      ||| ||||| |||||
Db 19 AGTAATGGCAAGCAC 5
```

## RESULT 10

```
US-11-101-244-248753
; Sequence 248753, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
```

```
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 248753
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-248753
```

```
Query Match 55.0%; Score 13.2; DB 8; Length 19;
Best Local Similarity 77.8%; Pred. No. 1.8e+03;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 3 GCGGAGTGATGGCAAGCA 20
||| ||| ||| ||| |||
Db 1 GCGGAGAGAUGUCAAGCA 18
```

```
RESULT 11
US-11-101-244-287598
; Sequence 287598, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 287598
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-287598
```

```
Query Match 55.0%; Score 13.2; DB 8; Length 19;
Best Local Similarity 72.2%; Pred. No. 1.8e+03;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 3 GCGGAGTGATGGCAAGCA 20
||| ||| ||| ||| |||
Db 1 GCAAGAGAUGGCAAGAA 18
```

```
RESULT 12
US-11-101-244-341923
; Sequence 341923, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
```

```
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 341923
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-341923
```

```
Query Match 55.0%; Score 13.2; DB 8; Length 19;
Best Local Similarity 72.2%; Pred. No. 1.8e+03;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 3 GCGGAGTGATGGCAAGCA 20
||| ||| ||| ||| |||
Db 1 GCAGAGAGAUGUCAAGUA 18
```

```
RESULT 13
US-11-101-244-426653
; Sequence 426653, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 426653
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-426653
```

```
Query Match 55.0%; Score 13.2; DB 8; Length 19;
Best Local Similarity 77.8%; Pred. No. 1.8e+03;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 CAGCGGAGTGATGGCAAG 18
||| ||| ||| ||| |||
Db 1 CAGCUGAGAUGGCAAG 18
```

```
RESULT 14
US-11-101-244-770754
; Sequence 770754, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
```

```

; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 770754
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-083-784-248753

```

```

Query Match      55.0%; Score 13.2; DB 8; Length 19;
Best Local Similarity 77.8%; Pred. No. 1.8e+03;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 6 GAGTGTGGCAAGCAGCA 23
    |||:||||| |||
Db 2 GAGUGACGCAAGAAGCA 19

```

```

RESULT 15
US-11-083-784-248753
; Sequence 248753, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 248753
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-083-784-248753

```

```

Query Match      55.0%; Score 13.2; DB 9; Length 19;
Best Local Similarity 77.8%; Pred. No. 1.8e+03;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 3 GCGGAGTGTGGCAAGCA 20
    |||||:||| |||
Db 1 GCGGAGAGAGUUGCAUGCA 18

```

```

RESULT 16
US-11-083-784-287598
; Sequence 287598, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin

```

```

; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 287598
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-083-784-287598

```

```

Query Match      55.0%; Score 13.2; DB 9; Length 19;
Best Local Similarity 72.2%; Pred. No. 1.8e+03;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 3 GCGGAGTGTGGCAAGCA 20
    |||:||| |||
Db 1 GCAAAGUGAUGCAAGAA 18

```

```

RESULT 17
US-11-083-784-341923
; Sequence 341923, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 341923
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-083-784-341923

```

```

Query Match      55.0%; Score 13.2; DB 9; Length 19;
Best Local Similarity 72.2%; Pred. No. 1.8e+03;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 3 GCGGAGTGTGGCAAGCA 20
    |||:||| |||
Db 1 GCAGAGUGAUGCAAGAA 18

```

```

RESULT 18
US-11-083-784-426653
; Sequence 426653, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.

```

; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 426653  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
; OTHER INFORMATION: oligonucleotide probe  
US-11-083-784-426653

Query Match 55.0%; Score 13.2; DB 9; Length 19;  
Best Local Similarity 77.8%; Pred. No. 1.8e+03;  
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAG 18  
||||| ||||| ||||| |||||  
Db 1 CAGCUGAGAUUGGCAAG 18

RESULT 19  
US-11-083-784-770754  
; Sequence 770754, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 770754  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-770754

Query Match 55.0%; Score 13.2; DB 9; Length 19;  
Best Local Similarity 77.8%; Pred. No. 1.8e+03;  
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 GAGTGATGGCAAGCAGA 23  
||||| ||||| ||||| |||||  
Db 2 GAGUGACGCGAAGAGGA 19

RESULT 20  
US-10-939-294A-17174  
; Sequence 17174, Application US/10939294A

; Publication No. US20050266417A1  
; GENERAL INFORMATION:  
; APPLICANT: Barany, Francis  
; APPLICANT: Turner, Daniel  
; APPLICANT: Pingle, Maneesh  
; APPLICANT: Pincas, Hanna  
; TITLE OF INVENTION: Methods for identifying target nucleic acid molecules  
; FILE REFERENCE: 19603/4121 (CRF D-2995-02)  
; CURRENT APPLICATION NUMBER: US/10/939,294A  
; CURRENT FILING DATE: 2004-09-10  
; PRIOR APPLICATION NUMBER: 60/502/731  
; PRIOR FILING DATE: 2003-09-12  
; NUMBER OF SEQ ID NOS: 3895  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 17174  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide probe  
US-10-939-294A-17174

Query Match 55.0%; Score 13.2; DB 6; Length 32;  
Best Local Similarity 83.3%; Pred. No. 1.9e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAG 18  
||||| ||||| ||||| |||||  
Db 8 CAGCGGGTGACGGCGAG 25

RESULT 21  
US-11-101-244-332886  
; Sequence 332886, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 332886  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-332886

Query Match 54.2%; Score 13; DB 8; Length 19;  
Best Local Similarity 84.6%; Pred. No. 2.2e+03;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAGTGATGGCAAG 18  
||||| ||||| ||||| |||||  
Db 4 GAGUGAGGCGCAAG 16

RESULT 22  
US-11-083-784-332886  
; Sequence 332886, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.



; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 332886  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-332886

Query Match 54.2%; Score 13; DB 9; Length 19;  
Best Local Similarity 84.6%; Pred. No. 2.2e+03;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAGTGATGGCAAG 18  
|||:|||||  
Db 4 GAGUGAUGGCAAG 16

## RESULT 23

US-10-770-726-27035  
; Sequence 27035, Application US/10770726  
; Publication No. US20050266409A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Brown, Eugene  
; APPLICANT: Liu, Wei

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING  
; FILE REFERENCE: AM101079 (031896-010000)  
; CURRENT APPLICATION NUMBER: US/10/770,726  
; CURRENT FILING DATE: 2004-02-04  
; NUMBER OF SEQ ID NOS: 48640  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 27035  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-770-726-27035

Query Match 54.2%; Score 13; DB 6; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAGTGATGGCAAG 18  
|||||  
Db 3 GAGTGATGGCAAG 15

## RESULT 24

US-10-770-726-27036  
; Sequence 27036, Application US/10770726  
; Publication No. US20050266409A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Brown, Eugene  
; APPLICANT: Liu, Wei

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING  
; FILE REFERENCE: AM101079 (031896-010000)

; CURRENT APPLICATION NUMBER: US/10/770,726  
; CURRENT FILING DATE: 2004-02-04  
; NUMBER OF SEQ ID NOS: 48640  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 27036  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: RNAi  
US-10-770-726-27036

Query Match 54.2%; Score 13; DB 6; Length 21;  
Best Local Similarity 84.6%; Pred. No. 2.3e+03;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAGTGATGGCAAG 18  
|||||  
Db 1 GAGUGAUGGCAAG 13

## RESULT 25

US-10-770-726-27533  
; Sequence 27533, Application US/10770726  
; Publication No. US20050266409A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Brown, Eugene  
; APPLICANT: Liu, Wei

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING  
; FILE REFERENCE: AM101079 (031896-010000)  
; CURRENT APPLICATION NUMBER: US/10/770,726  
; CURRENT FILING DATE: 2004-02-04  
; NUMBER OF SEQ ID NOS: 48640  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 27533  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-770-726-27533

Query Match 54.2%; Score 13; DB 6; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAGTGATGGCAAG 18  
|||||  
Db 7 GAGTGATGGCAAG 19

## RESULT 26

US-10-770-726-27534  
; Sequence 27534, Application US/10770726  
; Publication No. US20050266409A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Brown, Eugene  
; APPLICANT: Liu, Wei

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING  
; FILE REFERENCE: AM101079 (031896-010000)  
; CURRENT APPLICATION NUMBER: US/10/770,726  
; CURRENT FILING DATE: 2004-02-04  
; NUMBER OF SEQ ID NOS: 48640  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 27534  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: RNAi  
US-10-770-726-27534

Query Match 54.2%; Score 13; DB 6; Length 21;  
Best Local Similarity 84.6%; Pred. No. 2.3e+03;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
QY      6 GAGTGATGGCAAG 18
Db      5 GAGUGAUGGCAAG 17

RESULT 27
US-10-770-726-27536
; Sequence 27536, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27536
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-27536

Query Match      54.2%; Score 13; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAGTGATGGCAAG 18
Db      1 GAGTGATGGCAAG 13

RESULT 30
US-10-770-726-27989
; Sequence 27989, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27989
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-27989

Query Match      54.2%; Score 13; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAGTGATGGCAAG 18
Db      3 GAGTGATGGCAAG 15

RESULT 31
US-10-770-726-27990
; Sequence 27990, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27990
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAI
US-10-770-726-27990

QY      6 GAGTGATGGCAAG 18
Db      3 GAGTGATGGCAAG 15

RESULT 32
US-10-770-726-27990
; Sequence 27990, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27990
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAI
US-10-770-726-27990

QY      6 GAGTGATGGCAAG 18
Db      2 GAGUGAUGGCAAG 14

RESULT 29
US-10-770-726-27539
; Sequence 27539, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
```

```
Query Match          54.2%; Score 13; DB 6; Length 21;
Best Local Similarity 84.6%; Pred. No. 2.3e+03;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAGTGATGGCAAG 18
Db 1 GAGUGAUGGCAAG 13

RESULT 32
US-10-770-726-28073
; Sequence 28073, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28073
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-28073

Query Match          54.2%; Score 13; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAGTGATGGCAAG 18
Db 7 GAGTGATGGCAAG 19

RESULT 33
US-10-770-726-28074
; Sequence 28074, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28074
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNai
US-10-770-726-28074

Query Match          54.2%; Score 13; DB 6; Length 21;
Best Local Similarity 84.6%; Pred. No. 2.3e+03;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAGTGATGGCAAG 18
Db 5 GAGUGAUGGCAAG 17

RESULT 34
US-10-770-726-28076
; Sequence 28076, Application US/10770726
```

```
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28076
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-28076

Query Match          54.2%; Score 13; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAGTGATGGCAAG 18
Db 4 GAGTGATGGCAAG 16

RESULT 35
US-10-770-726-28077
; Sequence 28077, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28077
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNai
US-10-770-726-28077

Query Match          54.2%; Score 13; DB 6; Length 21;
Best Local Similarity 84.6%; Pred. No. 2.3e+03;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAGTGATGGCAAG 18
Db 2 GAGUGAUGGCAAG 14

RESULT 36
US-10-770-726-28079
; Sequence 28079, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28079
```

```
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-28079

Query Match      54.2%; Score 13; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAGTGATGGCAAG 18
Db      1 GAGTGATGGCAAG 13

RESULT 37
US-10-939-294A-17960
; Sequence 17960, Application US/10939294A
; Publication No. US20050266417A1
; GENERAL INFORMATION:
; APPLICANT: Barany, Francis
; APPLICANT: Turner, Daniel
; APPLICANT: Pingle, Maneesh
; APPLICANT: Pincas, Hanna
; TITLE OF INVENTION: Methods for identifying target nucleic acid molecules
; FILE REFERENCE: 19603/4121 (CRF D-2995-02)
; CURRENT APPLICATION NUMBER: US/10/939,294A
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US 60/502/731
; PRIOR FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 38895
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17960
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide probe
US-10-939-294A-17960

Query Match      54.2%; Score 13; DB 6; Length 32;
Best Local Similarity 76.2%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 CAGCGGAGTGATGGCAAGC 21
Db      4 CAGCGGGGTGACGCGCAACGC 24

RESULT 38
US-11-101-244-385942
; Sequence 385942, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 385942
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
```

```
US-11-101-244-385942

Query Match      53.3%; Score 12.8; DB 8; Length 19;
Best Local Similarity 75.0%; Pred. No. 2.8e+03;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      5 GGAGTGATGGCAAGCA 20
Db      1 GGAGUGAUGGCAGGUA 16

RESULT 39
US-11-101-244-394642
; Sequence 394642, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 394642
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-394642

Query Match      53.3%; Score 12.8; DB 8; Length 19;
Best Local Similarity 81.2%; Pred. No. 2.8e+03;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      5 GGAGTGATGGCAAGCA 20
Db      2 GGAGUGACUGCAAGCA 17

RESULT 40
US-11-101-244-394667
; Sequence 394667, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 394667
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-394667
```

Query Match 53.3%; Score 12.8; DB 8; Length 19;  
Best Local Similarity 81.2%; Pred. No. 2.8e+03;  
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCA 20  
||||:||||  
Db 1 GGAGUGACUGCAAGCA 16  
||||:||||

Search completed: December 13, 2005, 16:24:34  
Job time : 214.5 secs

**THIS PAGE BLANK (USPTO)**



; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 6679  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4303  
; LENGTH: 37  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-780-533A-4303

Query Match 75.8%; Score 18.2; DB 3; Length 37;  
Best Local Similarity 78.3%; Pred. No. 90;  
Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCGAGTGATGCGCAAGCACGA 23  
||| ||||:|||||||  
Db 1 CAGAGGAGUGGCAUGGCACUA 23

RESULT 3  
US-09-730-289B-2709  
; Sequence 2709, Application US/09730289B  
; Publication No. US20030050259A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease  
; FILE REFERENCE: MBH00-864-A (400/006)  
; CURRENT APPLICATION NUMBER: US/09/730,289B  
; CURRENT FILING DATE: 2000-12-05  
; PRIOR APPLICATION NUMBER: US 60/169,100  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 3897  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2709  
; LENGTH: 37  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-730-289B-2709

Query Match 71.7%; Score 17.2; DB 3; Length 37;  
Best Local Similarity 77.3%; Pred. No. 2.7e+02;  
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGCGAGTGATGCGCAAGCACGA 23  
||| ||||:|||||||  
Db 2 AGCUGAGUGGCAUGGCACUA 23

RESULT 4  
US-09-776-474-1941  
; Sequence 1941, Application US/09776474  
; Publication No. US20030087847A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Jarvis, Thale  
; APPLICANT: Boher, Robert  
; APPLICANT: Holman, Patricia  
; APPLICANT: Fattaey, Ali  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK  
; FILE REFERENCE: MBH00-955-A (400/008)  
; CURRENT APPLICATION NUMBER: US/09/776,474  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,983  
; PRIOR FILING DATE: 2000-03-02  
; NUMBER OF SEQ ID NOS: 2992  
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1941  
; LENGTH: 37  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
US-09-776-474-1941

Query Match 71.7%; Score 17.2; DB 3; Length 37;  
Best Local Similarity 77.3%; Pred. No. 2.7e+02;  
Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGCGAGTGATGCGCAAGCACGA 23  
||| ||||:|||||||  
Db 2 AGAGGAGUGGCAUGGCACUA 23

RESULT 5  
US-10-712-672-4389  
; Sequence 4389, Application US/10712672  
; Publication No. US20040102413A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme  
; FILE REFERENCE: MBH00-882-C (400/019)  
; CURRENT APPLICATION NUMBER: US/10/712,672  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: US/09/653,225  
; PRIOR FILING DATE: 2000-08-31  
; PRIOR APPLICATION NUMBER: 60/197,769  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/150,713  
; PRIOR FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 5586  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4389  
; LENGTH: 36  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-10-712-672-4389

Query Match 70.0%; Score 16.8; DB 7; Length 36;  
Best Local Similarity 80.0%; Pred. No. 4.3e+02;  
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 CGGAGTGATGCGCAAGCACGA 23  
||| ||||:|||||||  
Db 1 CGGAGUGGCAUGGCACUA 20

RESULT 6  
US-11-060-756-223011  
; Sequence 223011, Application US/11060756  
; Publication No. US20050221354A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William Martin  
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug  
; FILE REFERENCE: AM101083 (031896-042000)  
; CURRENT APPLICATION NUMBER: US/11/060,756  
; CURRENT FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 303284  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 223011  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: probe



US-11-060-756-223011

Query Match 69.2%; Score 16.6; DB 10; Length 25;  
Best Local Similarity 82.6%; Pred. No. 5.3e+02;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AGCGGAGTGATGGCAAGCAGC 24  
Db 2 AGCGGAGTGACAGTAAGCAGGAC 24

RESULT 7

US-09-730-2898-2718  
; Sequence 2718, Application US/097302898  
; Publication No. US20030050259A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for Treatment of Cardiac Disease  
; FILE REFERENCE: MBH00-864-A (400/006)  
; CURRENT APPLICATION NUMBER: US/09/730,289B  
; CURRENT FILING DATE: 2000-12-05  
; PRIOR APPLICATION NUMBER: US 60/169,100  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 3897  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 2718  
; LENGTH: 37  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-730-2898-2718

Query Match 69.2%; Score 16.6; DB 3; Length 37;  
Best Local Similarity 73.9%; Pred. No. 5.3e+02;  
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAGCA 23  
Db 1 CAGAGAAGUGAUGGCAUGCAGCA 23

RESULT 8

US-09-780-533A-4266  
; Sequence 4266, Application US/09780533A  
; Publication No. US20030060611A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: Haeblerli, Pete  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
; FILE REFERENCE: MBH00,878-A (400/011)  
; CURRENT APPLICATION NUMBER: US/09/780,533A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,797  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 6679  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 4266  
; LENGTH: 37  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-780-533A-4266

Query Match 69.2%; Score 16.6; DB 3; Length 37;  
Best Local Similarity 73.9%; Pred. No. 5.3e+02;  
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAGCA 23  
Db 1 CAGGGGCGUGAUGGCAUGCAGCA 23

RESULT 9

US-09-927-046-3502  
; Sequence 3502, Application US/09927046  
; Publication No. US20030064946A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Thompson, Jim  
; APPLICANT: McKenzie, Tim  
; APPLICANT: Ayers, Dave  
; APPLICANT: Grupe, Andrew  
; APPLICANT: Szymkowski, Edmund  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlor  
; FILE REFERENCE: 249/021  
; CURRENT APPLICATION NUMBER: US/09/927,046  
; CURRENT FILING DATE: 2001-08-09  
; NUMBER OF SEQ ID NOS: 5450  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 3502  
; LENGTH: 37  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-927-046-3502

Query Match 69.2%; Score 16.6; DB 3; Length 37;  
Best Local Similarity 73.9%; Pred. No. 5.3e+02;  
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAGCA 23  
Db 1 CAGGGUAGUGAUGGCAUGCAGCA 23

RESULT 10

US-09-877-478-4013  
; Sequence 4013, Application US/09877478  
; Publication No. US20030068301A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Draper, Kenneth  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Morrissey, Dave  
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication  
; FILE REFERENCE: MBH00-845-H (400/029)  
; CURRENT APPLICATION NUMBER: US/09/877,478  
; CURRENT FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: US 07/882,712  
; PRIOR FILING DATE: 1992-05-14  
; PRIOR APPLICATION NUMBER: US 09/531,025  
; PRIOR FILING DATE: 2000-03-20  
; PRIOR APPLICATION NUMBER: US 09/636,385  
; PRIOR FILING DATE: 2000-08-09  
; PRIOR APPLICATION NUMBER: US 09/696,347  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 08/193,627  
; PRIOR FILING DATE: 1994-02-07  
; PRIOR APPLICATION NUMBER: US 08/433,993  
; PRIOR FILING DATE: 1995-05-04  
; PRIOR APPLICATION NUMBER: US 08/434,504  
; PRIOR FILING DATE: 1995-05-04  
; PRIOR APPLICATION NUMBER: US 09/436,430  
; PRIOR FILING DATE: 1999-11-08  
; NUMBER OF SEQ ID NOS: 6586

```
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 4013
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-877-478-4013

Query Match          69.2%; Score 16.6; DB 3; Length 37;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGCGCAAGCACGA 23
    ||||| |:|:|:|:|:|:|:|
DB 1 CAGCCUAGUGAUGGCAUGCACUA 23

RESULT 11
US-09-930-423-2746
; Sequence 2746, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBHB00.918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2746
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-930-423-2746

Query Match          69.2%; Score 16.6; DB 3; Length 37;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGCGCAAGCACGA 23
    ||||| |:|:|:|:|:|:|:|
DB 1 CCGCGGCGUGAUGGCAUGCACUA 23

RESULT 12
US-09-930-423-2764
; Sequence 2764, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBHB00.918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2764
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-930-423-2764

Query Match          69.2%; Score 16.6; DB 3; Length 37;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGCGCAAGCACGA 23
    ||||| |:|:~|:~|:~|:~|:~|
DB 1 CCGCGGCGUGAUGGCAUGCACUA 23

RESULT 13
US-09-930-423-2765
; Sequence 2765, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBHB00.918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2765
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-930-423-2765

Query Match          69.2%; Score 16.6; DB 3; Length 37;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGCGCAAGCACGA 23
    ||||| |:|:~|:~|:~|:~|:~|
DB 1 CCGCAGAGUGAUGGCAUGCACUA 23

RESULT 14
US-09-930-423-2786
; Sequence 2786, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBHB00.918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2786
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-930-423-2786

Query Match          69.2%; Score 16.6; DB 3; Length 37;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGCGCAAGCACGA 23
    ||||| |:|:~|:~|:~|:~|:~|
DB 1 CCGCAGAGUGAUGGCAUGCACUA 23

RESULT 15
US-09-745-237A-2746
; Sequence 2746, Application US/09745237A
; Publication No. US20030143708A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2746
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-745-237A-2746

Query Match          69.2%; Score 16.6; DB 3; Length 37;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCACGA 23
Db 1 CGCGGGGUGAUGGCAUGCACUA 23

RESULT 16
US-09-745-237A-2764
; Sequence 2764, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2764
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-745-237A-2764

Query Match          69.2%; Score 16.6; DB 3; Length 37;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCACGA 23
Db 1 CGCGGGGUGAUGGCAUGCACUA 23

RESULT 17
US-09-745-237A-2765
; Sequence 2765, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2765
```

```
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-745-237A-2765

Query Match          69.2%; Score 16.6; DB 3; Length 37;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCACGA 23
Db 1 CGCGAGAGUGGCAUGCACUA 23

RESULT 18
US-09-745-237A-2786
; Sequence 2786, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2786
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-745-237A-2786

Query Match          69.2%; Score 16.6; DB 3; Length 37;
Best Local Similarity 73.9%; Pred. No. 5.3e+02;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAAGCACGA 23
Db 1 CAGCGGGUGAUGGCAUGCACUA 23

RESULT 19
US-10-342-902-4013
; Sequence 4013, Application US/10342902
; Publication No. US20040054156A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: 400/075 (MBHB00-845-1)
; CURRENT APPLICATION NUMBER: US/10/342,902
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 09/877,478
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
```

;; PRIOR APPLICATION NUMBER: US 09/436,430  
;; PRIOR FILING DATE: 1999-11-08  
;; NUMBER OF SEQ ID NOS: 6592  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 4013  
;; LENGTH: 37  
;; TYPE: RNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-10-342-902-4013

Query Match 69.2%; Score 16.6; DB 7; Length 37;  
Best Local Similarity 73.9%; Pred. No. 5.3e+02;  
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCGAGTGATGGCAAGCACGA 23  
||| |||:|||||  
Db 1 CAGCCUAGUGAUGGCAUGACUA 23

RESULT 20  
US-10-669-841-8904  
;; Sequence 8904, Application US/10669841  
;; Publication No. US20040127446A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Sirna Therapeutics, Inc.  
;; APPLICANT: Lawrence, Blatt  
;; APPLICANT: Dennis, Macejak  
;; APPLICANT: James, McSwiggen  
;; APPLICANT: David, Morrissey  
;; APPLICANT: Pamela, Pavco  
;; APPLICANT: Patricia, Lee  
;; APPLICANT: Kenneth, Draper  
;; APPLICANT: Elisabeth, Roberts  
;; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP  
;; TITLE OF INVENTION: VIRUS REPLICATION  
;; FILE REFERENCE: 400/04205 (MBHB02-249-B)  
;; CURRENT APPLICATION NUMBER: US/10/669,841  
;; CURRENT FILING DATE: 2003-09-23  
;; PRIOR APPLICATION NUMBER: PCT/US02/09187  
;; PRIOR FILING DATE: 2002-03-26  
;; PRIOR APPLICATION NUMBER: US 60/296,876  
;; PRIOR FILING DATE: 2001-06-08  
;; PRIOR APPLICATION NUMBER: US 60/335,059  
;; PRIOR FILING DATE: 2001-10-24  
;; PRIOR APPLICATION NUMBER: US 60/337,055  
;; PRIOR FILING DATE: 2001-12-05  
;; PRIOR APPLICATION NUMBER: US 60/358,580  
;; PRIOR FILING DATE: 2002-02-20  
;; PRIOR APPLICATION NUMBER: US 60/363,124  
;; PRIOR FILING DATE: 2002-03-11  
;; PRIOR APPLICATION NUMBER: US 09/817,879  
;; PRIOR FILING DATE: 2001-03-26  
;; PRIOR APPLICATION NUMBER: US 09/740,332  
;; PRIOR FILING DATE: 2000-12-18  
;; PRIOR APPLICATION NUMBER: US 09/611,931  
;; PRIOR FILING DATE: 2000-07-07  
;; PRIOR APPLICATION NUMBER: US 09/504,321  
;; PRIOR FILING DATE: 2000-02-15  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 16207  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 8904  
;; LENGTH: 37  
;; TYPE: RNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-10-669-841-8904

Query Match 69.2%; Score 16.6; DB 7; Length 37;  
Best Local Similarity 73.9%; Pred. No. 5.3e+02;

Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 1 CAGCGAGTGATGGCAAGCACGA 23  
||| |||:|||||  
Db 1 CAGCCUAGUGAUGGCAUGACUA 23  
RESULT 21  
US-09-780-533A-4274  
;; Sequence 4274, Application US/09780533A  
;; Publication No. US20030060611A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
;; APPLICANT: Blatt, Larry  
;; APPLICANT: McSwiggen, Jim  
;; APPLICANT: Chowiriza, Bharat  
;; APPLICANT: Haerberli, Pete  
;; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
;; FILE REFERENCE: MBHB00,878-A (400/011)  
;; CURRENT APPLICATION NUMBER: US/09/780,533A  
;; CURRENT FILING DATE: 2001-02-09  
;; PRIOR APPLICATION NUMBER: US 60/181,797  
;; PRIOR FILING DATE: 2000-02-11  
;; NUMBER OF SEQ ID NOS: 6679  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 4274  
;; LENGTH: 37  
;; TYPE: RNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-780-533A-4274

Query Match 67.5%; Score 16.2; DB 3; Length 37;  
Best Local Similarity 76.2%; Pred. No. 8.3e+02;  
Matches 16; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCGGAGTGCAGCAAGCACGA 23  
||| |||:|||||  
Db 3 GGGGAGUGAUGGCAUGACUA 23

RESULT 22  
US-09-877-478-3997  
;; Sequence 3997, Application US/09877478  
;; Publication No. US20030068301A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
;; APPLICANT: Draper, Kenneth  
;; APPLICANT: Blatt, Larry  
;; APPLICANT: McSwiggen, Jim  
;; APPLICANT: Morrissey, Dave  
;; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication  
;; FILE REFERENCE: MBHB00-845-H (400/029)  
;; CURRENT APPLICATION NUMBER: US/09/877,478  
;; CURRENT FILING DATE: 2001-12-31  
;; PRIOR APPLICATION NUMBER: US 07/882,712  
;; PRIOR FILING DATE: 1992-05-14  
;; PRIOR APPLICATION NUMBER: US 09/531,025  
;; PRIOR FILING DATE: 2000-03-20  
;; PRIOR APPLICATION NUMBER: US 09/636,385  
;; PRIOR FILING DATE: 2000-08-09  
;; PRIOR APPLICATION NUMBER: US 09/696,347  
;; PRIOR FILING DATE: 2000-10-24  
;; PRIOR APPLICATION NUMBER: US 08/193,627  
;; PRIOR FILING DATE: 1994-02-07  
;; PRIOR APPLICATION NUMBER: US 08/433,993  
;; PRIOR FILING DATE: 1995-05-04  
;; PRIOR APPLICATION NUMBER: US 08/434,504  
;; PRIOR FILING DATE: 1995-05-04  
;; PRIOR APPLICATION NUMBER: US 09/436,430  
;; PRIOR FILING DATE: 1999-11-08  
;; NUMBER OF SEQ ID NOS: 6586

```
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3997
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-877-478-3997

Query Match          67.5%; Score 16.2; DB 3; Length 37;
Best Local Similarity 76.2%; Pred. No. 8.3e+02;
Matches 16; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GCGGAGTGATGCGCAGCAGCA 23
Db 3 GCCGAGUGAUGGCAUGCACUA 23

RESULT 23
US-10-342-902-3997
; Sequence 3997, Application US/10342902
; Publication No. US20040054156A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, Jaim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: 400/075 (MBHB00-845-I)
; CURRENT APPLICATION NUMBER: US/10/342,902
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 09/877,478
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6592
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3997
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-342-902-3997

Query Match          67.5%; Score 16.2; DB 7; Length 37;
Best Local Similarity 76.2%; Pred. No. 8.3e+02;
Matches 16; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GCGGAGTGATGCGCAGCAGCA 23
Db 3 GCCGAGUGAUGGCAUGCACUA 23

RESULT 24
US-10-669-841-8888
; Sequence 8888, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
```

```
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP
; TITLE OF INVENTION: VIRUS REPLICATION
; FILE REFERENCE: 400/042US (MBHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8888
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-669-841-8888

Query Match          67.5%; Score 16.2; DB 7; Length 37;
Best Local Similarity 76.2%; Pred. No. 8.3e+02;
Matches 16; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GCGGAGTGATGCGCAGCAGCA 23
Db 3 GCCGAGUGAUGGCAUGCACUA 23

RESULT 25
US-10-182-049-35/c
; Sequence 35, Application US/10182049
; Publication No. US20050113322A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF INDUCIBLE NITRIC OXIDE SYNTHASE EXPRES
; FILE REFERENCE: RTSP-0360
; CURRENT APPLICATION NUMBER: US/10/182,049
; CURRENT FILING DATE: 2002-07-27
; PRIOR APPLICATION NUMBER: 09/490,208
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 35
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
```

US-10-182-049-35

Query Match 66.7%; Score 16; DB 9; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGATGGCAAGCAGC 24  
|||:|||||:|||||  
DB 18 TGATGGCAAGCAGC 3

RESULT 26

US-10-719-956-607979/c

; Sequence 607979, Application US/10719956

; Publication No. US20040146910A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Rat

; FILE REFERENCE: 3527.1

; CURRENT APPLICATION NUMBER: US/10/719,956

; CURRENT FILING DATE: 2003-11-20

; PRIOR APPLICATION NUMBER: 60/427,836

; PRIOR FILING DATE: 2002 11 20

; NUMBER OF SEQ ID NOS: 699466

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 607979

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Rattus norvegicus

US-10-719-956-607979

Query Match 66.7%; Score 16; DB 7; Length 25;

Best Local Similarity 79.2%; Pred. No. 1e+03;

Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAGCGAGTGATGGCAAGCAGC 24

DB 25 CAGCAGAGTGTGGCAGTCACGTC 2  
|||:|||||:|||||

RESULT 27

US-11-036-317-435997

; Sequence 435997, Application US/11036317

; Publication No. US20050214823A1

; GENERAL INFORMATION:

; APPLICANT: Williams, Alan

; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

; FILE REFERENCE: 3654.1

; CURRENT APPLICATION NUMBER: US/11/036,317

; CURRENT FILING DATE: 2005-01-13

; PRIOR APPLICATION NUMBER: US 60/536,639

; PRIOR FILING DATE: 2004-01-13

; NUMBER OF SEQ ID NOS: 991174

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 435997

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-11-036-317-435997

Query Match 65.8%; Score 15.8; DB 10; Length 25;

Best Local Similarity 89.5%; Pred. No. 1.3e+03;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GAGTGATGGCAAGCAGC 24

DB 1 GACTGATGGCAAGCATGAC 19  
|||:|||||:|||||

RESULT 28

US-10-138-674-15256

; Sequence 15256, Application US/10138674

; Publication No. US20040077565A1

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Pavco, Pam

; APPLICANT: McSwiggen, Jim

; APPLICANT: Stinchcomb, Dan

; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

; FILE REFERENCE: MBHB00-876-N (400/049)

; CURRENT APPLICATION NUMBER: US/10/138,674

; CURRENT FILING DATE: 2002-05-03

; NUMBER OF SEQ ID NOS: 20822

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 15256

; LENGTH: 36

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

US-10-138-674-15256

Query Match 65.8%; Score 15.8; DB 7; Length 36;

Best Local Similarity 78.9%; Pred. No. 1.3e+03;

Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCAGCA 23

DB 2 GGAGUGAUGGCAUGCACUA 20  
|||:|||||:|||||

RESULT 29

US-10-138-674-15277

; Sequence 15277, Application US/10138674

; Publication No. US20040077565A1

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Pavco, Pam

; APPLICANT: McSwiggen, Jim

; APPLICANT: Stinchcomb, Dan

; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

; FILE REFERENCE: MBHB00-876-N (400/049)

; CURRENT APPLICATION NUMBER: US/10/138,674

; CURRENT FILING DATE: 2002-05-03

; NUMBER OF SEQ ID NOS: 20822

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 15277

; LENGTH: 36

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

US-10-138-674-15277

Query Match 65.8%; Score 15.8; DB 7; Length 36;

Best Local Similarity 78.9%; Pred. No. 1.3e+03;

Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCAGCA 23

DB 2 GGAGUGAUGGCAUGCACUA 20  
|||:|||||:|||||

RESULT 30

US-10-287-949A-15256

; Sequence 15256, Application US/10287949A

; Publication No. US20040102389A1

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Pavco, Pam

; APPLICANT: McSwiggen, Jim

```
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MH000-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15256
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-15256

Query Match          65.8%; Score 15.8; DB 7; Length 36;
Best Local Similarity 78.9%; Pred. No. 1.3e+03;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCACGA 23
   ||||:|||||
Db 2 GGAGUGAUGGCAUGCACUA 20

RESULT 31
US-10-287-949A-15277
; Sequence 15277, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MH000-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15277
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-15277

Query Match          65.8%; Score 15.8; DB 7; Length 36;
Best Local Similarity 78.9%; Pred. No. 1.3e+03;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCACGA 23
   ||||:|||||
Db 2 GGAGUGAUGGCAUGCACUA 20

RESULT 32
US-10-712-672-4241
; Sequence 4241, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MH000-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
```

```
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4241
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-712-672-4241

Query Match          65.8%; Score 15.8; DB 7; Length 36;
Best Local Similarity 78.9%; Pred. No. 1.3e+03;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCACGA 23
   ||||:|||||
Db 2 GGAGUGAUGGCAUGCACUA 20

RESULT 33
US-10-712-672-4246
; Sequence 4246, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MH000-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4246
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-712-672-4246

Query Match          65.8%; Score 15.8; DB 7; Length 36;
Best Local Similarity 78.9%; Pred. No. 1.3e+03;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCACGA 23
   ||||:|||||
Db 2 GGAGUGAUGGCAUGCACUA 20

RESULT 34
US-10-712-672-4375
; Sequence 4375, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
```

; FILE REFERENCE: MBH00-882-C (400/019)  
; CURRENT APPLICATION NUMBER: US/10/712,672  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: US/09/653,225  
; PRIOR FILING DATE: 2000-08-31  
; PRIOR APPLICATION NUMBER: 60/197,769  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/150,713  
; PRIOR FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 5586  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4375  
; LENGTH: 36  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-10-712-672-4375

Query Match 65.8%; Score 15.8; DB 7; Length 36;  
Best Local Similarity 78.9%; Pred. No. 1.3e+03;  
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCACGA 23  
||||:|||||  
Db 2 GGAGUGAUGGCAUGCACUA 20

RESULT 35  
US-10-712-672-4498  
; Sequence 4498, Application US/10712672  
; Publication No. US20040102413A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme  
; FILE REFERENCE: MBH00-882-C (400/019)  
; CURRENT APPLICATION NUMBER: US/10/712,672  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: US/09/653,225  
; PRIOR FILING DATE: 2000-08-31  
; PRIOR APPLICATION NUMBER: 60/197,769  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/150,713  
; PRIOR FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 5586  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4498  
; LENGTH: 36  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-10-712-672-4498

Query Match 65.8%; Score 15.8; DB 7; Length 36;  
Best Local Similarity 78.9%; Pred. No. 1.3e+03;  
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCACGA 23  
||||:|||||  
Db 2 GGAGUGAUGGCAUGCACUA 20

RESULT 36  
US-09-780-533A-4335  
; Sequence 4335, Application US/09780533A  
; Publication No. US2003006011A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry

; APPLICANT: McSwiggen, Jim  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: Haeberli, Pete  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
; FILE REFERENCE: MBH00,878-A (400/011)  
; CURRENT APPLICATION NUMBER: US/09/780,533A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,797  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 6679  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4335  
; LENGTH: 37  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-780-533A-4335

Query Match 65.8%; Score 15.8; DB 3; Length 37;  
Best Local Similarity 78.9%; Pred. No. 1.3e+03;  
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCACGA 23  
||||:|||||  
Db 5 GGAGUGAUGGCAUGCACUA 23

RESULT 37  
US-09-927-046-3492  
; Sequence 3492, Application US/09927046  
; Publication No. US20030064946A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Thompson, Jim  
; APPLICANT: McKenzie, Tim  
; APPLICANT: Ayers, Dave  
; APPLICANT: Grupe, Andrew  
; APPLICANT: Szymkowski, Edmund  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlori  
; FILE REFERENCE: 249/021  
; CURRENT APPLICATION NUMBER: US/09/927,046  
; CURRENT FILING DATE: 2001-08-09  
; NUMBER OF SEQ ID NOS: 5450  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3492  
; LENGTH: 37  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-927-046-3492

Query Match 65.8%; Score 15.8; DB 3; Length 37;  
Best Local Similarity 78.9%; Pred. No. 1.3e+03;  
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCACGA 23  
||||:|||||  
Db 5 GGAGUGAUGGCAUGCACUA 23

RESULT 38  
US-09-927-046-3526  
; Sequence 3526, Application US/09927046  
; Publication No. US20030064946A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Thompson, Jim  
; APPLICANT: McKenzie, Tim



; APPLICANT: Avers, Dave  
; APPLICANT: Grupe, Andrew  
; APPLICANT: Szymkowski, Edmund  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloride Channel-1  
; FILE REFERENCE: 249/021  
; CURRENT APPLICATION NUMBER: US/09/927,046  
; CURRENT FILING DATE: 2001-08-09  
; NUMBER OF SEQ ID NOS: 5450  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 3526  
; LENGTH: 37  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-927-046-3526

Query Match 65.8%; Score 15.8; DB 3; Length 37;  
Best Local Similarity 78.9%; Pred. No. 1.3e+03;  
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCACGA 23  
||||:|||||  
DB 5 GGAGUGAUGGCAUGCACUA 23

RESULT 39  
US-09-927-046-3549  
; Sequence 3549, Application US/09927046  
; Publication No. US20030064946A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Thompson, Jim  
; APPLICANT: McKenzie, Tim  
; APPLICANT: Avers, Dave  
; APPLICANT: Grupe, Andrew  
; APPLICANT: Szymkowski, Edmund  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloride Channel-1  
; FILE REFERENCE: 249/021  
; CURRENT APPLICATION NUMBER: US/09/927,046  
; CURRENT FILING DATE: 2001-08-09  
; NUMBER OF SEQ ID NOS: 5450  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 3549  
; LENGTH: 37  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-927-046-3549

Query Match 65.8%; Score 15.8; DB 3; Length 37;  
Best Local Similarity 78.9%; Pred. No. 1.3e+03;  
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCACGA 23  
||||:|||||  
DB 5 GGAGUGAUGGCAUGCACUA 23

RESULT 40  
US-09-776-474-1927  
; Sequence 1927, Application US/09776474  
; Publication No. US20030087847A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Jarvis, Thale  
; APPLICANT: Boher, Robert  
; APPLICANT: Holman, Patricia  
; APPLICANT: Fattaey, Ali

; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CI)  
; FILE REFERENCE: MHB00-955-A (400/008)  
; CURRENT APPLICATION NUMBER: US/09/776,474  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,983  
; NUMBER OF SEQ ID NOS: 2992  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 1927  
; LENGTH: 37  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
US-09-776-474-1927

Query Match 65.8%; Score 15.8; DB 3; Length 37;  
Best Local Similarity 78.9%; Pred. No. 1.3e+03;  
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCACGA 23  
||||:|||||  
DB 5 GGAGUGAUGGCAUGCACUA 23

Search completed: December 13, 2005, 16:17:14  
Job time : 661 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 13:14:34 ; Search time 104.5 Seconds  
(without alignments)  
408.244 Million cell updates/sec

Title: US-10-713-137-2

Perfect score: 24

Sequence: 1 cagcggagtgcgaagcagcag 24

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1299706

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*  
1: /cgn2\_6/ptodata/1/ina/1 COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5 COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/H COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/PCTUS COMB.seq.\*  
7: /cgn2\_6/ptodata/1/ina/PP COMB.seq.\*  
8: /cgn2\_6/ptodata/1/ina/RE COMB.seq.\*  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.8	65.8	36	US-09-371-772B-12979	Sequence 12979, A
2	15.8	65.8	36	US-09-371-772B-13000	Sequence 13000, A
3	15.8	65.8	36	US-09-479-005A-597	Sequence 597, App
4	15.2	63.3	36	US-09-371-772B-12711	Sequence 12711, A
5	15.2	63.3	36	US-09-371-772B-12725	Sequence 12725, A
6	15.2	63.3	36	US-09-371-772B-14177	Sequence 14177, A
7	15.2	63.3	36	US-09-371-772B-14200	Sequence 14200, A
8	15.2	63.3	36	US-09-479-005A-825	Sequence 825, App
9	15.2	63.3	36	US-09-479-005A-1014	Sequence 1014, Ap
10	15	62.5	39	US-09-430-221-27	Sequence 27, Appl
11	14.8	61.7	25	US-09-866-108A-4012	Sequence 4012, Ap
12	14.8	61.7	25	US-09-866-108A-4013	Sequence 4013, Ap
13	14.8	61.7	25	US-09-866-108A-4014	Sequence 4014, Ap
14	14.8	61.7	25	US-09-866-108A-4015	Sequence 4015, Ap
15	14.8	61.7	25	US-09-866-108A-4016	Sequence 4016, Ap
16	14.8	61.7	25	US-09-866-108A-4017	Sequence 4017, Ap
17	14.8	61.7	25	US-09-866-108A-4018	Sequence 4018, Ap
18	14.8	61.7	25	US-09-866-108A-4019	Sequence 4019, Ap
19	14.8	61.7	36	US-09-371-772B-12719	Sequence 12719, A
20	14.8	61.7	36	US-09-371-772B-12797	Sequence 12797, A
21	14.8	61.7	36	US-09-371-772B-12964	Sequence 12964, A
22	14.8	61.7	36	US-09-371-772B-13173	Sequence 13173, A
23	14.8	61.7	36	US-09-371-772B-14087	Sequence 14087, A
24	14.8	61.7	36	US-09-371-772B-14110	Sequence 14110, A

25	14.8	61.7	36	3	US-09-371-772B-14162	Sequence 14162, A
26	14.8	61.7	36	3	US-09-479-005A-665	Sequence 665, App
27	14.8	61.7	36	3	US-09-479-005A-785	Sequence 785, App
28	14.8	61.7	36	3	US-09-479-005A-938	Sequence 938, App
29	14.4	60.0	25	3	US-09-396-196G-42756	Sequence 42756, A
30	14.4	60.0	35	9	5519127-6	Patent No. 5519127
31	14.2	59.2	36	3	US-09-371-772B-12724	Sequence 12724, A
32	14.2	59.2	36	3	US-09-371-772B-12727	Sequence 12727, A
33	14.2	59.2	36	3	US-09-371-772B-12754	Sequence 12754, A
34	14.2	59.2	36	3	US-09-371-772B-12767	Sequence 12767, A
35	14.2	59.2	36	3	US-09-371-772B-12819	Sequence 12819, A
36	14.2	59.2	36	3	US-09-371-772B-12861	Sequence 12861, A
37	14.2	59.2	36	3	US-09-371-772B-12890	Sequence 12890, A
38	14.2	59.2	36	3	US-09-371-772B-12939	Sequence 12939, A
39	14.2	59.2	36	3	US-09-371-772B-12962	Sequence 12962, A
40	14.2	59.2	36	3	US-09-371-772B-12978	Sequence 12978, A
41	14.2	59.2	36	3	US-09-371-772B-12980	Sequence 12980, A
42	14.2	59.2	36	3	US-09-371-772B-13014	Sequence 13014, A
43	14.2	59.2	36	3	US-09-371-772B-13062	Sequence 13062, A
44	14.2	59.2	36	3	US-09-371-772B-13065	Sequence 13065, A
45	14.2	59.2	36	3	US-09-371-772B-13067	Sequence 13067, A

ALIGNMENTS

RESULT 1  
US-09-371-772B-12979  
; Sequence 12979, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MHB00.876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371.772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 12979  
; LENGTH: 36  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-12979

Query Match 65.8%; Score 15.8; DB 3; Length 36;  
Best Local Similarity 78.9%; Pred. No. 4.4e+02;  
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGCGAAGCAGCA 23  
|||||:|||||  
Db 2 GGAGUGAUGGCAUGCAGCA 20

RESULT 2  
US-09-371-772B-13000  
; Sequence 13000, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan

```
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13000
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-13000

Query Match          65.8%; Score 15.8; DB 3; Length 36;
Best Local Similarity 78.9%; Pred. No. 4.4e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTCATGCCAGCAGCA 23
Db 2 GGAGUGAUGGCAUGCACUA 20

RESULT 3
US-09-479-005A-597
; Sequence 597, Application US/09479005A
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
; FILE REFERENCE: MBH00-884-C
; CURRENT APPLICATION NUMBER: US/09/479,005A
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/444,209
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: US 09/159,274
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: US 60/059,473
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 597
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-479-005A-597

Query Match          65.8%; Score 15.8; DB 3; Length 36;
Best Local Similarity 78.9%; Pred. No. 4.4e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTCATGCCAGCAGCA 23
Db 2 GGAGUGAUGGCAUGCACUA 20

RESULT 4
US-09-371-772B-12711
; Sequence 12711, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
```

```
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12711
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-12711

Query Match          63.3%; Score 15.2; DB 3; Length 36;
Best Local Similarity 75.0%; Pred. No. 8.3e+02;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 CGGAGTCATGCCAAGCAGCA 23
Db 1 CUGAGUGAUGGCAUGCACUA 20

RESULT 5
US-09-371-772B-12725
; Sequence 12725, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12725
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-12725

Query Match          63.3%; Score 15.2; DB 3; Length 36;
Best Local Similarity 75.0%; Pred. No. 8.3e+02;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 CGGAGTCATGCCAAGCAGCA 23
Db 1 CUGAGUGAUGGCAUGCACUA 20

RESULT 6
US-09-371-772B-14177
; Sequence 14177, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
```

; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBH00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 14177  
; LENGTH: 36  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-14177

Query Match 63.3%; Score 15.2; DB 3; Length 36;  
Best Local Similarity 75.0%; Pred. No. 8.3e+02;  
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CGGAGTGATGGCAAGCACGA 23  
|||:|:|:|:|:|:|  
Db 1 CUGAGUGAUGGCAUGCACUA 20

RESULT 7  
US-09-371-772B-14200  
; Sequence 14200, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBH00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 14200  
; LENGTH: 36  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-14200

Query Match 63.3%; Score 15.2; DB 3; Length 36;  
Best Local Similarity 75.0%; Pred. No. 8.3e+02;  
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CGGAGTGATGGCAAGCACGA 23  
|||:|:|:|:|:|:|  
Db 1 CUGAGUGAUGGCAUGCACUA 20

RESULT 8  
US-09-479-005A-825  
; Sequence 825, Application US/09479005A

; Patent No. 6656731  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity  
; FILE REFERENCE: MBH00-884-C  
; CURRENT APPLICATION NUMBER: US/09/479,005A  
; CURRENT FILING DATE: 2000-01-07  
; PRIOR APPLICATION NUMBER: US 09/444,209  
; PRIOR FILING DATE: 1999-11-19  
; PRIOR APPLICATION NUMBER: US 09/159,274  
; PRIOR FILING DATE: 1998-09-22  
; PRIOR APPLICATION NUMBER: US 60/059,473  
; PRIOR FILING DATE: 1997-09-22  
; NUMBER OF SEQ ID NOS: 1208  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 825  
; LENGTH: 36  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-479-005A-825

Query Match 63.3%; Score 15.2; DB 3; Length 36;  
Best Local Similarity 75.0%; Pred. No. 8.3e+02;  
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CGGAGTGATGGCAAGCACGA 23  
|||:|:~|:|:|:|:|:|  
Db 1 CGUAGUGAUGGCAUGCACUA 20

RESULT 9  
US-09-479-005A-1014  
; Sequence 1014, Application US/09479005A  
; Patent No. 6656731  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity  
; FILE REFERENCE: MBH00-884-C  
; CURRENT APPLICATION NUMBER: US/09/479,005A  
; CURRENT FILING DATE: 2000-01-07  
; PRIOR APPLICATION NUMBER: US 09/444,209  
; PRIOR FILING DATE: 1999-11-19  
; PRIOR APPLICATION NUMBER: US 09/159,274  
; PRIOR FILING DATE: 1998-09-22  
; PRIOR APPLICATION NUMBER: US 60/059,473  
; PRIOR FILING DATE: 1997-09-22  
; NUMBER OF SEQ ID NOS: 1208  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1014  
; LENGTH: 36  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-479-005A-1014

Query Match 63.3%; Score 15.2; DB 3; Length 36;  
Best Local Similarity 75.0%; Pred. No. 8.3e+02;  
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CGGAGTGATGGCAAGCACGA 23  
|||:|:~|:|:|:|:|:|  
Db 1 CGGGGUGAUGGCAUGCACUA 20

RESULT 10  
US-09-430-221-27/c  
; Sequence 27, Application US/09430221  
; Patent No. 6521425  
; GENERAL INFORMATION:  
; APPLICANT: Perler, Francine B.

; APPLICANT: Adam, Eric E.  
; TITLE OF INVENTION: Screening And Use Of Reagents Which Block Or Activate  
; FILE OF INVENTION: Intein Splicing Utilizing Natural Or Homologous Extreins  
; FILE REFERENCE: PROTEIN SPLICING (FRAN/ERIC)  
; CURRENT APPLICATION NUMBER: US/09/430,221  
; CURRENT FILING DATE: 1999-10-29  
; EARLIER APPLICATION NUMBER: 08/811,492  
; EARLIER FILING DATE: 1997-03-05  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 27  
; LENGTH: 39  
; TYPE: DNA  
; ORGANISM: Streptomyces griseoruber  
US-09-430-221-27

Query Match 62.5%; Score 15; DB 3; Length 39;  
Best Local Similarity 78.3%; Pred. No. 1e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 AGCGAGTGATGGCAAGCAGC 24  
||| ||||| ||||| ||||| |||||  
Db 29 AGCCAAGCGATGCAAGCAAG 7

RESULT 11  
US-09-866-108A-4012  
; Sequence 4012, Application US/09866108A  
; Patent No. 6686188  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108A  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; SOFTWARE: Aecomica Sequence Listing Engine  
; NUMBER OF SEQ ID NOS: 15755  
; Patent No. 6686188  
; SEQ ID NO 4012  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108A-4012

Query Match 61.7%; Score 14.8; DB 3; Length 25;  
Best Local Similarity 88.9%; Pred. No. 1.2e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 5 GGAGTGATGGCAAGCAGC 22  
||||| ||||| ||||| |||||  
Db 8 GGAGTGAAGGAAGCAGC 25

RESULT 12  
US-09-866-108A-4013  
; Sequence 4013, Application US/09866108A  
; Patent No. 6686188  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108A  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; SOFTWARE: Aecomica Sequence Listing Engine  
; NUMBER OF SEQ ID NOS: 15755  
; Patent No. 6686188  
; SEQ ID NO 4013  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108A-4013

Query Match 61.7%; Score 14.8; DB 3; Length 25;  
Best Local Similarity 88.9%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCAGC 22  
||||| ||||| ||||| |||||  
Db 7 GGAGTGAAGGAAGCAGC 24

RESULT 13  
US-09-866-108A-4014  
; Sequence 4014, Application US/09866108A  
; Patent No. 6686188  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng

```
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 4014
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-4014

Query Match 61.7%; Score 14.8; DB 3; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GGAGTGATGCGAAGCAGC 22
Db 6 GGAGTGAAGCGAAGCAGC 23

RESULT 14
US-09-866-108A-4015
; Sequence 4015, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 4014
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-4014

Query Match 61.7%; Score 14.8; DB 3; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GGAGTGATGCGAAGCAGC 22
Db 6 GGAGTGAAGCGAAGCAGC 23

RESULT 15
US-09-866-108A-4016
; Sequence 4016, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 4016
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-4016

Query Match 61.7%; Score 14.8; DB 3; Length 25;
```

```
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 4015
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-4015

Query Match 61.7%; Score 14.8; DB 3; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GGAGTGATGCGAAGCAGC 22
Db 5 GGAGTGAAGCGAAGCAGC 22

RESULT 15
US-09-866-108A-4016
; Sequence 4016, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 4016
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-4016

Query Match 61.7%; Score 14.8; DB 3; Length 25;
```

Best Local Similarity 88.9%; Pred. No. 1.2e+03; Mismatches 2; Indels 0; Gaps 0;  
Matches 16; Conservative 0;  
QY 5 GGAGTGATGCGCAAGCAGC 22  
Db 4 GGAGTGAAGGGAAGCAGC 21

RESULT 16  
US-09-866-108A-4017  
; Sequence 4017, Application US/09866108A  
; Patent No. 6686188  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEWICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108A  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 15755  
; SOFTWARE: Aemica Sequence Listing Engine  
; Patent No. 6686188  
; SEQ ID NO 4017  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108A-4017

Query Match 61.7%; Score 14.8; DB 3; Length 25;  
Best Local Similarity 88.9%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 5 GGAGTGATGCGCAAGCAGC 22  
Db 3 GGAGTGAAGGGAAGCAGC 20

RESULT 17  
US-09-866-108A-4018  
; Sequence 4018, Application US/09866108A  
; Patent No. 6686188  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEWICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108A  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 15755  
; SOFTWARE: Aemica Sequence Listing Engine  
; Patent No. 6686188  
; SEQ ID NO 4018  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108A-4018

Query Match 61.7%; Score 14.8; DB 3; Length 25;  
Best Local Similarity 88.9%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 5 GGAGTGATGCGCAAGCAGC 22  
Db 2 GGAGTGAAGGGAAGCAGC 19

RESULT 18  
US-09-866-108A-4019  
; Sequence 4019, Application US/09866108A  
; Patent No. 6686188  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEWICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108A  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30



```
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6586188
; SEQ ID NO 4019
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-4019

Query Match      61.7%; Score 14.8; DB 3; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GGAGTGATGGCAAGCAG 22
Db 1 GGAGTGAAGGCAAGCAG 18

RESULT 19
US-09-371-772B-12719
; Sequence 12719, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12719
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-12719

Query Match      61.7%; Score 14.8; DB 3; Length 36;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GAGTGATGGCAAGCAG 23
Db 3 GAGUGAUGGCAUGCACUA 20

RESULT 20
US-09-371-772B-12797
; Sequence 12797, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
```

```
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; FILE REFERENCE: MHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12797
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-12797

Query Match      61.7%; Score 14.8; DB 3; Length 36;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GAGTGATGGCAAGCAG 23
Db 3 GAGUGAUGGCAUGCACUA 20

RESULT 21
US-09-371-772B-12964
; Sequence 12964, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions f
; FILE REFERENCE: MHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12964
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-12964

Query Match      61.7%; Score 14.8; DB 3; Length 36;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GAGTGATGGCAAGCAG 23
Db 3 GAGUGAUGGCAUGCACUA 20

RESULT 22
US-09-371-772B-13173
; Sequence 13173, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
```

; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBHB00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 13173  
; LENGTH: 36  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-13173

Query Match 61.7%; Score 14.8; DB 3; Length 36;  
Best Local Similarity 77.8%; Pred. No. 1.3e+03;  
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 GAGTGATGGCAAGCACGA 23  
|||:|||||  
DB 3 GAGUGAUGGCAUGCACUA 20

RESULT 23  
US-09-371-772B-14087  
; Sequence 14087, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBHB00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 14087  
; LENGTH: 36  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-14087

Query Match 61.7%; Score 14.8; DB 3; Length 36;  
Best Local Similarity 77.8%; Pred. No. 1.3e+03;  
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 GAGTGATGGCAAGCACGA 23  
|||:|||||  
DB 3 GAGUGAUGGCAUGCACUA 20

RESULT 24  
US-09-371-772B-14110

; Sequence 14110, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBHB00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 14110  
; LENGTH: 36  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-14110

Query Match 61.7%; Score 14.8; DB 3; Length 36;  
Best Local Similarity 77.8%; Pred. No. 1.3e+03;  
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 GAGTGATGGCAAGCACGA 23  
|||:|||||  
DB 3 GAGUGAUGGCAUGCACUA 20

RESULT 25  
US-09-371-772B-14162  
; Sequence 14162, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBHB00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 14162  
; LENGTH: 36  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-14162

Query Match 61.7%; Score 14.8; DB 3; Length 36;  
Best Local Similarity 77.8%; Pred. No. 1.3e+03;  
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 GAGTGATGGCAAGCACGA 23  
|||:|||||  
DB 3 GAGUGAUGGCAUGCACUA 20

```
RESULT 26
US-09-479-005A-665
; Sequence 665, Application US/09479005A
; Patent No. 6656731
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
; FILE REFERENCE: MBH00-884-C
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/479,005A
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: US 09/444,209
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: US 09/159,274
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: US 60/059,473
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 665
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-479-005A-665

Query Match 61.7%; Score 14.8; DB 3; Length 36;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GAGTGTGGCAAGCACGA 23
Db 3 GAGUGAUGGCAUGCACUA 20

RESULT 27
US-09-479-005A-785
; Sequence 785, Application US/09479005A
; Patent No. 6656731
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
; FILE REFERENCE: MBH00-884-C
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/479,005A
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: US 09/444,209
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: US 09/159,274
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: US 60/059,473
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 785
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-479-005A-785

Query Match 61.7%; Score 14.8; DB 3; Length 36;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GAGTGTGGCAAGCACGA 23
Db 3 GAGUGAUGGCAUGCACUA 20

RESULT 28
US-09-479-005A-938
; Sequence 938, Application US/09479005A
; Patent No. 6656731
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
; FILE REFERENCE: MBH00-884-C
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/479,005A
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: US 09/444,209
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: US 09/159,274
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: US 60/059,473
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 938
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-479-005A-938

Query Match 61.7%; Score 14.8; DB 3; Length 36;
Best Local Similarity 77.8%; Pred. No. 1.3e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GAGTGTGGCAAGCACGA 23
Db 3 GAGUGAUGGCAUGCACUA 20

RESULT 29
US-09-396-196G-42756/c
; Sequence 42756, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42756
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-42756

Query Match 60.0%; Score 14.4; DB 3; Length 25;
Best Local Similarity 75.0%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGTGGCAAGCACGAC 24
Db 24 CAGCAGGTGTGGCAGCCAATAC 1

RESULT 30
5519127-6/c
; Patent No. 5519127
; APPLICANT: SHAH, JYOTSNA;BUHARIN, AMELIA;LANE, DAVID J.
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE DETECTION OF
; PNEUMOCYSTIS CARINII
; NUMBER OF SEQUENCES: 57
; CURRENT APPLICATION DATA:
```

5519127-6

D<sub>b</sub> 25 CAGCGGGCTGTTGGCAACGATGAC 2

; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26

; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 12767  
; LENGTH: 36  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-12767

Query Match 59.2%; Score 14.2; DB 3; Length 36;  
Best Local Similarity 73.7%; Pred. No. 2.4e+03;  
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GGAGTGATGGCAAGCACGA 23  
|||:|||||  
Db 2 GUAGUGAUGGCAUGCACUA 20

## RESULT 35

US-09-371-772B-12819  
; Sequence 12819, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBH00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 12819  
; LENGTH: 36  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-12819

Query Match 59.2%; Score 14.2; DB 3; Length 36;  
Best Local Similarity 73.7%; Pred. No. 2.4e+03;  
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GGAGTGATGGCAAGCACGA 23  
|||:|||||  
Db 2 GGAUGAUGGCAUGCACUA 20

## RESULT 36

US-09-371-772B-12861  
; Sequence 12861, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBH00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 12861  
; LENGTH: 36  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-12861

Query Match 59.2%; Score 14.2; DB 3; Length 36;  
Best Local Similarity 73.7%; Pred. No. 2.4e+03;  
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GGAGTGATGGCAAGCACGA 23  
|||:|||||  
Db 2 GGUGUGAUGGCAUGCACUA 20

## RESULT 37

US-09-371-772B-12890  
; Sequence 12890, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions  
; FILE REFERENCE: MBH00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 12890  
; LENGTH: 36  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-12890

Query Match 59.2%; Score 14.2; DB 3; Length 36;  
Best Local Similarity 73.7%; Pred. No. 2.4e+03;  
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GGAGTGATGGCAAGCACGA 23  
|||:|||||  
Db 2 GGUGUGAUGGCAUGCACUA 20

## RESULT 38

US-09-371-772B-12939  
; Sequence 12939, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim

; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBH00.876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 12939  
; LENGTH: 36  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-12939

Query Match 59.2%; Score 14.2; DB 3; Length 36;  
Best Local Similarity 73.7%; Pred. No. 2.4e+03;  
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 GGAGTGTGGCAAGCACGA 23  
| |:|:|:|:|:|:|:|  
Db 2 GAAGUGAUGGCAUGCACUA 20

RESULT 39  
US-09-371-772B-12962  
; Sequence 12962, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBH00.876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 12962  
; LENGTH: 36  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-12962

Query Match 59.2%; Score 14.2; DB 3; Length 36;  
Best Local Similarity 73.7%; Pred. No. 2.4e+03;  
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 GGAGTGTGGCAAGCACGA 23  
| |:|:|:|:|:|:|  
Db 2 GAAGUGAUGGCAUGCACUA 20

RESULT 40  
US-09-371-772B-12978  
; Sequence 12978, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R  
; FILE REFERENCE: MBH00.876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 12978  
; LENGTH: 36  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-12978

Query Match 59.2%; Score 14.2; DB 3; Length 36;  
Best Local Similarity 73.7%; Pred. No. 2.4e+03;  
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 GGAGTGTGGCAAGCACGA 23  
| |:|:|:|:|:|:|  
Db 2 GCAGUGAUGGCAUGCACUA 20

Search completed: December 13, 2005, 15:54:59  
Job time : 105.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 12:51:49 ; Search time 2984 Seconds  
(without alignments)  
376.304 Million cell updates/sec

Title: US-10-713-137-2

Perfect score: 24

Sequence: 1 cagcgagtgatggcaagcagcagc 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 179606

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_est3: \*  
4: gb\_hic: \*  
5: gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_est7: \*  
9: gb\_gse1: \*  
10: gb\_gse2: \*  
11: gb\_gse3: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15.2	63.3	50	9	CC326423 XN495 Bay
C 2	13.6	56.7	31	8	CV933697 PMrpcm 36
C 3	13.6	56.7	49	1	AW100845 sd62b05.Y
C 4	13.4	55.8	42	1	AJ795163 AJ795163
C 5	13.2	55.0	40	6	CF331176 NACL--07-
C 6	13	54.2	40	1	AV839593 AV839593
C 7	13	54.2	46	1	A1019594 ua91a06.r
C 8	12.8	53.3	28	11	CT017058 KBRH128N1
C 9	12.8	53.3	33	9	A2776950 2M0011H04
C 10	12.8	53.3	49	9	A2840176 2M0136B09
C 11	12.8	53.3	49	11	AL981974 Danio rer
C 12	12.8	53.3	50	1	AU104990 AU104990
C 13	12.8	53.3	50	1	AU104991 AU104991
C 14	12.8	53.3	50	1	AU104992 AU104992
C 15	12.6	52.5	42	6	CA913527 PCS01597X
C 16	12.6	52.5	50	1	AU108033 AU108033
C 17	12.4	51.7	23	9	A2823791 2M0098H06
C 18	12.4	51.7	31	1	A1443308 sa30a08.x
C 19	12.4	51.7	37	2	BF347447 602020763
C 20	12.4	51.7	44	9	BH620252 1007061G0
C 21	12.2	50.8	32	3	BJ032969 BJ032969
C 22	12.2	50.8	33	10	CZ472229 d01430-3p

23	12.2	50.8	38	1	AV833104	AV833104
24	12.2	50.8	38	9	AZ773196	AZ773196 IM0584P01
25	12.2	50.8	38	10	CZ473186	CZ473186 d03124-5p
26	12.2	50.8	47	1	AJ669015	AJ669015 AJ669015
27	12.2	50.8	44	1	AV947544	AV947544 AV947544
28	12	50.0	42	9	BH863108	BH863108 SALK_0931
29	12	50.0	42	9	BH863111	BH863111 SALK_0931
30	12	50.0	42	9	BH863117	BH863117 SALK_0932
31	12	50.0	44	9	BH863151	BH863151 SALK_0932
32	12	50.0	44	9	AQ902826	AQ902826 K071087-T
33	12	50.0	47	9	CC039454	CC039454 3591.1.10
34	12	50.0	49	9	BH891758	BH891758 3526-1-19
35	12	50.0	50	10	AJ600111	AJ600111 Arabidops
36	12	50.0	50	11	CR086418	CR086418 Reverse s
37	11.8	49.2	30	10	CZ473756	CZ473756 d04146-3p
38	11.8	49.2	41	9	AZ821223	AZ821223 2M0093G24
39	11.8	49.2	41	9	AZ386728	AZ386728 IM0145C20
40	11.8	49.2	43	1	AI497819	AI497819 tm89G04.x
41	11.8	49.2	43	10	CZ481370	CZ481370 e03617-3p
42	11.8	49.2	46	9	BZ384414	BZ384414 SALK_1355
43	11.8	49.2	49	4	AK209013	AK209013 Mus muscu
44	11.8	49.2	50	1	AU103111	AU103111 AU103111
45	11.8	49.2	50	1	AU103122	AU103122 AU103122

ALIGNMENTS

RESULT 1  
CC326423/c  
LOCUS  
XN495 BayGenomics Gene Trap Library pGT2Lxf Mus musculus cDNA, mRNA  
DEFINITION  
sequence.  
ACCESSION  
CC326423  
VERSION  
CC326423.1  
KEYWORDS  
GI:30795594  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 50)  
TITLES  
BayGenomics.  
AUTHORS  
http://baygenomics.ucsf.edu/  
JOURNAL  
Unpublished (2001)  
COMMENT  
Contact: BayGenomics  
Bay Area Functional Genomics Consortium (BayGenomics)  
Email: info@baygenomics.ucsf.edu  
Sequence tag generated by 5' RACE of total RNA from gene trap ES  
cell line. ES cell lines harboring insertion mutation of target  
gene are available upon request from BayGenomics. Annotation  
information available from  
http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=  
CELL\_LINE&KEY=XN495  
Class: Gene Trap.

FEATURES

source  
1..50  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129 ola"  
/db\_xref="taxon:10090"  
/sex="Male"  
/cell\_type="Embryonic stem cell"  
/clone\_lib="BayGenomics Gene Trap Library pGT2Lxf"  
/note="Vector: pGT2Lxf"

ORIGIN

Query Match 63.3%; Score 15.2; DB 9; Length 50;  
Best Local Similarity 85.0%; Pred. No. 3e+04; 3; Indels 0; Gaps 0;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCGAGTGTGCGAAGCAGCA 23

| ||||| ||||| ||||| ||





```

PUBMED 15539471
COMMENT Contact: Schwarz-Sommer Z
Molekulare Pflanzen-genetik
MPI fuer Zuechtungs-forschung
Carl-von-Linne Weg 10, D-50829, Germany.
FEATURES
source 1. .42
/organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:4151"
/clone="018_3_07_e21"
/tissue_type="whole plant"
/clone_lib="Antirrhinum majus whole plant"

ORIGIN
Query Match 55.8%; Score 13.4; DB 1; Length 42;
Best Local Similarity 73.9%; Pred. No. 1.9e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGCGCAGCA 23
Db 40 CACCGCGTCAGGTAAGCTCGA 18

RESULT 5
CF331176/c
LOCUS
DEFINITION NACL--07-D03.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--07-D03, mRNA
sequence.
ACCESSION CF331176.1 GI:33810575
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 40)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source 1. .40
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--07-D03"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E. coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="vector: pCR4-ROPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN
Query Match 55.0%; Score 13.2; DB 6; Length 40;
Best Local Similarity 83.3%; Pred. No. 2.4e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGCGCAG 18
Db 25 CATCGGAGTGATGGAGG 8

RESULT 6
AV839593
LOCUS
DEFINITION AV839593 Nori Satoh unpublished cDNA library, young adult Ciona
intestinalis cDNA clone rciad06f24, mRNA sequence.
ACCESSION AV839593.1 GI:16783744
VERSION
KEYWORDS
SOURCE
ORGANISM
Ciona intestinalis
Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Ciona.
REFERENCE 1 (bases 1 to 40)
AUTHORS Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
TITLE Expressed genes in Ciona intestinalis
JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: sato@ascidian.zool.kyoto-u.ac.jp.
FEATURES
source 1. .40
Location/Qualifiers
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="rciad06f24"
/tissue_type="whole animal"
/dev_stage="young adult"
/clone_lib="Nori Satoh unpublished cDNA library, young
adult"

ORIGIN
Query Match 54.2%; Score 13; DB 1; Length 40;
Best Local Similarity 66.7%; Pred. No. 2.9e+05;
Matches 16; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGCGCAGCAGC 24
Db 8 CNGCGGTTCGCGGCGCANGCAG 31

RESULT 7
AI019594/c
LOCUS
DEFINITION AI019594
r1 Soares mammary gland NbMMG Mus musculus cDNA clone
IMAGE:1364818 5' Similar to SW:HPB HUMAN Q00341 HIGH DENSITY
LIPOPROTEIN BINDING PROTEIN ;, mRNA sequence.
ACCESSION AI019594.1 GI:3233930
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eumarkaria; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 46)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gaisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,N. and
Waterston,R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800

```

Class: BAC ends.	Location/Qualifiers
1. .28	/organism="Brassica rapa subsp. pekinensis"
	/mol_type="genomic DNA"
	/strain="Chiifu type 401-42"
	/cultivar="Chiifu"
	/sub_species="pekinensis"
	/db_xref="taxon:51351"
	/clone="KBrHI28N12"
	/clone_lib="KBrH, Brassica rapa HindIII BAC library
	GF-SCF-1002, Vector: pCUGISacI"
	/lab_host="E.coli DH10B"

```

/clone="KBrH128N12"
/clone lib="KBrH, Brassica rapa HindIII BAC library
GF-SCF-1002, Vector: pCUGIBac1"
/lab_host="E.coli DH10B"
ORIGIN

```

Query Match	53.3%	Score 12.8;	DB 11;	Length 28;
Best Local Similarity	70.8%	Pred. No. 3.5e+05;		
Matches 17;	Conservative	0;	Mismatches 7;	Indels 0;
Matches 17;	Conservative	0;	Mismatches 7;	Indels 0;

Qy 1 CAGCGAGTGTGGCAAGCAGAC 24  
| | | | | | | | | | | | | | | | | | | | | | | |  
Db 1 CAGCAGAGAGAGAGCAACAGGCG 24  
| | | | | | | | | | | | | | | | | | | | | | | |

RESULT 9	AZ776950	LOCUS	AZ776950	33 bp	DNA	linear	GSS 16-FEB-2001
DEFINITION	2M0011H04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0011H04 F. genomic survey sequence.						

ACCESSION	AZ776950
VERSION	AZ776950.1
KEYWORDS	GSS, GI:12905041
SOURCE	Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCES  
1. DUNN, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.

**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
**JOURNAL** Unpublished (2000)

COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 383 3606  
 Fax: 801 385 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0011 row: H column: 04  
 Seq primer: CGTTGTAACACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 33.

FEATURES	source
1	33
Location/Qualifiers	
organism="Mus musculus"	
/mol_type="genomic DNA"	
/strain="C57BL/6J"	
/db_xref="taxon:10090"	
/clone="TUGC2M0011H04"	
/sex="Male"	

```

"sex_mate"="E. Coli strain XL10-Gold, T1-resistant, F-"/
"lab_host"="E. Coli strain XL10-Gold, T1-resistant, F-"/
"clone_lib"="Mouse 10kb plasmid UUGC1M library"
"/note"="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrotynamically sheared by repeated passage through a

```

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 53.3%; Score 12.8; DB 9; Length 33;  
Best Local Similarity 87.5%; Pred. No. 3.5e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCA 20  
||||| ||||| |||||  
Db 18 GGAGTGAGGCGCAGCA 33

## RESULT 10

AZ840176/c  
LOCUS  
DEFINITION  
2M0136B09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0136B09 R, genomic survey sequence.

ACCESSION  
AZ840176  
VERSION  
A2840176.1 GI:13010084  
GSS.

SOURCE  
Mus musculus (house mouse)

ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Ielam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0136 row: B column: 09  
Seq primer: CACACGAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 49.

## FEATURES

source

Location/Qualifiers  
1. .49  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0136B09"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, P-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 53.3%; Score 12.8; DB 9; Length 49;  
Best Local Similarity 87.5%; Pred. No. 3.7e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCA 20  
||||| ||||| |||||  
Db 20 GGTGTGGTGGCAAGCA 5

## RESULT 11

DR49P1S/c  
LOCUS  
DEFINITION  
49 bp DNA linear GSS 22-NOV-2002  
Danio rerio genomic clone DKEY-49p1, genomic survey sequence.

ACCESSION  
AL981974  
VERSION  
AL981974.1 GI:25187155  
GSS.

KEYWORDS  
Danio rerio (zebrafish)

SOURCE  
Danio rerio

ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.

## REFERENCE

AUTHORS  
Humphray, S.J., Huckle, E. and Hunt, S.E.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome  
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:  
humquerry@sanger.ac.uk Unpublished  
This sequence was generated from the SP6 end of BAC 49p1. 49p1 is  
part of the Daniokey BAC Library created by R. Plasterk and N.V.  
Keygene.

Further details: [http://www.sanger.ac.uk/Projects/D\\_rerio/](http://www.sanger.ac.uk/Projects/D_rerio/).

## FEATURES

source

Location/Qualifiers  
1. .49  
/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone="DKEY-49p1"  
/tissue\_type="Testis"  
/note="Vector pindigoBAC-536"

## ORIGIN

Query Match 53.3%; Score 12.8; DB 11; Length 49;  
Best Local Similarity 87.5%; Pred. No. 3.7e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TGATGGCAAGCAGCAC 24  
||||| ||||| |||||  
Db 44 TGATGAGAGAGCAGCAC 29

## RESULT 12

AU104990  
LOCUS  
DEFINITION  
50 bp mRNA linear EST 28-JAN-2004  
AUI04990 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
HRC07124, mRNA sequence.

ACCESSION  
AU104990







source

ORIGIN

Qy  
Db

RESULT 20	ACCESSION	REFERENCE
BH620252/c	VERSION	
LOCUS	KEYWORDS	
DEFINITION	SOURCE	
	ORGANISM	

**AUTHORS**  
**TITLE**  
**JOURNAL**  
**COMMENT**

## FEATURES

```

ACCESSION      C2472229
VERSION        C2472229.1  GI:62966242
KEYWORDS
SOURCE
ORGANISM       Drosophila melanogaster (fruit fly)
               Drosophila melanogaster
               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
               Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
               Ephydroidea; Drosophilidae; Drosophila.
REFERENCE      1 (bases 1 to 33)
AUTHORS       Thibault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A.,
               Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.L.,
               Ryner,L., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.W.,
               Greer,K., Harouni,S.R., Howie,E., Jakkula,L., Joo,D., Killpack,K.,
               Laufer,A., Mazotta,J., Smith,R.D., Stevens,L.M., Stuber,C.,
               Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F.,
               Swimmer,C., Kopcynski,C., Duyk,G., Winberg,M.L. and Margolis,J.
TITLE         A complementary transposon tool kit for Drosophila melanogaster
               using P and piggyBac
JOURNAL        Nat. Genet. 36 (3), 283-287 (2004)
PUBMED        14981521
COMMENT       Contact: Roger A Hoskins
               Berkeley Drosophila Genome Project
               Lawrence Berkeley National Laboratory
               Mailstop 64-121 One Cyclotron Road, Berkeley, CA 94720, USA
               Tel: 510 486 4015
               Fax: 510 486 6798
               Email: RHoskins@lbl.gov
               Sequence recovery method was inverse PCR.
               Sequence orientation is forward strand relative to 5' end of P
               element.
               The P element insertion position is 1 in the 33 bases. This
               insertion position refers to the first base of the 8 base target
               recognition sequence.
               Class: transposon insertion site.
               Location/Qualifiers
                 1..33
                 /organism="Drosophila melanogaster"
                 /mol_type="genomic DNA"
                 /strain="isogenic w- strain"
                 /db_xref="taxon:7227"
                 /clone_lib="Exelixis P element XP insertions"
                 /notes="Vector: P element XP (GenBank accession number
                 AV515149); An isogenic w- Drosophila melanogaster strain
                 was mutagenized by remobilization of transposable
                 elements. For the P element XP, we selected an easily
                 mobilized ammunition element among inserts hopped onto the
                 Binsyncy balancer. New insertions were collected in vials
                 from dysgenic females using the standard chromosomal
                 source of transposase, delta2-3. All lines were mapped to
                 a chromosome by standard genetic methods, examined for
                 homozygous viability and used for recovery of flanking
                 genomic sequence by inverse PCR."

ORGANISM       Hordeum vulgare subsp. vulgare
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Poideae; Triticeae; Hordeum.
REFERENCE      1 (bases 1 to 38)
AUTHORS       Sato,K.
TITLE         Barley EST sequencing project in NIG and Okayama Univ
               Unpublished (2001)
JOURNAL        Research Institute for Bioresources
               Okayama University, Barley Germplasm Center
               Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
               Email: kzsato@rib.okayama-u.ac.jp,
               URL:http://www.rib.okayama-u.ac.jp/barley/
               Sato,K., Saisho,D., Takeda,K., Shini,T. and Kohara,Y. Direct
               submission;
               database:http://www.shigen.nig.ac.jp/barley/Barley.html.
               Location/Qualifiers
                 1..38
                 /organism="Hordeum vulgare subsp. vulgare"
                 /mol_type="mRNA"
                 /cultivar="Haruna Nijo"
                 /sub_species="vulgare"
                 /db_xref="taxon:112509"
                 /clone="bags11124"
                 /tissue_type="shoots"
                 /dev_stage="germination"
                 /clone_lib="K. Sato unpublished cDNA library: Hordeum
                 vulgare subsp. vulgare shoots germination"

ORIGIN
Query Match      50.8%; Score 12.2; DB 1; Length 38;
Best Local Similarity 82.4%; Pred. No. 6.8e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCGAGTGATGGCAA 17
    ||| ||||| ||||| |||
Db 14 CACGAGAGTGATGGGAA 30

RESULT 24
LOCUS      AZ773196/c
DEFINITION AZ773196 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
             clone UUGC1M0584P01 R, genomic survey sequence.
ACCESSION  AZ773196
VERSION     AZ773196.1  GI:12897306
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
             Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 38)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
             Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
             Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
             Niederhausern,A. and Wright,D., Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
             plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
             University of Utah Genome Center
             Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
             84112, USA
             Tel: 801 585 5606
             Fax: 801 585 7177
             Email: ddunn@genetics.utah.edu
             Insert Length: 10000 Std Error: 0.00
             Plate: 0584 row: P column: 01
             Seq primer: CACACGAGAAACAGCTATGACC
             Class: plasmid ends

ORGANISM       Hordeum vulgare subsp. vulgare
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Poideae; Triticeae; Hordeum.
REFERENCE      1 (bases 1 to 38)
AUTHORS       Sato,K.
TITLE         Barley EST sequencing project in NIG and Okayama Univ
               Unpublished (2001)
JOURNAL        Research Institute for Bioresources
               Okayama University, Barley Germplasm Center
               Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
               Email: kzsato@rib.okayama-u.ac.jp,
               URL:http://www.rib.okayama-u.ac.jp/barley/
               Sato,K., Saisho,D., Takeda,K., Shini,T. and Kohara,Y. Direct
               submission;
               database:http://www.shigen.nig.ac.jp/barley/Barley.html.
               Location/Qualifiers
                 1..38
                 /organism="Hordeum vulgare subsp. vulgare"
                 /mol_type="mRNA"
                 /cultivar="Haruna Nijo"
                 /sub_species="vulgare"
                 /db_xref="taxon:112509"
                 /clone="bags11124"
                 /tissue_type="shoots"
                 /dev_stage="germination"
                 /clone_lib="K. Sato unpublished cDNA library: Hordeum
                 vulgare subsp. vulgare shoots germination"

ORIGIN
Query Match      50.8%; Score 12.2; DB 1; Length 38;
Best Local Similarity 82.4%; Pred. No. 6.8e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCGAGTGATGGCAA 17
    ||| ||||| ||||| |||
Db 14 CACGAGAGTGATGGGAA 30

RESULT 24
LOCUS      AV833104
DEFINITION AV833104 K. Sato unpublished cDNA library: Hordeum vulgare subsp.
             vulgare shoots germination Hordeum vulgare subsp. vulgare cDNA
             clone bags11124, mRNA sequence.
ACCESSION  AV833104
VERSION     AV833104.1  GI:14525193
KEYWORDS    EST.
SOURCE      Hordeum vulgare subsp. vulgare

```





```

ORIGIN
Query Match      50.8%; Score 12.2; DB 1; Length 44;
Best Local Similarity 82.4%; Pred. No. 6.9e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GGAGTGATGCGCAGCAC 21
    ||||| ||||| ||||| ||
Db 7 GGAGGATGTCAGGCAC 23
    ||||| ||||| ||||| ||

RESULT 27
AV947544 47 bp mRNA linear EST 14-MAR-2002
LOCUS
DEFINITION AV947544 Nori Satoh unpublished cDNA library, young adult Ciona
intestinalis cDNA clone ciad01b12 5', mRNA sequence.
ACCESSION AV947544
VERSION AV947544.1 GI:19425303
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
REFERENCE Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
AUTHORS 1 (bases 1 to 47)
TITLE Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
JOURNAL Expressed genes in Ciona intestinalis
COMMENT Unpublished (2000)
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES
source
1..47
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="ciad01b12"
/tissue_type="whole animal"
/dev_stage="young adult"
/clone_lib="Nori Satoh unpublished cDNA library, young
adult"

ORIGIN
Query Match      50.8%; Score 12.2; DB 1; Length 47;
Best Local Similarity 82.4%; Pred. No. 7e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAGCGGATGATGCGCAA 17
    ||||| ||||| ||||| ||
Db 13 CAGCGGATGATGCTAA 29
    ||||| ||||| ||||| ||

RESULT 28
BH863108 42 bp DNA linear GSS 05-AUG-2002
LOCUS
DEFINITION SALK_093178 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_093178, genomic survey sequence.
ACCESSION BH863108
VERSION BH863108.1 GI:22098437
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 42)

, REFERENCE 1 (bases 1 to 42)

```

```

AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At2g10530.
Class: TDNA tagged.
FEATURES
Location/Qualifiers
1..42
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotye="Col-0"
/db_xref="taxon:3702"
/clone="SALK_093178"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match      50.0%; Score 12; DB 9; Length 42;
Best Local Similarity 75.0%; Pred. No. 8.5e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 GGAGTGATGCGCAGCAGCAC 24
    ||||| ||||| ||||| ||
Db 15 GGAGTGATTTCAAAACTAC 34
    ||||| ||||| ||||| ||

RESULT 29
BH863111 42 bp DNA linear GSS 05-AUG-2002
LOCUS
DEFINITION SALK_093187 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_093187, genomic survey sequence.
ACCESSION BH863111
VERSION BH863111.1 GI:22098440
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 42)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At2g10530.
Class: TDNA tagged.
FEATURES
Location/Qualifiers
1..42

```

/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/ecotype="Col-0"  
/db\_xref="taxon:3702"  
/clone\_lib="SALK\_093197"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

## ORIGIN

Query Match 50.0%; Score 12; DB 9; Length 42;  
Best Local Similarity 75.0%; Pred. No. 8.5e+05;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 GGAGTGATGGCAAGCAGC 24  
||||| ||| |||  
Db 15 GGAGTGATTTCAAAACTAC 34

RESULT 30  
BH863117  
LOCUS  
DEFINITION SALK\_093195 Arabidopsis thaliana TDNA insertion lines Arabidopsis  
thaliana genomic clone SALK\_093195, genomic survey sequence.

ACCESSION BH863117  
VERSION BH863117.1 GI:22098446  
KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

## ORGANISM

Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 42)

## AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
Shinn,P., Zimmerman,J. and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

## JOURNAL

Comment: Unpublished (2001)  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGnAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of  
TDNA. This sequence lies within an annotated exon of At2g10530.  
Class: TDNA tagged.

## FEATURES

Location/Qualifiers

1..42  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/ecotype="Col-0"  
/db\_xref="taxon:3702"  
/clone\_lib="SALK\_093195"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

## ORIGIN

Query Match 50.0%; Score 12; DB 9; Length 42;  
Best Local Similarity 75.0%; Pred. No. 8.5e+05;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 GGAGTGATGGCAAGCAGC 24  
||||| ||| |||  
Db 15 GGAGTGATTTCAAAACTAC 34

## RESULT 31

BH863151

## LOCUS

DEFINITION BH863151 42 bp DNA linear GSS 05-AUG-2002  
SALK\_093283 Arabidopsis thaliana TDNA insertion lines Arabidopsis  
thaliana genomic clone SALK\_093283, genomic survey sequence.

## ACCESSION

BH863151

## VERSION

BH863151.1 GI:22098480

## KEYWORDS

GSS.

## SOURCE

Arabidopsis thaliana (thale cress)

## ORGANISM

Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 42)

## AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
Shinn,P., Zimmerman,J. and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

## JOURNAL

Comment: Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGnAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within an annotated exon of At2g10530.

Class: TDNA tagged.

Location/Qualifiers

1..42

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/ecotype="Col-0"

/db\_xref="taxon:3702"

/clone\_lib="SALK\_093283"

/clone\_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

## ORIGIN

Query Match 50.0%; Score 12; DB 9; Length 42;  
Best Local Similarity 75.0%; Pred. No. 8.5e+05;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 GGAGTGATGGCAAGCAGC 24

||||| ||| |||

Db 15 GGAGTGATTTCAAAACTAC 34

## RESULT 32

AQ902826/c

## LOCUS

DEFINITION AQ902826 44 bp DNA linear GSS 06-NOV-2000  
K071087-T7 Library RP11.3-5 Human PAC Homo sapiens genomic clone  
RPC1P704K071087, genomic survey sequence.

## ACCESSION

AQ902826

## VERSION

AQ902826.1 GI:7673877

## KEYWORDS

GSS.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

```

REFERENCE
AUTHORS      1 (bases 1 to 44)
TITLE        Alexander, C., Bernstein, S.L., Rocchi, M. and Auburger, G.
JOURNAL      Saturating Density of STRs (1/6 kb) in a 1.1 Mb Region on 3q28-q29:
COMMENT      A Valuable Resource for Cloning of Disease Genes
              Unpublished (2000)
              Contact: Alexander C
              Department of Molecular Genetics
              Institute of Ophthalmology, University College London
              11-43 Bath Street, London EC1V9EL, UK
              Tel: +44 171 608 6839
              Fax: +44 171 608 6863
              Email: calexand@hmp.mrc.ac.uk
              Seq primer: 'nested' T7-Primer cggtcgagcttgacattgtag
              Class: PAC end

FEATURES
source
1..44
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="RPCIP704K071087"
/clone_lib="Library RPC11,3-5 Human PAC"
/note="Human genomic PAC library RPC1 (Ioannou et al.,
1994)"

ORIGIN
Query Match      50.0%; Score 12; DB 9; Length 44;
Best Local Similarity 75.0%; Pred. No. 8.5e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3 GCGGAGTGATGGCAAGCACG 22
      ||||| ||||| ||||| |||||
Db      23 GCGGTCTGTGGGAGCAATG 4

RESULT 33
CC039454/c
LOCUS      3591_1_104_1_E12.1EL_x_2 3591 - RescueMu Grid P Zea mays genomic,
DEFINITION      genomic survey sequence.
ACCESSION      CC039454
VERSION        CC039454.1 GI:29454345
KEYWORDS      GSS.
SOURCE        Zea mays
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
              clade; Panicoideae; Andropogoneae; Zea.
              1 (bases 1 to 47)
              Walbot, V.
              Maize genomic sequences found using engineered RescueMu transposon
              Unpublished (2001)
              Contact: Walbot V
              Department of Biological Sciences
              Stanford University
              855 California Ave, Palo Alto, CA 94304, USA
              Tel: 650 723 2227
              Fax: 650 725 8221
              Email: walbot@stanford.edu
              Possible ligation site of ends cut by single endonuclease.
              Reverse complemented post-ligation sequence from source sequence.
              Plate: 3591_1_104_1 row: 17
              Class: transposon-tagged.
              Location/Qualifiers
                1..47
                  /organism="Zea mays"
                  /mol_type="genomic DNA"
                  /cultivar="mixed background W23/A188/B73/K55"
                  /db_xref="taxon:4577"
                  /tissue_type="leaf"
                  /dev_stage="adult"
                  /lab_host="DH10B"
                  /clone_lib="3591 - RescueMu Grid P"
                  /note="Organ: leaf; Vector: RescueMu (engineered from
                  pBlueScript backbone)"

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid P was grown at Molokai in 2002. DNA was
extracted from leaf strips, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

FEATURES
source
1..47
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="3591 - RescueMu Grid P"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid K was grown at Molokai, Hawaii in Winter
2000-2001. DNA was extracted from leaf punches, double
digested using BamHI and BglII, and ligated to form
circular plasmids. DH10B cells were transformed and then
screened on LB plates with ampicillin."

```

```

ORIGIN
Query Match      50.0%; Score 12; DB 9; Length 47;
Best Local Similarity 75.0%; Pred. No. 8.6e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 AGCGGAGTGATGGCAAGCAC 21
      ||||| ||||| ||||| |||||
Db      23 AGCGGGGGGTGGCCAGCAC 4

RESULT 34
BH891758
LOCUS      BH891758
DEFINITION      3526_1_19_1_B08.2EL_x_1 3526 - RescueMu Grid K Zea mays genomic,
              genomic survey sequence.
ACCESSION      BH891758
VERSION        BH891758.1 GI:22222805
KEYWORDS      GSS.
SOURCE        Zea mays
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
              clade; Panicoideae; Andropogoneae; Zea.
              1 (bases 1 to 49)
              Walbot, V.
              Maize genomic sequences found using engineered RescueMu transposon
              Unpublished (2001)
              Contact: Walbot V
              Department of Biological Sciences
              Stanford University
              855 California Ave, Palo Alto, CA 94304, USA
              Tel: 650 723 2227
              Fax: 650 725 8221
              Email: walbot@stanford.edu
              Possible ligation site of ends cut by 2 different endonucleases.
              Reverse complemented post-ligation sequence from source sequence.
              Plate: 3526_1_19_1 row: 29
              Class: transposon-tagged.
              Location/Qualifiers
                1..49
                  /organism="Zea mays"
                  /mol_type="genomic DNA"
                  /cultivar="mixed background W23/A188/B73"
                  /db_xref="taxon:4577"
                  /tissue_type="leaf"
                  /dev_stage="adult"
                  /lab_host="DH10B"
                  /clone_lib="3526 - RescueMu Grid K"
                  /note="Organ: leaf; Vector: RescueMu (engineered from
                  pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
                  RescueMu is a 4.9 kb, modified maize Mu transposon
                  designed to allow plasmid rescue from total genomic DNA.
                  Mu elements insert preferentially into transcription
                  units. For more information on RescueMu, go to the web
                  site 'www.zmdb.iastate.edu' and follow the links for
                  'RescueMu.' Grid K was grown at Molokai, Hawaii in Winter
                  2000-2001. DNA was extracted from leaf punches, double
                  digested using BamHI and BglII, and ligated to form
                  circular plasmids. DH10B cells were transformed and then
                  screened on LB plates with ampicillin."

ORIGIN

```

```

Query Match          50.0%; Score 12; DB 9; Length 49;
Best Local Similarity 75.0%; Pred. No. 8.7e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AGCGGAGTGATGGCAAGCAC 21
Db 26 AGCGGAGAGAGCTAGGCC 45

RESULT 35
AJ600111
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence, right border, clone
500C09 genomic survey sequence.
ACCESSION
AJ600111.1 GI:37949739
VERSION
AJ600111.1
KEYWORDS
GSS; right border; T-DNA flanking sequence.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1
REFERENCE
AUTHORS
Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F.,
Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
Lepiniec, L., Caboche, M., and Lecharny, A.
TITLE
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
JOURNAL
EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED
12446565
REFERENCE
2 (bases 1 to 50)
AUTHORS
Balzergue, S.
TITLE
Direct Submission
COMMENT
Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
FEATURES
Location/Qualifiers
source
1..50
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="500C09"
/ecotype="Wassilewskija"
misc_feature
1..50
/note="T-DNA flanking sequence
right border"
ORIGIN
Query Match          50.0%; Score 12; DB 10; Length 50;
Best Local Similarity 75.0%; Pred. No. 8.7e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCA 20
Db 18 CAACGGAGTGATGATAGGAA 37

RESULT 36
CR086418
LOCUS
DEFINITION
Reverse strand read from insert in 3'HPRT insertion targeting and

```

```

chromosome engineering clone MHPp182e10, genomic survey sequence.
CR086418
VERSION
GI:49820010
KEYWORDS
GSS; genome survey sequence; MICER.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1
(bases 1 to 50)
REFERENCE
AUTHORS
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,
Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,
Rogers, J. and Bradley, A.
TITLE
Direct Submission
JOURNAL
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICER
FEATURES
Location/Qualifiers
source
1..50
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPp182e10"
/clone_lib="MHPP"
ORIGIN
Query Match          50.0%; Score 12; DB 11; Length 50;
Best Local Similarity 75.0%; Pred. No. 8.7e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 GGAGTGATGGCAAGCACGAC 24
Db 32 GGATTAAGGATGCACAC 13

RESULT 37
CZ473756/c
LOCUS
DEFINITION
d04146-3prime Exelixis P element XP insertions Drosophila
melanogaster genomic sequence recovered from 3' end of P element,
genomic survey sequence.
ACCESSION
CZ473756
VERSION
CZ473756.1 GI:62967769
KEYWORDS
GSS.
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1
(bases 1 to 30)
REFERENCE
AUTHORS
Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A.,
Singh, C.M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H.L.,
Ryner, L., Cheung, L.M., Chong, A., Erickson, C., Fisher, W.W.,
Greer, K., Hartzouni, S.R., Howie, E., Jakkula, L., Joo, D., Killpack, K.,
Lauffer, A., Mazzotta, J., Smith, R.D., Stevens, L.M., Stuber, C.,
Tan, L.R., Ventura, R., Woo, A., Zakrajsek, I., Zhao, L., Chen, F.,
Swimmer, C., Koczynski, C., Duyk, G., Winberg, M.L. and Margolis, J.
TITLE
A complementary transposon tool kit for Drosophila melanogaster
using P and piggyBac
JOURNAL
Nat. Genet. 36 (3), 283-287 (2004)
PUBMED
14981521
COMMENT
Contact: Roger A Hoskins
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
Email: RHoskins@lbl.gov
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of P
element.
The P element insertion position is 1 in the 30 bases. This
insertion position refers to the first base of the 8 base target
recognition sequence.

```

Class: transposon insertion site.  
Location/Qualifiers  
1. .30  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/strain="isogenic w- strain"  
/db\_xref="taxon:7227"  
/clone\_lib="Exelixis 7227"  
/note="Vector: P element XP (GenBank accession number AY15149); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. For the P element XP, we selected an easily mobilized amminution element among inserts hopped onto the Binsinsky balancer. New insertions were collected in vials from dysgenic females using the standard chromosomal source of transposase, delta2-3. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability and used for recovery of flanking genomic sequence by inverse PCR."

ORIGIN

Query Match 49.2%; Score 11.8; DB 10; Length 30;  
Best Local Similarity 86.7%; Pred. No. 1e+06;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGCC 15  
||| ||||| ||||| |||||  
DB 21 CACCGGAGTGAGGC 7

RESULT 38  
AZ821223/c 40 bp DNA linear GSS 20-FEB-2001  
LOCUS  
DEFINITION  
2M0093G24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0093G24 R, genomic survey sequence.  
AZ821223  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 40)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
JOURNAL  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0093 row: G column: 24  
Seq primer: CACACAGGAACAGCATGACC  
Class: plasmid ends  
High quality sequence stop: 40.  
Location/Qualifiers  
1. .40  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0093G24"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"

Class: transposon insertion site.  
Location/Qualifiers  
1. .30  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/strain="isogenic w- strain"  
/db\_xref="taxon:7227"  
/clone\_lib="Exelixis 7227"  
/note="Vector: P element XP (GenBank accession number AY15149); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. For the P element XP, we selected an easily mobilized amminution element among inserts hopped onto the Binsinsky balancer. New insertions were collected in vials from dysgenic females using the standard chromosomal source of transposase, delta2-3. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability and used for recovery of flanking genomic sequence by inverse PCR."

ORIGIN

Query Match 49.2%; Score 11.8; DB 9; Length 40;  
Best Local Similarity 69.6%; Pred. No. 1e+06;  
Matches 16; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGCCAAGCACGA 23  
||| ||||| ||||| ||||| |||||  
DB 23 CAGTGGAGTTTGAGCATGCATGA 1

RESULT 39  
AZ386728/c 41 bp DNA linear GSS 02-OCT-2000  
LOCUS  
DEFINITION  
1M0145C20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0145C20 R, genomic survey sequence.  
AZ386728  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 41)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
JOURNAL  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0145 row: C column: 20  
Seq primer: CACACAGGAACAGCATGACC  
Class: plasmid ends  
High quality sequence stop: 41.  
Location/Qualifiers  
1. .41  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0145C20"  
/sex="Male"

/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

ORIGIN

Query Match 49.2%; Score 11.8; DB 9; Length 41;  
Best Local Similarity 69.6%; Pred. No. 1e+06;  
Matches 16; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGGCAAGCAGCA 23  
Db 35 CTGCAGCAAGATGGCAAGACCA 13

RESULT 40

AI497819/c

LOCUS

DEFINITION

AI497819 tm89g04.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2165334 3'  
similar to SW:WASP MOUSE P70315 WISKOTT-ALDRICH SYNDROME PROTEIN  
HOMOLOG ; mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AI497819.1 GI:4389801  
EST.  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

1 (bases 1 to 43)  
NCI/NIHNS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute / National Institute of Neurological  
Disorders and Stroke, Brain Tumor Genome Anatomy Project  
(CGAP/BTGA), Tumor Gene Index

JOURNAL

COMMENT

Unpublished (1998)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 1418 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1..43

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

FEATURES

source

/clone="IMAGE:2165334"  
/tissue\_type="anaplastic oligodendroglioma"  
/lab host="DH10B"  
/clone lib="NCI CGAP Brn25"  
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a  
modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTACAATCTGAGTGGAGCGCCGATAGGTTTTTTTTTTTTTTTTTTT  
T 3']; double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified pT7T3 vector.  
Library is normalized, and was constructed by Bento  
Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 49.2%; Score 11.8; DB 1; Length 43;  
Best Local Similarity 69.6%; Pred. No. 1e+06;  
Matches 16; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 AGCGGAGTGATGGCAAGCAGCAG 24  
Db 32 AGAGGCTCGGCGCAAGCAAGAC 10

Search completed: December 13, 2005, 15:51:21  
Job time : 2988 secs

**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 11:03:03 ; Search time 368.5 Seconds  
(without alignments)  
434.064 Million cell updates/sec

Title: US-10-713-137-2

Perfect score: 24

Sequence: 1 cagcgagtgatggaagcagcagc 24

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 4879314

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq 21:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1980s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004as:\*
- 13: Geneseqn2004bs:\*
- 14: Geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	14	ADZ75765 Human ind
2	18.2	75.8	37	4	ABK05395 Human NOG
3	17.2	71.7	37	4	Aah96727 Human Chk
4	17.2	71.7	37	5	ADV17621 Human PLN
5	16.8	70.0	36	5	ADU94766 Human TER
6	16.6	69.2	37	4	ABK05358 Human NOG
7	16.6	69.2	37	5	ADV47962 HBV G-cle
8	16.6	69.2	37	5	ADV04075 Human BAC
9	16.6	69.2	37	5	ADV04149 Human BAC
10	16.6	69.2	37	5	ADV04093 Human BAC
11	16.6	69.2	37	5	ADV17630 Human PLN
12	16.6	69.2	37	5	ADV04128 Human BAC
13	16.6	69.2	37	6	ABK59131 Human CLC
14	16.6	69.2	37	8	ACD53318 HBV G-cle
15	16.6	69.2	37	12	ADM61879 Hepatitis
16	16.4	68.3	45	10	ADC33588 Human loc
17	16.2	67.5	32	3	AAD00496 Clone cgm
18	16.2	67.5	37	4	ABK05366 Human NOG
19	16.2	67.5	37	5	ADV47946 HBV G-cle

20	16.2	67.5	37	6	ABK20721	Abk20721 Human ERG
21	16.2	67.5	37	8	ACD53251	ACD53251 HBV G-cle
22	16.2	67.5	37	12	ADM61863	ADM61863 Hepatitis
23	16	66.7	18	4	AH47991	Aah47991 Human ind
24	15.8	65.8	36	5	ADU85578	Adu85578 Anti huma
25	15.8	65.8	36	5	ADU94721	Adu94721 Human TER
26	15.8	65.8	36	5	ADU94968	Adu94968 Human TER
27	15.8	65.8	36	5	ADU94463	Adu94463 Human TER
28	15.8	65.8	36	5	ADM90363	Adm90363 Human PTP
29	15.8	65.8	36	5	ADU85545	Adu85545 Human Met
30	15.8	65.8	36	5	ADM90361	Adm90361 Human PTP
31	15.8	65.8	36	5	ADU94468	Adu94468 Human TER
32	15.8	65.8	37	4	AH96713	Aah96713 Human Chk
33	15.8	65.8	37	4	ABK05427	Abk05427 Human NOG
34	15.8	65.8	37	4	ABK08475	Abk08475 Human CD2
35	15.8	65.8	37	6	ABK59121	Abk59121 Human CLC
36	15.8	65.8	37	6	ABK59178	Abk59178 Human CLC
37	15.8	65.8	37	6	ABK59155	Abk59155 Human CLC
38	15.6	65.0	37	4	ABK05394	Abk05394 Human NOG
39	15.6	65.0	37	4	ABK05401	Abk05401 Human NOG
40	15.6	65.0	37	4	ABK05385	Abk05385 Human NOG
41	15.6	65.0	37	5	ADV04196	Adv04196 Human BAC
42	15.6	65.0	37	5	ADV48009	Adv48009 HBV G-cle
43	15.6	65.0	37	8	ACD53331	ACD53331 HBV G-cle
44	15.6	65.0	37	12	ADM61892	Adm61892 Hepatitis
45	15.2	63.3	36	5	ADM90417	Adm90417 Human PTP

## ALIGNMENTS

RESULT 1

ADZ75765

ID ADZ75765 standard; DNA; 24 BP.

XX AC ADZ75765;

XX XX

XX 28-JUL-2005 (first entry)

XX DE Human inducible nitric oxide synthase gene exon 7 forward PCR primer.

XX KW ss; PCR; high altitude pulmonary edema; pulmonary edema;

XX KW respiratory-gen.; respiratory disease; SNP detection; allelic variation;

XX KW primer; exon.

XX OS Homo sapiens.

XX XX US2005106573-A1.

XX XX 19-MAY-2005.

XX PD

XX PF 13-NOV-2003; 2003US-00713137.

XX XX 13-NOV-2003; 2003US-00713137.

XX PR

XX XX (COUN-) COUNCIL SCI & IND RES INDIA.

XX XX Pasha AQM, Ahsan A;

XX XX WPI; 2005-384299/39.

XX PT Detecting predisposition to high altitude pulmonary edema (HAPE) by

XX PT amplifying intron 7 of human inducible nitric oxide synthase gene, and

XX PT predicting and analyzing differences in the distribution of allelic

XX PS Claim 6; SEQ ID NO 2; 13pp; English.

XX CC The invention relates to a novel method for detecting predisposition to

XX CC high altitude pulmonary edema (HAPE). The method comprises amplifying

XX CC intron 7 of the human inducible nitric oxide synthase (iNOS) gene

XX CC (ADZ75764) by designing and synthesizing forward and reverse

XX CC oligonucleotide primers (ADZ75765+ADZ75766), and predicting and

CC statistically analyzing differences in the distribution of the allelic  
 CC variants in the populations, where GG genotype at 19480 position are at  
 CC low risk of HAPE, and AA genotype at 19480 position are at high risk of  
 CC HAPE. The present sequence represents the forward oligonucleotide primer  
 CC of the invention.

XX Sequence 24 BP; 7 A; 6 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 14; Length 24;

Best Local Similarity 100.0%; Pred. No. 0.18;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCGAGTGATGGCAAGCAGAC 24

Db 1 CAGCGAGTGATGGCAAGCAGAC 24

RESULT 2

ABK05395

ID ABK05395 standard; RNA; 37 BP.

XX AC ABK05395;

XX DT 12-MAR-2002 (first entry)

XX DE Human NOGO G-Cleaver substrate sequence #58.

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;  
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;  
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
 KW DNzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;  
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
 KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;  
 KW inflammatory arthropathy; central nervous system injury;  
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
 KW Parkinson's disease; ataxia; Huntington's disease; substrate sequence;  
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

OS Homo sapiens.

OS Synthetic.

PN WO200159103-A2.

XX PD 16-AUG-2001.

XX PF 09-FEB-2001; 2001WO-US004273.

XX PR 11-FEB-2000; 2000US-0181797P.

PR 28-FEB-2000; 2000US-0185516P.

PR 06-MAR-2000; 2000US-0187128P.

XX PA (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (CHOW/) CHOWRIRA B M.

XX PI Blatt L, Mcswiggen J, Chowrira BM;

XX WPI; 2001-607195/69.

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
 PT constructs, which down regulate expression of a CD20 gene or neurite  
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
 PT central nervous system injury.

XX Claim 89; Page 92; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates  
 CC expression of a CD20 gene and a nucleic acid molecule which down  
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The  
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a

CC DNzyme) an inozyme (an endolytic nucleic acid cleaving a an RNA molecule  
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr  
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA  
 CC with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA  
 CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
 CC the cell and treat a patient having a condition associated with the level  
 CC of CD20. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the CD20 targetting nucleic acid may be used to  
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-  
 CC targetting nucleic acid is used to cleave RNA of the NOGO gene in the  
 CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the  
 CC cell and treat a patient having a condition associated with the level of  
 CC NOGO. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the NOGO-targetting nucleic acid may be used to  
 CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NOGO expression. The present  
 CC sequence is a substrate sequence for a nucleic acid of the invention  
 CC based on the human NOGO sequence

XX Sequence 37 BP; 10 A; 8 C; 12 G; 0 T; 7 U; 0 Other;

Query Match 75.8%; Score 18.2; DB 4; Length 37;

Best Local Similarity 78.3%; Pred. No. 1.1e+02;

Matches 18; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCGAGTGATGGCAAGCAGCA 23

Db 1 CAGAGGAGUGAUGCAUGCACUA 23

RESULT 3

AAH96727

ID AAH96727 standard; RNA; 37 BP.

XX AC AAH96727;

XX DT 09-OCT-2001 (first entry)

XX DE Human Chk1 ribozyme SEQ ID NO: 2152.

XX Human; checkpoint kinase-1; Chk1; antisense; ribozyme; gene therapy;

KW RNA cleavage; cancer; ss.

XX OS Homo sapiens.

XX WO200157206-A2.

XX PD 09-AUG-2001.

XX PF 02-FEB-2001; 2001WO-US003504.

XX PR 03-FEB-2000; 2000US-0179983P.

XX PA (RIBO-) RIBOZYME PHARM INC.

PA (FATT/) FATTAEY A R.

XX PI Fattaey AR, Jarvis T, Mcswiggen J, Booher RN, Holman PS;

XX WPI; 2001-496922/54.

DR Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid

XX molecules, which downregulates expression of a checkpoint kinase-1 gene,  
 PT useful for treating colorectal, lung, breast or prostate cancers.

XX Claim 5; Page 68; 115pp; English.

XX The present invention provides nucleic acid molecules capable of

CC downregulating the expression of the human checkpoint kinase-1 (Chk1)

CC gene. These may be antisense or ribozyme sequences, and are useful in the

CC treatment of diseases associated with conditions affected by Chk1 levels,

CC including cancer. The present sequence is an oligonucleotide described in

CC the exemplification of the invention

XX Sequence 37 BP; 11 A; 6 C; 13 G; 0 T; 7 U; 0 Other;

SQ

Query Match 71.7%; Score 17.2; DB 4; Length 37;

Best Local Similarity 77.3%; Pred. No. 3.1e+02;

Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGCGAGTGTGTCGACGACGCA 23

DB 2 AGAGGAGUGGCAUGGACGACUA 23

RESULT 4

ADVI7621

ID ADVI7621 standard; RNA; 37 BP.

XX

AC ADVI7621;

XX

XX 10-FEB-2005 (first entry)

XX

XX Human PLN G-cleaver ribozyme sequence #9.

XX

XX Enzymatic nucleic acid molecule; gene expression; down regulation;

KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;

KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;

KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;

KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;

KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;

KW amberyne; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;

KW diabetes; obesity; cardiac disease; heart disease; age-related disease;

KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;

ss.

XX Homo sapiens.

XX

XX WO200116312-A2.

XX

XX 08-MAR-2001.

XX

XX 30-AUG-2000; 2000WO-US023998.

XX

XX 31-AUG-1999; 99US-0151713P.

XX 27-SEP-1999; 99US-00406643.

XX 27-SEP-1999; 99US-0156236P.

XX 27-SEP-1999; 99US-0156467P.

XX 08-NOV-1999; 99US-00436430.

XX 06-DEC-1999; 99US-0169100P.

XX 29-DEC-1999; 99US-00474432.

XX 29-DEC-1999; 99US-0173612P.

XX 30-DEC-1999; 99US-00476387.

XX 04-FEB-2000; 2000US-00498824.

XX 20-MAR-2000; 2000US-00531025.

XX 14-APR-2000; 2000US-0197769P.

XX 23-MAY-2000; 2000US-00578223.

XX 09-AUG-2000; 2000US-00636385.

XX (RIBO-) RIBOZYME PHARM INC.

XX

XX Mcawiggen J, Usman N, Blatt L, Beigelman L, Burgin A;

PI Karpeisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;

PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;

XX

XX WPT; 2001-244406/25.

XX

PT Enzymatic nucleic acid molecules able to cleave separate RNA molecules

PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,

PT obesity and heart disease.

XX Example 5; Page 428; 717pp; English.

XX

XX The present invention relates to the use of enzymatic nucleic acid

CC molecules (e.g. ribozymes) to modulate gene expression. The invention

CC also methods for their use to down regulate or inhibit the expression of

CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine

CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C

CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor

CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),

CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic

CC nucleic acid molecules used to inhibit the expression of the said genes

CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberyne,

CC zinzyme, and/or DNazyme motifs. The methods of the invention are useful

CC for treating cancer, in particular breast cancer, Alzheimer's disease,

CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related

CC diseases, hepatitis B infections, and hepatitis and hepatocellular

CC carcinoma. The enzymatic nucleic acid molecules can also be used as

CC diagnostic tools to examine genetic drift and mutations within diseased

CC cells and to detect the presence of specific RNA in a cell. The present

CC sequence represents a ribozyme used in the examples of the present

CC invention. Note: Some SEQ ID Nos are repeated more than once in the

CC specification, but these have different sequences associated with them.

XX

XX Sequence 37 BP; 8 A; 6 C; 15 G; 0 T; 8 U; 0 Other;

SQ

Query Match 71.7%; Score 17.2; DB 5; Length 37;

Best Local Similarity 77.3%; Pred. No. 3.1e+02;

Matches 17; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGCGAGTGTGTCGACGACGCA 23

DB 2 AGCUGAGUGGCAUGGACGACUA 23

RESULT 5

ADU94766

ID ADU94766 standard; RNA; 36 BP.

XX

XX ADU94766;

XX

XX 10-FEB-2005 (first entry)

XX

XX Human TERT G-cleaver ribozyme sequence #157.

XX

XX Enzymatic nucleic acid molecule; gene expression; down regulation;

KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;

KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;

KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;

KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;

KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;

KW amberyne; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;

KW diabetes; obesity; cardiac disease; heart disease; age-related disease;

KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;

ss.

XX Homo sapiens.

XX

XX WO200116312-A2.

XX

XX 08-MAR-2001.

XX

XX 30-AUG-2000; 2000WO-US023998.

XX

XX 31-AUG-1999; 99US-0151713P.

XX 27-SEP-1999; 99US-00406643.

XX 27-SEP-1999; 99US-0156236P.

XX 27-SEP-1999; 99US-0156467P.

XX 08-NOV-1999; 99US-00436430.

XX 06-DEC-1999; 99US-0169100P.

XX 29-DEC-1999; 99US-00474432.

XX 29-DEC-1999; 99US-0173612P.

XX 30-DEC-1999; 99US-00476387.

XX 04-FEB-2000; 2000US-00498824.

XX 20-MAR-2000; 2000US-00531025.

XX 14-APR-2000; 2000US-0197769P.

XX 23-MAY-2000; 2000US-00578223.

XX 09-AUG-2000; 2000US-00636385.

XX (RIBO-) RIBOZYME PHARM INC.

XX

XX Mcawiggen J, Usman N, Blatt L, Beigelman L, Burgin A;

PI Karpeisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;

PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;

XX

XX WPT; 2001-244406/25.

XX

PR 29-DEC-1999; 99US-00474432.  
 PR 29-DEC-1999; 99US-0173612P.  
 PR 30-DEC-1999; 99US-00476387.  
 PR 04-FEB-2000; 2000US-00498824.  
 PR 20-MAR-2000; 2000US-00531025.  
 PR 14-APR-2000; 2000US-0197769P.  
 PR 23-MAY-2000; 2000US-00578223.  
 PR 09-AUG-2000; 2000US-00636385.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX  
 XX Mcswiggen J, Usman N, Blatt L, Beigelman L, Burgin A;  
 PI Karpeisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;  
 PI Stinchcomb D, Beaudry A, Zinnen S, Lugwig J, Sproat BS;  
 XX WPI; 2001-244406/25.  
 XX  
 XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules  
 PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,  
 PT obesity and heart disease.  
 PT  
 XX Example 1; Page 304; 717pp; English.  
 PS  
 XX The present invention relates to the use of enzymatic nucleic acid  
 CC molecules (e.g. ribozymes) to modulate gene expression. The invention  
 CC also methods for their use to down regulate or inhibit the expression of  
 CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine  
 CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C  
 CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor  
 CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),  
 CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic  
 CC nucleic acid molecules used to inhibit the expression of the said genes  
 CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,  
 CC zynzyme, and/or DNAzyme motifs. The methods of the invention are useful  
 CC for treating cancer, in particular breast cancer, Alzheimer's disease,  
 CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related  
 CC diseases, hepatitis B infections, and hepatitis and hepatocellular  
 CC carcinoma. The enzymatic nucleic acid molecules can also be used as  
 CC diagnostic tools to examine genetic drift and mutations within diseased  
 CC cells and to detect the presence of specific RNA in a cell. The present  
 CC sequence represents a ribozyme used in the examples of the present  
 CC invention. Note: Some SEQ ID Nos are repeated more than once in the  
 CC specification, but these have different sequences associated with them.  
 XX  
 SQ Sequence 36 BP; 8 A; 10 C; 12 G; 0 T; 6 U; 0 Other;  
 Query Match 70.0%; Score 16.8; DB 5; Length 36;  
 Best Local Similarity 80.0%; Pred. No. 4.8e+02;  
 Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 4 CGGAGTGATGGCAACGACA 23  
 |||||:|||||  
 Db 1 CGGAGUGAUGGCAUGACUA 20  
 RESULT 6  
 ABK05358  
 ID ABK05358 standard; RNA; 37 BP.  
 AC ABK05358;  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX  
 XX Human NOGO G-Cleaver substrate sequence #21.  
 DE  
 XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;  
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;  
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
 KW DNAzyme; inozyme; G-cleaver; amberzyme; zynzyme; lymphoma; leukaemia;  
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
 KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;  
 KW inflammatory arthropathy; central nervous system injury;  
 KW

KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
 KW Parkinson's disease; ataxia; Huntington's disease; substrate sequence;  
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
 OS Homo sapiens.  
 OS Synthetic.  
 XX WO200159103-A2.  
 XX  
 XX 16-AUG-2001.  
 PD  
 PD 09-FEB-2001; 2001WO-US004273.  
 PF  
 PF 11-FEB-2000; 2000US-0181797P.  
 XX 28-FEB-2000; 2000US-0185516P.  
 PR 06-MAR-2000; 2000US-0187128P.  
 PR  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (CHOW/) CHOWRIRA B M.  
 XX  
 XX Blatt L, Mcswiggen J, Chowrira BM;  
 PI WPI; 2001-607195/69.  
 DR  
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
 PT constructs, which down regulate expression of a CD20 gene or neurite  
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
 PT central nervous system injury.  
 XX  
 XX Claim 89; Page 92; 200pp; English.  
 PS  
 XX The invention relates to a nucleic acid molecule which down regulates  
 CC expression of a CD20 gene and a nucleic acid molecule which down  
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The  
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
 CC DNAzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule  
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or  
 CC an amberzyme (cleaving RNA with an NGN triplet), a zynzyme (cleaving RNA  
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
 CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
 CC the cell and treat a patient having a condition associated with the level  
 CC of CD20. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-  
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the  
 CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the  
 CC cell and treat a patient having a condition associated with the level of  
 CC NOGO. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to  
 CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states, which respond to the modulation of NOGO expression. The present  
 CC sequence is a substrate sequence for a nucleic acid of the invention  
 CC based on the human NOGO sequence  
 XX  
 SQ Sequence 37 BP; 5 A; 10 C; 17 G; 0 T; 5 U; 0 Other;  
 Query Match 69.2%; Score 16.6; DB 4; Length 37;  
 Best Local Similarity 73.9%; Pred. No. 6e+02;  
 Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAGCACGA 23  
 ||||| :|||:|||||  
 Db 1 CAGGGGGUGAUGGCAUGCACUA 23

RESULT 7  
 ADV47962  
 ID ADV47962 standard; RNA; 37 BP.  
 XX  
 AC ADV47962;  
 XX  
 DT 10-FEB-2005 (first entry)  
 XX  
 DE HBV G-cleaver ribozyme sequence #57.  
 XX  
 KW Enzymatic nucleic acid molecule; gene expression; down regulation;  
 KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;  
 KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
 KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;  
 KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;  
 KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;  
 KW amberyzyme; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;  
 KW diabetes; obesity; cardiac disease; heart disease; age-related disease;  
 KW hepatitis B infection; hepatocellular carcinoma; genetic drift; ss.  
 KW  
 OS Hepatitis B virus.  
 XX  
 XX WO200116312-A2.  
 XX  
 XX 08-MAR-2001.  
 XX  
 XX 30-AUG-2000; 2000WO-US023398.  
 XX  
 XX 31-AUG-1999; 99US-0151713P.  
 PR 27-SEP-1999; 99US-00406643.  
 PR 27-SEP-1999; 99US-0156236P.  
 PR 27-SEP-1999; 99US-0156467P.  
 PR 08-NOV-1999; 99US-00436430.  
 PR 06-DEC-1999; 99US-0169100P.  
 PR 29-DEC-1999; 99US-00474432.  
 PR 30-DEC-1999; 99US-0173612P.  
 PR 29-DEC-1999; 99US-00476387.  
 PR 30-DEC-1999; 99US-00498824.  
 PR 04-FEB-2000; 2000US-00498824.  
 PR 20-MAR-2000; 2000US-00531025.  
 PR 14-APR-2000; 2000US-0197769P.  
 PR 23-MAY-2000; 2000US-00578223.  
 PR 09-AUG-2000; 2000US-00636385.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX  
 XX Mcswiggen J, Ueman N, Blatt L, Beigelman L, Burgin A;  
 PI Karpeisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;  
 PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;  
 XX  
 DR WPI; 2001-244406/25.  
 XX  
 XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules  
 XX are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,  
 XX obesity and heart disease.  
 XX  
 XX Example 6; Page 531; 717pp; English.  
 XX  
 XX The present invention relates to the use of enzymatic nucleic acid  
 XX molecules (e.g. ribozymes) to modulate gene expression. The invention  
 XX also methods for their use to down regulate or inhibit the expression of  
 XX genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine  
 XX aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C  
 XX alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor  
 XX receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),  
 XX presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic  
 XX nucleic acid molecules used to inhibit the expression of the said genes  
 XX include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberyzyme,  
 XX zinzyme, and/or DNazyme motifs. The methods of the invention are useful

CC for treating cancer, in particular breast cancer, Alzheimer's disease,  
 CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related  
 CC diseases, hepatitis B infections, and hepatitis and hepatocellular  
 CC carcinoma. The enzymatic nucleic acid molecules can also be used as  
 CC diagnostic tools to examine genetic drift and mutations within diseased  
 CC cells and to detect the presence of specific RNA in a cell. The present  
 CC sequence represents a ribozyme used in the examples of the present  
 CC invention. Note: Some SEQ ID Nos are repeated more than once in the  
 CC specification, but these have different sequences associated with them.  
 XX  
 SQ Sequence 37 BP; 8 A; 10 C; 12 G; 0 T; 7 U; 0 Other;

Query Match 69.2%; Score 16.6; DB 5; Length 37;  
 Best Local Similarity 73.9%; Pred. No. 6e+02;  
 Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAGCACGA 23  
 ||||| :|||:|||||  
 Db 1 CAGCCUAGUGAUGGCAUGCACUA 23

## RESULT 8

ADV04075  
 ID ADV04075 standard; RNA; 37 BP.  
 XX

AC ADV04075;

XX 10-FEB-2005 (first entry)

XX Human BACE G-cleaver ribozyme sequence #12.

XX Enzymatic nucleic acid molecule; gene expression; down regulation;  
 KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;  
 KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
 KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;  
 KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;  
 KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;  
 KW amberyzyme; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;  
 KW diabetes; obesity; cardiac disease; heart disease; age-related disease;  
 KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;  
 KW ss.

XX Homo sapiens.

XX WO200116312-A2.

XX 08-MAR-2001.

XX 30-AUG-2000; 2000WO-US023398.

XX 31-AUG-1999; 99US-0151713P.

PR 27-SEP-1999; 99US-00406643.

PR 27-SEP-1999; 99US-0156236P.

PR 27-SEP-1999; 99US-0156467P.

PR 08-NOV-1999; 99US-00436430.

PR 06-DEC-1999; 99US-0169100P.

PR 29-DEC-1999; 99US-00474432.

PR 30-DEC-1999; 99US-0173612P.

PR 30-DEC-1999; 99US-00476387.

PR 04-FEB-2000; 2000US-00498824.

PR 20-MAR-2000; 2000US-00531025.

PR 14-APR-2000; 2000US-0197769P.

PR 23-MAY-2000; 2000US-00578223.

PR 09-AUG-2000; 2000US-00636385.

XX (RIBO-) RIBOZYME PHARM INC.

XX Mcswiggen J, Ueman N, Blatt L, Beigelman L, Burgin A;  
 PI Karpeisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;  
 PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;

XX WPI; 2001-244406/25.

PT Enzymatic nucleic acid molecules able to cleave separate RNA molecules  
 PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,  
 PT obesity and heart disease.

XX Example 4; Page 364; 717pp; English.

XX The present invention relates to the use of enzymatic nucleic acid  
 CC molecules (e.g. ribozymes) to modulate gene expression. The invention  
 CC also methods for their use to down regulate or inhibit the expression of  
 CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine  
 CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C  
 CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor  
 CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),  
 CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic  
 CC nucleic acid molecules used to inhibit the expression of the said genes  
 CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,  
 CC zinyne, and/or DNzyme motifs. The methods of the invention are useful  
 CC for treating cancer, in particular breast cancer, Alzheimer's disease,  
 CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related  
 CC diseases, hepatitis B infections, and hepatitis and hepatocellular  
 CC carcinoma. The enzymatic nucleic acid molecules can also be used as  
 CC diagnostic tools to examine genetic drift and mutations within diseased  
 CC cells and to detect the presence of specific RNA in a cell. The present  
 CC sequence represents a ribozyme used in the examples of the present  
 CC invention. Note: Some SEQ ID Nos are repeated more than once in the  
 CC specification, but these have different sequences associated with them.

XX Sequence 37 BP; 5 A; 9 C; 18 G; 0 T; 5 U; 0 Other;

Query Match 69.2%; Score 16.6; DB 5; Length 37;

Best Local Similarity 73.9%; Pred. No. 6e+02;

Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGCCAAGCAGCA 23

Db 1 CGCGCGCGUGAUGGCAUGCACA 23

RESULT 9

ADV04149

ID ADV04149 standard; RNA; 37 BP.

AC ADV04149;

DT 10-FEB-2005 (first entry)

DE Human BACE G-cleaver ribozyme sequence #52.

XX Enzymatic nucleic acid molecule; gene expression; down regulation;  
 KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;  
 KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
 KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;  
 KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;  
 KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;  
 KW amberzyme; zinyne; DNzyme; cancer; breast cancer; Alzheimer's disease;  
 KW diabetes; obesity; cardiac disease; heart disease; age-related disease;  
 KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;  
 KW ss.

OS Homo sapiens.

XX WO200116312-A2.

PN 08-MAR-2001.

PD 30-AUG-2000; 2000WO-US023998.

PF 31-AUG-1999; 99US-0151713P.

PR 27-SEP-1999; 99US-00406643.

PR 27-SEP-1999; 99US-0156236P.

PR 27-SEP-1999; 99US-0156467P.

PR 08-NOV-1999; 99US-00436430.

PR 06-DEC-1999; 99US-0169100P.

PR 29-DEC-1999; 99US-00474432.

PR 29-DEC-1999; 99US-0173612P.

PR 29-DEC-1999; 99US-00476387.

PR 04-FEB-2000; 2000US-00498824.

PR 20-MAR-2000; 2000US-00531025.

PR 14-APR-2000; 2000US-0197769P.

PR 23-MAY-2000; 2000US-00578223.

PR 09-AUG-2000; 2000US-00636395.

XX (RIBO-) RIBOZYME PHARM INC.

XX McSwiggen J, Uman N, Blatt L, Beigelman L, Burgin A,

PI Karpelisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;

PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;

XX WPI; 2001-244406/25.

XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules  
 PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,  
 PT obesity and heart disease.

XX Example 4; Page 365; 717pp; English.

XX The present invention relates to the use of enzymatic nucleic acid  
 CC molecules (e.g. ribozymes) to modulate gene expression. The invention  
 CC also methods for their use to down regulate or inhibit the expression of  
 CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine  
 CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C  
 CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor  
 CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),  
 CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic  
 CC nucleic acid molecules used to inhibit the expression of the said genes  
 CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,  
 CC zinyne, and/or DNzyme motifs. The methods of the invention are useful  
 CC for treating cancer, in particular breast cancer, Alzheimer's disease,  
 CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related  
 CC diseases, hepatitis B infections, and hepatitis and hepatocellular  
 CC carcinoma. The enzymatic nucleic acid molecules can also be used as  
 CC diagnostic tools to examine genetic drift and mutations within diseased  
 CC cells and to detect the presence of specific RNA in a cell. The present  
 CC sequence represents a ribozyme used in the examples of the present  
 CC invention. Note: Some SEQ ID Nos are repeated more than once in the  
 CC specification, but these have different sequences associated with them.

XX Sequence 37 BP; 6 A; 12 C; 14 G; 0 T; 5 U; 0 Other;

Query Match 69.2%; Score 16.6; DB 5; Length 37;

Best Local Similarity 73.9%; Pred. No. 6e+02;

Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGATGCCAAGCAGCA 23

Db 1 CAGCGCGUGAUGGCAUGCACA 23

RESULT 10

ADV04093

ID ADV04093 standard; RNA; 37 BP.

XX ADV04093;

XX 10-FEB-2005 (first entry)

XX Human BACE G-cleaver ribozyme sequence #30.

XX Enzymatic nucleic acid molecule; gene expression; down regulation;  
 KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;  
 KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
 KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;  
 KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;  
 KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;  
 KW amberzyme; zinyne; DNzyme; cancer; breast cancer; Alzheimer's disease;  
 KW diabetes; obesity; cardiac disease; heart disease; age-related disease;







XX The invention relates to enzymatic nucleic acid molecules that down  
 CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes  
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are  
 CC useful as pharmaceutical agents for treating conditions such as chronic  
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic  
 CC fibrosis, obstructive bowel syndrome and any other diseases or conditions  
 CC that are related to or will respond to the levels of CLCA1 in a cell or  
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,  
 CC hence, are useful for treatment of a patient having a condition  
 CC associated with the level of CLCA1, where the invention further comprises  
 CC the use of one or more therapies under conditions suitable for the  
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,  
 CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The  
 CC nucleic acids of the invention are also used as diagnostic tools to  
 CC examine genetic drift and mutations within diseased cells or to detect  
 CC the presence of CLCA1 RNA in a cell. This sequence represents an  
 CC enzymatic nucleic acid molecule of the invention  
 XX  
 SQ Sequence 37 BP; 8 A; 7 C; 14 G; 0 T; 8 U; 0 Other;  
 Query Match 69.2%; Score 16.6; DB 6; Length 37;  
 Best Local Similarity 73.9%; Pred. No. 6e+02;  
 Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 CAGCGGAGTGATGGCAAGCAGCA 23  
 DB 1 CAGGGUAGUGAUGGCAUGCACUA 23  
 RESULT 14  
 ACDS3318  
 ID ACD53318 standard; RNA; 37 BP.  
 XX  
 AC ACD53318;  
 DT 24-SEP-2003 (first entry)  
 XX  
 DE HBV G-cleaver sequence #57.  
 XX  
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;  
 KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW virucide; antiinflammatory; ss.  
 XX  
 OS Hepatitis B virus.  
 XX  
 XX WO200281494-A1.  
 XX  
 PD 17-OCT-2002.  
 XX  
 XX 26-MAR-2002; 2002WO-US009187.  
 XX  
 XX 26-MAR-2001; 2001US-00817879.  
 PR 08-JUN-2001; 2001US-00877478.  
 PR 08-JUN-2001; 2001US-0296876P.  
 PR 24-OCT-2001; 2001US-0335059P.  
 PR 05-DEC-2001; 2001US-0337055P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MACE/) MACEJAK D.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (MORR/) MORRISSEY D.  
 PA (PAVC/) PAVCO P.  
 PA (LEEF/) LEE P.  
 PA (DRAP/) DRAPER K.  
 PA (ROBE/) ROBERTS E.

PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
 PI Draper K, Roberts E;  
 XX  
 DR WPI; 2003-229207/22.  
 XX  
 XX Novel compound useful for treating cirrhosis, liver failure,  
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
 PT infection.  
 XX  
 XX Example 1; Page 166; 387pp; English.  
 PS  
 XX The present invention relates to nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
 CC inozymes, zinzymes, amberyne, and G-cleaver ribozymes. Also disclosed  
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
 CC DNA. The nucleic acids may be used to modulate the expression of HBV  
 CC genes and HBV viral replication. Also disclosed is a method for screening  
 CC compounds and/or potential therapies directed against HBV, and compounds  
 CC that modulate the expression and/or replication of HCV. The compounds and  
 CC methods of the invention are useful for the treatment of degenerative and  
 CC disease states related to HBV and HCV infection, replication and gene  
 CC expression such as cirrhosis, liver failure, and hepatocellular  
 CC carcinoma. The present sequence represents one of the HBV ribozyme,  
 CC inozyme, G-cleaver, zinzyme, DNzyme or amberyne sequences disclosed in  
 CC the present invention  
 XX  
 SQ Sequence 37 BP; 8 A; 10 C; 12 G; 0 T; 7 U; 0 Other;  
 Query Match 69.2%; Score 16.6; DB 8; Length 37;  
 Best Local Similarity 73.9%; Pred. No. 6e+02;  
 Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 CAGCGGAGTGATGGCAAGCAGCA 23  
 DB 1 CAGCCUAGUGAUGGCAUGCACUA 23  
 RESULT 15  
 ADMG1879  
 ID ADMG1879 standard; RNA; 37 BP.  
 XX  
 AC ADMG1879;  
 XX  
 XX 03-JUN-2004 (first entry)  
 DT  
 XX  
 DE Hepatitis B virus (HBV) enzymatic nucleic acid #1471.  
 XX  
 KW Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;  
 KW Hepatitis B virus infection; hepatitis; hepatocellular carcinoma;  
 KW cirrhosis; liver failure; lamivudine; interferon; genetic drift;  
 KW virucide; hepatotropic; antiinflammatory; cytostatic.  
 XX  
 OS Hepatitis B virus.  
 XX  
 XX US2004054156-A1.  
 XX  
 XX 18-MAR-2004.  
 XX  
 XX 15-JAN-2003; 2003US-00342902.  
 XX  
 XX 14-MAY-1992; 92US-00882712.  
 PR 07-FEB-1994; 94US-00193627.  
 PR 08-NOV-1999; 99US-00436430.  
 PR 20-MAR-2000; 2000US-00531025.  
 PR 09-AUG-2000; 2000US-00636385.  
 PR 24-OCT-2000; 2000US-00696347.  
 PR 08-JUN-2001; 2001US-00877478.  
 XX  
 XX (DRAP/) DRAPER K.

```
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
PA (MORR/) MORRISSEY D.
XX
PI Draper K, Blatt L, Mcswiggen JA, Morrissey D;
XX WPI; 2004-247781/23.
DR
XX
XX Novel enzymatic nucleic acid molecule such as DNAzymes and inozymes
PT specifically cleaving RNA derived from hepatitis B virus and comprising
PT one or more binding arms, useful for treating hepatitis and cirrhosis.
XX
XX Disclosure; SEQ ID NO 4013; 122pp; English.
XX
XX The invention relates to an enzymatic nucleic acid molecule that
CC specifically cleaves RNA derived from hepatitis B virus (HBV) and
CC comprising one or more binding arms, without requiring the presence of a
CC 2'-OH group within the molecule for activity. The nucleic acids are
CC useful for treating hepatitis B virus infection, hepatitis,
CC hepatocellular carcinoma, cirrhosis and liver failure, either alone or in
CC combination with other therapies such as lamivudine and interferons. The
CC nucleic acids are useful as diagnostic tools to examine genetic drift and
CC mutations within diseased cells, for detecting the presence of HBV RNA in
CC a cell, for the study of RNA and for down-regulating gene expression of
CC target genes in bacterial, fungal, viral, plant or mammalian cells. This
CC sequence represents an enzymatic nucleic acid molecule which cleaves HBV
CC RNA of the invention. Note: The sequence data for this patent is also
CC available in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 37 BP; 8 A; 10 C; 12 G; 0 T; 7 U; 0 Other;

Query Match 69.2%; Score 16.6; DB 12; Length 37;
Best Local Similarity 73.9%; Pred. No. 6e+02;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAACGCA 23
Db 1 CAGCCUAGUGAUGGCAUGCACUA 23

RESULT 16
ADC33588
ID ADC33588 standard; DNA; 45 BP.
XX
AC ADC33588;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human locus DYS271 30C-44A-168A variant PCR primer #4.
XX
XX Human; Y chromosome; DYS271; SNP; single nucleotide polymorphism; ss;
KW mutation detection; denaturing high performance liquid chromatography;
KW DHPLC; nitrogen containing composition; PCR; primer.
XX
XX Homo sapiens.
XX
XX US2003082557-A1.
XX
XX 01-MAY-2003.
XX
XX 29-OCT-2001; 2001US-00033104.
XX
XX 30-OCT-2000; 2000US-024436P.
XX 03-JAN-2001; 2001US-0259847P.
XX
PA (TAYL/) TAYLOR P D.
XX Taylor PD;
PI
DR WPI; 2003-743884/70.
XX
XX Preparing a double stranded DNA fragment for mutation detection by
```

```
PT denaturing high performance liquid chromatography, comprises including
PT during hybridization composition comprising a nitrogen-containing organic
XX compound.
XX Example 4; SEQ ID NO 4; 24pp; English.
XX
XX The invention relates to preparing a double stranded DNA fragment for
CC mutation detection by denaturing high performance liquid chromatography
CC (DHPLC) comprising including during the hybridisation, a nitrogen
CC containing composition (of structure detailed in the specification). The
CC double stranded DNA fragment corresponds to a wild type double stranded
CC DNA fragment having a known nucleotide sequence. The method further
CC comprises: (a) amplifying a section of the double stranded DNA fragment
CC for mutation detection by PCR using a set of primers flanking the
CC section, where at least one primer of the set incorporates a sequence
CC comprising solely GC content on the 5' end; (b) hybridising the
CC amplification product of (a) with wild type double stranded DNA
CC corresponding to the section, where a mixture comprising one or more
CC heteroduplexes is formed if the section includes a mutation; and (c)
CC including during the hybridisation, an amount of the nitrogen containing
CC composition. The composition is included to increase the amount of
CC heteroduplex DNA double stranded DNA fragment for mutation detection.
CC Also included are a product of the method above, a kit for preparing a
CC double stranded DNA for mutation detection by liquid chromatography, a
CC kit for hybridising a target nucleotide sequence with wild type DNA
CC corresponding to the target sequence, and a kit for analysing a double
CC stranded DNA for mutation detection by liquid chromatography. The method
CC is useful for preparing a double stranded DNA fragment for mutation
CC analysis, and for diagnosing a disease. The method improves the
CC resolution between heteroduplex and homoduplex peaks even for mutations
CC that are difficult to detect. The present sequence is a PCR primer used
CC to amplify variants of the human Y chromosome locus DYS271 (which
CC contains 3 single nucleotide polymorphisms) and is used to demonstrate
XX the method of the invention.
XX
SQ Sequence 45 BP; 8 A; 11 C; 14 G; 7 T; 0 U; 5 Other;

Query Match 68.3%; Score 16.4; DB 10; Length 45;
Best Local Similarity 70.8%; Pred. No. 7.6e+02;
Matches 17; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCGGAGTGATGGCAACGACGAC 24
Db 10 CAGMTGTMGTGTCATACAGGAC 33

RESULT 17
AAD00496
ID AAD00496 standard; RNA; 32 BP.
XX
AC AAD00496;
XX
DT 29-AUG-2000 (first entry)
XX
DE Clone cGMP-5 for allosteric modulation of hammerhead ribozyme by cGMP.
XX
XX Hammerhead ribozyme; molecular sensor; signalling agent; ligand; FMN;
KW flavin mononucleotide; conformational change; molecular switch; CM;
KW communication module; allosteric; sensing element; environmental;
KW agricultural; clinical; industrial; genetic control; cGMP; ss.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
FH misc_feature 1..4
FT /tag= a
FT /label= Communication_module
FT /note= "Comprises substitution mutations"
FT misc_feature 1
FT /tag= b
FT /note= "Cytosine substituted with Uracil"
FT misc_feature 3
FT /tag= c
```

```

FT misc_feature /note= "Uracil substituted with Guanine"
FT 5..28 /tag= d
FT /note= "Corresponds to aptamer domain"
FT 29..32
FT /tag= e
FT /label= Communication module
FT /note= "Comprises substitution mutations"
FT 29
FT /tag= f
FT /note= "Adenine substituted with Uracil"
FT 30
FT /tag= g
FT /note= "Cytosine substituted with Adenine"
FT 31
FT /tag= h
FT /note= "Guanine substituted with Cytosine"
FT 32
FT /tag= i
FT /note= "Uracil substituted with Guanine"
XX
XX WO200026226-A1.
XX
XX 11-MAY-2000.
XX
XX 29-OCT-1999; 99WO-US025497.
XX
XX 03-NOV-1998; 98US-0106829P.
XX 29-MAR-1999; 99US-0126683P.
XX (UYUA ) UNIV YALE.
XX
XX Breaker RR, Soukup GA;
XX
XX WPI; 2000-365558/31.
XX
XX Novel functional polynucleotides comprising an actuator domain, a
XX receptor domain, and a bridging domain useful for generating highly
XX specific polynucleotide sensors and as genetic control elements.
XX
XX Example 3; Fig 10A; 83pp; English.
XX
XX The patent discloses multidomain polynucleotide molecular sensors,
XX constructed using hammerhead ribozyme RNAs, comprising an actuator or
XX catalytic domain, bridging domain and receptor or aptamer domain. The
XX interaction of the receptor with a signalling agent like a ligand e.g.,
XX flavin mononucleotide (FMN) or physical signal, triggers a conformational
XX change in the bridging domain, that modulates the catalytic or reporter
XX activity of the actuator domain. It functions as a molecular switch.
XX Communication module (CM) sequences can be inserted as the bridging
XX domain, that enhances the allosteric properties. The ligand-specific
XX sensors may be used as sensing elements in clinical, agricultural,
XX industrial and environmental analyses and as genetic control or reporter
XX elements for the regulation of gene expression. The present RNA sequence
XX is the clone cGMP-5, isolated from G18' RNA population, after selective
XX amplification. It is used to study the allosteric modulation of
XX hammerhead ribozymes by cGMPs. This clone comprises mutations in the
XX aptamer domain (deletions) and communication module (substitutions)
XX
XX Sequence 32 BP; 7 A; 8 C; 11 G; 0 T; 6 U; 0 Other;
XX
XX Query Match 67.5%; Score 16.2; DB 3; Length 32;
XX Best Local Similarity 81.0%; Pred. No. 9.1e+02;
XX Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 2 AGCGGAGTGATGGCAAGCAGC 22
XX ||||| ||||| ||||| |||||
XX Db 8 AGCGGAGCGAUGGCGCCAGC 28
XX
XX RESULT 18
XX ABRK05366
XX ID ABRK05366 standard; RNA; 37 BP.

```

```

XX ABK05366;
XX
XX 12-MAR-2002 (first entry)
XX
XX Human NOGO G-Cleaver substrate sequence #29.
XX
XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
XX cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
XX musclar; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
XX DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
XX B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
XX human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
XX MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
XX inflammatory arthropathy; central nervous system injury;
XX cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
XX chemotherapy-induced neuropathy; ankyrotrophic lateral sclerosis; ALS;
XX Parkinson's disease; ataxia; Huntington's disease; substrate sequence;
XX Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO200159103-A2.
XX
XX 16-AUG-2001.
XX
XX 09-FEB-2001; 2001WO-US004273.
XX
XX 11-FEB-2000; 2000US-0181797P.
XX 28-FEB-2000; 2000US-0185516P.
XX 06-MAR-2000; 2000US-0187128P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J.
XX (CHOW/) CHOWRIRA B M.
XX
XX Blatt L, Mcswiggen J, Chowrira BM;
XX
XX WPI; 2001-607195/69.
XX
XX
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
XX constructs, which down regulate expression of a CD20 gene or neurite
XX growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
XX central nervous system injury.
XX
XX Claim 89; Page 92; 200pp; English.
XX
XX The invention relates to a nucleic acid molecule which down regulates
XX expression of a CD20 gene and a nucleic acid molecule which down
XX regulates expression of a neurite growth inhibitor gene (NOGO). The
XX nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
XX DNazyme) an inozyme (an endolytic nucleic acid cleaving a an RNA molecule
XX possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr
XX an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
XX with a VCY motif). The CD20-targeting nucleic acid is used to cleave RNA
XX of CD20 in the presence of a divalent cation that is preferably Mg2+.
XX Furthermore, it may be contacted with a cell to reduce CD20 activity of
XX the cell and treat a patient having a condition associated with the level
XX of CD20. The treatment may further comprise the use of one or more
XX therapies. In particular, the CD20 targeting nucleic acid may be used to
XX treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
XX Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
XX leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
XX lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
XX immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
XX targeting nucleic acid is used to cleave RNA of the NOGO gene in the
XX presence of a divalent cation that is preferably Mg2+. Furthermore, the
XX nucleic acid may be contacted with a cell to reduce NOGO activity of the
XX cell and treat a patient having a condition associated with the level of
XX NOGO. The treatment may further comprise the use of one or more
XX therapies. In particular, the NOGO-targeting nucleic acid may be used to

```

CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NCO expression. The present  
 CC sequence is a substrate sequence for a nucleic acid of the invention  
 CC based on the human NCO sequence  
 XX  
 SQ Sequence 37 BP; 6 A; 8 C; 18 G; 0 T; 5 U; 0 Other;  
 Query Match 67.5%; Score 16.2; DB 4; Length 37;  
 Best Local Similarity 76.2%; Pred. No. 9.2e+02;  
 Matches 16; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 GCGGAGTGATGCCAAGCACA 23  
 DB 3 GCGGAGUGAUGGCAUGCACUA 23  
 RESULT 19  
 ADV47946  
 ID ADV47946 standard; RNA; 37 BP.  
 XX  
 AC ADV47946;  
 XX  
 DT 10-FEB-2005 (first entry)  
 XX  
 DE HBV G-cleaver ribozyme sequence #41.  
 XX  
 KW Enzymatic nucleic acid molecule; gene expression; down regulation;  
 KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;  
 KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
 KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;  
 KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;  
 KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;  
 KW amberyze; zincyme; DNzyme; cancer; breast cancer; Alzheimer's disease;  
 KW diabetes; obesity; cardiac disease; heart disease; age-related disease;  
 KW hepatitis B infection; hepatocellular carcinoma; genetic drift; ss.  
 XX  
 OS Hepatitis B virus.  
 XX  
 XX WO200116312-A2.  
 XX  
 XX 08-MAR-2001.  
 XX  
 XX 30-AUG-2000; 2000WO-US023998.  
 XX  
 XX 31-AUG-1999; 99US-0151713P.  
 XX  
 XX 27-SEP-1999; 99US-00406643.  
 XX  
 XX 27-SEP-1999; 99US-0156236P.  
 XX  
 XX 27-SEP-1999; 99US-0156467P.  
 XX  
 XX 08-NOV-1999; 99US-00436430.  
 XX  
 XX 06-DEC-1999; 99US-0169100P.  
 XX  
 XX 29-DEC-1999; 99US-00474432.  
 XX  
 XX 29-DEC-1999; 99US-0173612P.  
 XX  
 XX 30-DEC-1999; 99US-00476387.  
 XX  
 XX 04-FEB-2000; 2000US-00498824.  
 XX  
 XX 20-MAR-2000; 2000US-00531025.  
 XX  
 XX 14-APR-2000; 2000US-0197769P.  
 XX  
 XX 23-MAY-2000; 2000US-00578223.  
 XX  
 XX 09-AUG-2000; 2000US-00636385.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX  
 XX Mcswiggen J, Usman N, Blatt L, Beigelman L, Burgin A;  
 XX Karpeisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;  
 XX Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;  
 XX  
 XX WPI; 2001-244406/25.  
 XX  
 DR Enzymatic nucleic acid molecules able to cleave separate RNA molecules  
 PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,

PT obesity and heart disease.  
 XX  
 PS Example 6; Page 531; 717pp; English.  
 XX  
 CC The present invention relates to the use of enzymatic nucleic acid  
 CC molecules (e.g. ribozymes) to modulate gene expression. The invention  
 CC also methods for their use to down regulate or inhibit the expression of  
 CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine  
 CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C  
 CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor  
 CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),  
 CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic  
 CC nucleic acid molecules used to inhibit the expression of the said genes  
 CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberyze,  
 CC zincyme, and/or DNzyme motifs. The methods of the invention are useful  
 CC for treating cancer, in particular breast cancer, Alzheimer's disease,  
 CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related  
 CC diseases, hepatitis B infections, and hepatitis and hepatocellular  
 CC carcinoma. The enzymatic nucleic acid molecules can also be used as  
 CC diagnostic tools to examine genetic drift and mutations within diseased  
 CC cells and to detect the presence of specific RNA in a cell. The present  
 CC sequence represents a ribozyme used in the examples of the present  
 CC invention. Note: Some SEQ ID Nos are repeated more than once in the  
 CC specification, but these have different sequences associated with them.  
 XX  
 SQ Sequence 37 BP; 7 A; 8 C; 14 G; 0 T; 8 U; 0 Other;  
 Query Match 67.5%; Score 16.2; DB 5; Length 37;  
 Best Local Similarity 76.2%; Pred. No. 9.2e+02;  
 Matches 16; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 GCGGAGTGATGCCAAGCACA 23  
 DB 3 GCGGAGUGAUGGCAUGCACUA 23  
 RESULT 20  
 ABK20721  
 ID ABK20721 standard; RNA; 37 BP.  
 XX  
 XX AC ABK20721;  
 XX  
 XX 09-APR-2002 (first entry)  
 XX  
 XX Human ERG G-cleaver ribozyme, Seq ID No 3368.  
 XX  
 KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;  
 KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;  
 KW vulnery; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;  
 KW tumour angiogenesis; diabetic retinopathy; macular degeneration;  
 KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;  
 KW angiofibroma of tuberosus sclerosis; port-wine stain; wound healing;  
 KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;  
 KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNzyme; inozyme;  
 XX amberyze.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200188124-A2.  
 XX  
 XX 22-NOV-2001.  
 XX  
 XX 16-MAY-2001; 2001WO-US015866.  
 XX  
 XX 16-MAY-2000; 2000US-00572021.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX  
 XX (GLAX ) GLAXO GROUP LTD.  
 XX  
 XX Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;  
 XX WPI; 2002-082995/11.  
 XX  
 DR  
 XX

PT Novel polynucleotide which down regulates expression of Ets-related gene,  
 PT useful for treating cancer, diabetic retinopathy, macular degeneration,  
 PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.  
 XX  
 PS Claim 5; Page 82; 149pp; English.

XX The invention relates to a nucleic acid molecule (I) which down regulates  
 CC expression of an Ets-related gene (ERG). (I) is useful for treating  
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,  
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration, verruca  
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca  
 CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge  
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu  
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for  
 CC treating a patient having a condition associated with the level of ERG,  
 CC by contacting cells of the patient with (I) under conditions suitable for  
 CC the treatment. The method comprises the use of one or more therapies  
 CC under conditions suitable for the treatment. Leukaemia or tumour  
 CC angiogenesis is treated by administering (I) to the patient in  
 CC conjunction with one or more of other therapies such as radiation or  
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a  
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of  
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent  
 CC cation such as Mg<sup>2+</sup>. (I) is useful for diagnosis of conditions and  
 CC diseases related to the expression of ERG, and as diagnostic tool to  
 CC examine genetic drift and mutations within diseased cells or to detect  
 CC the presence of ERG RNA in a cell. (I) is useful for specifically  
 CC targeting genes that share homology with ERG gene or ERG fusion genes.  
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and  
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and  
 CC related PCR primers of the invention

XX Sequence 37 BP; 7 A; 10 C; 12 G; 0 T; 8 U; 0 Other;

Query Match 67.5%; Score 16.2; DB 6; Length 37;  
 Best Local Similarity 76.2%; Pred. No. 9.2e+02;  
 Matches 16; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCGGAGTGATGCGAAGCAGCA 23  
 ||| |||:||||| |||||  
 DB 3 GCGUAGUGAUGGCAUGCACUA 23

RESULT 21  
 ACDS3251  
 ID ACDS3251 standard; RNA; 37 BP.

XX AC ACDS3251;

XX 24-SEP-2003 (first entry)

XX HBV G-cleaver sequence #41.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;  
 KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatitis; cytostatic;  
 KW virucide; antiinflammatory; ss.

XX Hepatitis B virus.

XX WO200281494-A1.

XX 17-OCT-2002.

XX 26-MAR-2002; 2002WO-US009187.

XX 26-MAR-2001; 2001US-00817879.

PR 08-JUN-2001; 2001US-00877478.

PR 08-JUN-2001; 2001US-0296876P.

PR 24-OCT-2001; 2001US-0335059P.  
 XX 05-DEC-2001; 2001US-0337055P.

PA (RIBO-) RIBOZYME PHARM INC.

PA (BLATY) BLATY L.

PA (MACE) MACEJAK D.

PA (MCSW) MCSWIGGEN J.

PA (MORR) MORRISSEY D.

PA (PAVC) PAVCO P.

PA (LEEP) LEE P.

PA (DRAP) DRAPER K.

PA (ROBE) ROBERTS E.

XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;

PI Draper K, Roberts E;

XX WPI; 2003-229207/22.

XX Novel compound useful for treating cirrhosis, liver failure,

PT hepatocellular carcinoma, or condition associated with hepatitis C virus

PT infection.

XX Example 1; Page 165; 387pp; English.

XX The present invention relates to nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNzymes,  
 CC inozymes, zinzymes, amberyne, and G-cleaver ribozymes. Also disclosed  
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
 CC DNA. The nucleic acids may be used to modulate the expression of HBV  
 CC genes and HBV viral replication. Also disclosed is a method for screening  
 CC compounds and/or potential therapies directed against HBV, and compounds  
 CC that modulate the expression and/or replication of HCV. The compounds and  
 CC methods of the invention are useful for the treatment of degenerative and  
 CC disease states related to HBV and HCV infection, replication and gene  
 CC expression such as cirrhosis, liver failure, and hepatocellular  
 CC carcinoma. The present sequence represents one of the HBV ribozyme.  
 CC inozyme, G-cleaver, zinzyme, DNzyme or amberyne sequences disclosed in  
 CC the present invention

XX Sequence 37 BP; 7 A; 8 C; 14 G; 0 T; 8 U; 0 Other;

Query Match 67.5%; Score 16.2; DB 8; Length 37;

Best Local Similarity 76.2%; Pred. No. 9.2e+02;

Matches 16; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCGGAGTGATGCGAAGCAGCA 23

DB 3 GCGGAGUGAUGGCAUGCACUA 23

RESULT 22

ADM61863

ID ADM61863 standard; RNA; 37 BP.

XX ADM61863;

XX 03-JUN-2004 (first entry)

XX Hepatitis B virus (HBV) enzymatic nucleic acid #1455.

XX Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;

KW hepatitis B virus infection; hepatitis; hepatocellular carcinoma;

KW cirrhosis; liver failure; lamivudine; interferon; genetic drift;

KW virucide; hepatotropic; antiinflammatory; cytostatic.

XX Hepatitis B virus.

XX US2004054156-A1.

```
PD 18-MAR-2004.
XX
PF 15-JAN-2003; 2003US-00342902.
XX
PR 14-MAY-1992; 92US-00882712.
PR 07-FEB-1994; 94US-00193627.
PR 08-NOV-1999; 99US-00436430.
PR 20-MAR-2000; 2000US-00531025.
PR 09-AUG-2000; 2000US-00636385.
PR 24-OCT-2000; 2000US-00696347.
PR 08-JUN-2001; 2001US-00877478.
XX
PA {DRAP/} DRAPER K.
PA {BLAT/} BLATT L.
PA {MCSW/} MCSWIGGEN J A.
PA {MORR/} MORRISSEY D.
XX
PI Draper K, Blatt L, Mcswiggen JA, Morrissey D;
XX WPI; 2004-247781/23.
DR
XX
PT Novel enzymatic nucleic acid molecule such as DNazymes and inozymes
PT specifically cleaving RNA derived from hepatitis B virus and comprising
PT one or more binding arms, useful for treating hepatitis and cirrhosis.
XX
PS Disclosure; SEQ ID NO 3997; 122pp; English.
XX
CC The invention relates to an enzymatic nucleic acid molecule that
CC specifically cleaves RNA derived from hepatitis B virus (HBV) and
CC comprising one or more binding arms, without requiring the presence of a
CC 2'-OH group within the molecule for activity. The nucleic acids are
CC useful for treating hepatitis B virus infection, hepatitis,
CC hepatocellular carcinoma, cirrhosis and liver failure, either alone or in
CC combination with other therapies such as lamivudine and interferons. The
CC nucleic acids are useful as diagnostic tools to examine genetic drift and
CC mutations within diseased cells; for detecting the presence of HBV RNA in
CC a cell, for the study of RNA and for down-regulating gene expression of
CC target genes in bacterial, fungal, viral, plant or mammalian cells. This
CC sequence represents an enzymatic nucleic acid molecule which cleaves HBV
CC RNA of the invention. Note: The sequence data for this patent is also
CC available in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 37 BP; 7 A; 8 C; 14 G; 0 T; 8 U; 0 Other;
Query Match 67.5%; Score 16.2; DB 12; Length 37;
Best Local Similarity 76.2%; Pred. No. 9.2e+02;
Matches 16; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 3 GCGGAGTGATGCGNAGCAGCA 23
DB |||||:|||||
3 GCGGAGUGAUGGCAUGCACUA 23
RESULT 23
AAH47991/C
ID AAH47991 standard; DNA; 18 BP.
XX
AC AAH47991;
XX
DT 02-OCT-2001 (first entry)
XX
DE Human inducible NOS antisense oligonucleotide SEQ ID NO 35.
XX
KW Antisense oligonucleotide; inducible nitric oxide synthase; NOS;
KW modulate expression; immunomodulator; antidiabetic; cardiovascular;
KW cardiant; neuroprotective; vasotropic; ischaemia; reperfusion injury;
KW 2'-O-methoxyethyl; phosphorothioate; human; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1. .18
```

```
FT /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone, 5' and 3' four
FT nucleotide 2'-MOE (2'-O-methoxyethyl) wings (the cytidine
FT residues in the 2'-MOE wings are 5-methylcytidines) and a
FT deoxy gap"
XX WO200152902-A1.
XX
PD 26-JUL-2001.
XX
XX 15-JAN-2001; 2001WO-US001381.
XX
PR 24-JAN-2000; 2000US-00490208.
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Dean NM, Cowseert LM;
XX WPI; 2001-465340/50.
XX
XX New antisense oligonucleotides for modulating the expression of inducible
XX nitric oxide synthase in cells or tissues, particularly useful for
XX treating e.g. immunological, cardiovascular or neurological disorders, or
XX ischemia.
XX
XX Example 15; Page 83; 144pp; English.
XX
CC The invention relates to antisense compounds, especially
CC oligonucleotides, which are targeted to a nucleic acid encoding inducible
CC nitric oxide synthase and which specifically hybridise to and modulate
CC expression of inducible nitric oxide synthase. The antisense compounds
CC have immunomodulator, antidiabetic, cardiovascular, cardiant,
CC neuroprotective, disorder and vasotropic activity. The antisense
CC oligonucleotides are useful for inhibiting the expression of inducible
CC nitric oxide synthase in cells or tissues. In particular, the antisense
CC oligonucleotides are useful for treating diseases or disorders associated
CC with inducible nitric oxide synthase, e.g. diabetes, immunological
CC disorder, cardiovascular disorder, neurological disorder or
CC ischaemia/reperfusion injury. The antisense oligonucleotides are also
CC useful for research and diagnostics. The present sequence is that of an
CC antisense 2'-O-methoxyethyl gapmer oligonucleotide with a
CC phosphorothioate backbone, a central "gap" region of ten nucleotides
CC flanked by four nucleotide 2'-MOE (2'-methoxyethyl) wings (cytidine
CC residues in the 2'-MOE wings are 5-methylcytidines) and targeted to human
CC inducible nitric oxide synthase (NOS) mRNA (AAH47959)
XX
SQ Sequence 18 BP; 4 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 66.7%; Score 16; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 TGATGGCAAGCAGCAGAC 24
DB |||||:|||||
18 TGATGGCAAGCAGCAGAC 3
RESULT 24
ADU85578
ID ADU85578 standard; RNA; 36 BP.
XX
AC ADU85578;
XX
DT 10-FEB-2005 (first entry)
XX
DE Anti human MetAP-2 G-cleaver ribozyme sequence #2.
XX
KW Enzymatic nucleic acid molecule; gene expression; down regulation;
KW protein-tyrosine-phosphatase-1b; PTB-18; methionine aminopeptidase;
KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
```

KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;  
KW amberzyme; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease;  
KW diabetes; obesity; cardiac disease; heart disease; age-related disease;  
KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;  
KW ss.  
XX Homo sapiens.  
XX WO200116312-A2.  
XX 08-MAR-2001.  
XX 30-AUG-2000; 2000WO-US023998.  
XX 31-AUG-1999; 99US-0151713P.  
XX 27-SEP-1999; 99US-00406643.  
XX 27-SEP-1999; 99US-0156236P.  
XX 27-SEP-1999; 99US-0156467P.  
XX 08-NOV-1999; 99US-00436430.  
XX 06-DEC-1999; 99US-0169100P.  
XX 29-DEC-1999; 99US-00474432.  
XX 29-DEC-1999; 99US-0173612P.  
XX 30-DEC-1999; 99US-00476387.  
XX 04-FEB-2000; 2000US-00498824.  
XX 20-MAR-2000; 2000US-00531025.  
XX 14-APR-2000; 2000US-0197769P.  
XX 23-MAY-2000; 2000US-00578223.  
XX 09-AUG-2000; 2000US-00636385.  
XX (RIBO-) RIBOZYME PHARM INC.  
XX Mcawiggen J, Usman N, Blatt L, Beigelman L, Burgin A;  
XX Karpelsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;  
XX Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;  
XX WPI; 2001-244406/25.  
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules  
XX are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,  
XX obesity and heart disease.  
XX Example 3; Page 266; 717pp; English.  
XX The present invention relates to the use of enzymatic nucleic acid  
XX molecules (e.g. ribozymes) to modulate gene expression. The invention  
XX also methods for their use to down regulate or inhibit the expression of  
XX genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine  
XX aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C  
XX alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor  
XX receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),  
XX presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic  
XX nucleic acid molecules used to inhibit the expression of the said genes  
XX include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,  
XX zinzyme, and/or DNAzyme motifs. The methods of the invention are useful  
XX for treating cancer, in particular breast cancer, Alzheimer's disease,  
XX diabetes, obesity, cardiac diseases e.g. heart disease, age-related  
XX diseases, hepatitis B infections, and hepatitis and hepatocellular  
XX carcinoma. The enzymatic nucleic acid molecules can also be used as  
XX diagnostic tools to examine genetic drift and mutations within diseased  
XX cells and to detect the presence of specific RNA in a cell. The present  
XX sequence represents an anti human ribozyme used in the examples of the  
XX present invention. Note: Some SEQ ID Nos are repeated more than once in  
XX the specification, but these have different sequences associated with  
XX them.  
SQ Sequence 36 BP; 8 A; 6 C; 13 G; 0 T; 9 U; 0 Other;  
Query Match 65.8%; Score 15.8; DB 5; Length 36;  
Best Local Similarity 78.9%; Pred. No. 1.4e+03;  
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
OY 5 GGAGTGTGCGAAGCACGA 23  
|||||:|||||

Db 2 GGAGUGAUGGCAUGCACUA 20  
RESULT 25  
ADU94721  
ID ADU94721 standard; RNA; 36 BP.  
XX AC  
XX ADU94721;  
XX 10-FEB-2005 (first entry)  
XX Human TERT G-cleaver ribozyme sequence #143.  
XX Enzymatic nucleic acid molecule; gene expression; down regulation;  
KW protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase;  
KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
KW beta-secretase; BACE; human epidermal growth factor receptor-2; HBR2;  
KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;  
KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;  
KW amberzyme; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease;  
KW diabetes; obesity; cardiac disease; heart disease; age-related disease;  
KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;  
KW ss.  
XX Homo sapiens.  
XX WO200116312-A2.  
XX 08-MAR-2001.  
XX 30-AUG-2000; 2000WO-US023998.  
XX 31-AUG-1999; 99US-0151713P.  
XX 27-SEP-1999; 99US-00406643.  
XX 27-SEP-1999; 99US-0156236P.  
XX 27-SEP-1999; 99US-0156467P.  
XX 08-NOV-1999; 99US-00436430.  
XX 06-DEC-1999; 99US-0169100P.  
XX 29-DEC-1999; 99US-00474432.  
XX 29-DEC-1999; 99US-0173612P.  
XX 30-DEC-1999; 99US-00476387.  
XX 04-FEB-2000; 2000US-00498824.  
XX 20-MAR-2000; 2000US-00531025.  
XX 14-APR-2000; 2000US-0197769P.  
XX 23-MAY-2000; 2000US-00578223.  
XX 09-AUG-2000; 2000US-00636385.  
XX (RIBO-) RIBOZYME PHARM INC.  
XX Mcawiggen J, Usman N, Blatt L, Beigelman L, Burgin A;  
XX Karpelsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;  
XX Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;  
XX WPI; 2001-244406/25.  
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules  
XX are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,  
XX obesity and heart disease.  
XX Example 1; Page 303; 717pp; English.  
XX The present invention relates to the use of enzymatic nucleic acid  
XX molecules (e.g. ribozymes) to modulate gene expression. The invention  
XX also methods for their use to down regulate or inhibit the expression of  
XX genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine  
XX aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C  
XX alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor  
XX receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),  
XX presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic  
XX nucleic acid molecules used to inhibit the expression of the said genes  
XX include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,  
XX zinzyme, and/or DNAzyme motifs. The methods of the invention are useful  
XX for treating cancer, in particular breast cancer, Alzheimer's disease,

CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related  
 CC diseases, hepatitis B infections, and hepatitis and hepatocellular  
 CC carcinoma. The enzymatic nucleic acid molecules can also be used as  
 CC diagnostic tools to examine genetic drift and mutations within diseased  
 CC cells and to detect the presence of specific RNA in a cell. The present  
 CC sequence represents a ribozyme used in the examples of the present  
 CC invention. Note: Some SEQ ID Nos are repeated more than once in the  
 CC specification, but these have different sequences associated with them.

XX  
 SQ Sequence 36 BP; 8 A; 9 C; 13 G; 0 T; 6 U; 0 Other;

Query Match 65.8%; Score 15.8; DB 5; Length 36;  
 Best Local Similarity 78.9%; Pred. No. 1.4e+03;  
 Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAGCACGA 23  
 ||||:|||||  
 Db 2 GGAGUGAUGGCAUGCACUA 20

RESULT 26  
 ADU94968  
 ID ADU94968 standard; RNA; 36 BP.  
 XX  
 AC ADU94968;  
 XX  
 DT 10-FEB-2005 (first entry)  
 XX  
 DE Human TERT G-cleaver ribozyme sequence #266.  
 XX  
 KW Enzymatic nucleic acid molecule; gene expression; down regulation;  
 KW protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase;  
 KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
 KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;  
 KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;  
 KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;  
 KW amberyzyme; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;  
 KW diabetes; obesity; cardiac disease; heart disease; age-related disease;  
 KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;  
 KW ss.

XX Homo sapiens.  
 XX  
 OS  
 PN WO200116312-A2.  
 XX  
 XX 08-MAR-2001.  
 XX  
 PD 30-AUG-2000; 2000WO-US023998.  
 XX  
 PF 31-AUG-1999; 99US-0151713P.  
 PR 27-SEP-1999; 99US-00406643.  
 PR 27-SEP-1999; 99US-0156236P.  
 PR 27-SEP-1999; 99US-0156467P.  
 PR 08-NOV-1999; 99US-00436430.  
 PR 06-DEC-1999; 99US-0169100P.  
 PR 29-DEC-1999; 99US-00474432.  
 PR 29-DEC-1999; 99US-0173612P.  
 PR 30-DEC-1999; 99US-00476387.  
 PR 04-FEB-2000; 2000US-00498824.  
 PR 20-MAR-2000; 2000US-00531025.  
 PR 14-APR-2000; 2000US-0197769P.  
 PR 23-MAY-2000; 2000US-00578223.  
 PR 09-AUG-2000; 2000US-00636385.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 XX Mcswiggen J, Usman N, Blatt L, Beigelman L, Burgin A;  
 PI Karpeisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;  
 PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;  
 XX  
 XX WPI; 2001-244406/25.  
 XX  
 XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules

PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,  
 PT obesity and heart disease.  
 XX  
 PS Example 1; Page 307; 717pp; English.  
 XX  
 CC The present invention relates to the use of enzymatic nucleic acid  
 CC molecules (e.g. ribozymes) to modulate gene expression. The invention  
 CC also methods for their use to down regulate or inhibit the expression of  
 CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine  
 CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C  
 CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor  
 CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),  
 CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic  
 CC nucleic acid molecules used to inhibit the expression of the said genes  
 CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberyzyme,  
 CC zinzyme, and/or DNazyme motifs. The methods of the invention are useful  
 CC for treating cancer, in particular breast cancer, Alzheimer's disease,  
 CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related  
 CC diseases, hepatitis B infections, and hepatitis and hepatocellular  
 CC carcinoma. The enzymatic nucleic acid molecules can also be used as  
 CC diagnostic tools to examine genetic drift and mutations within diseased  
 CC cells and to detect the presence of specific RNA in a cell. The present  
 CC sequence represents a ribozyme used in the examples of the present  
 CC invention. Note: Some SEQ ID Nos are repeated more than once in the  
 CC specification, but these have different sequences associated with them.

XX  
 SQ Sequence 36 BP; 7 A; 11 C; 12 G; 0 T; 6 U; 0 Other;

Query Match 65.8%; Score 15.8; DB 5; Length 36;  
 Best Local Similarity 78.9%; Pred. No. 1.4e+03;  
 Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAGCACGA 23  
 ||||:|||||  
 Db 2 GGAGUGAUGGCAUGCACUA 20

RESULT 27  
 ADU94463  
 ID ADU94463 standard; RNA; 36 BP.  
 XX  
 AC ADU94463;  
 XX  
 DT 10-FEB-2005 (first entry)  
 XX  
 DE Human TERT G-cleaver ribozyme sequence #9.  
 XX  
 KW Enzymatic nucleic acid molecule; gene expression; down regulation;  
 KW protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase;  
 KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
 KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;  
 KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;  
 KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;  
 KW amberyzyme; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;  
 KW diabetes; obesity; cardiac disease; heart disease; age-related disease;  
 KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;  
 KW ss.

XX Homo sapiens.  
 OS  
 PN WO200116312-A2.  
 XX  
 XX 08-MAR-2001.  
 XX  
 PD 30-AUG-2000; 2000WO-US023998.  
 XX  
 PF 31-AUG-1999; 99US-0151713P.  
 PR 27-SEP-1999; 99US-00406643.  
 PR 27-SEP-1999; 99US-0156236P.  
 PR 27-SEP-1999; 99US-0156467P.  
 PR 08-NOV-1999; 99US-00436430.  
 PR 06-DEC-1999; 99US-0169100P.  
 PR 29-DEC-1999; 99US-00474432.



```

PR 29-DEC-1999; 99US-0173612P.
PR 30-DEC-1999; 99US-00476387.
PR 04-FEB-2000; 2000US-00498824.
PR 20-MAR-2000; 2000US-00531025.
PR 14-APR-2000; 2000US-0197769P.
PR 23-MAY-2000; 2000US-00578223.
PR 09-AUG-2000; 2000US-00636385.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Meswiggen J, Usman N, Blatt L, Beigelman L, Burgin A;
XX Karpelsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
XX Stinchcomb D, Beaudry A, Zinnen S, Lugwig J, Sproat BS;
XX
XX WPI; 2001-244406/25.
XX
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules
XX are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
XX obesity and heart disease.
XX
XX Example 1; Page 299; 717pp; English.
XX
XX The present invention relates to the use of enzymatic nucleic acid
XX molecules (e.g. ribozymes) to modulate gene expression. The invention
XX also methods for their use to down regulate or inhibit the expression of
XX genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine
XX C
XX aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase
XX alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
XX receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
XX presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
XX nucleic acid molecules used to inhibit the expression of the said genes
XX include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,
XX zinzyme, and/or DNzyme motifs. The methods of the invention are useful
XX for treating cancer, in particular breast cancer, Alzheimer's disease,
XX diabetes, obesity, cardiac diseases e.g. heart disease, age-related
XX diseases, hepatitis B infections, and hepatitis and hepatocellular
XX carcinoma. The enzymatic nucleic acid molecules can also be used as
XX diagnostic tools to examine genetic drift and mutations within diseased
XX cells and to detect the presence of specific RNA in a cell. The present
XX sequence represents a ribozyme used in the examples of the present
XX invention. Note: Some SEQ ID Nos are repeated more than once in the
XX specification, but these have different sequences associated with them.
XX
XX Sequence 36 BP; 6 A; 9 C; 15 G; 0 T; 6 U; 0 Other;
XX
XX Query Match 65.8%; Score 15.8; DB 5; Length 36;
XX Best Local Similarity 78.9%; Pred. No. 1.4e+03;
XX Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 5 GGAGTGATGGCAAGCAGCA 23
XX Db 2 GGAGUGAUGGCAUGCAGCA 20
XX
XX RESULT 28
XX ADM90363
XX ID ADM90363 standard; RNA; 36 BP.
XX
XX AC ADM90363;
XX
XX DT 10-FEB-2005 (first entry)
XX
XX DE Human PTP-1B G-cleaver ribozyme sequence #110.
XX
XX KW Enzymatic nucleic acid molecule; gene expression; down regulation;
XX protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase;
XX MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
XX beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
XX c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
XX hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
XX amberzyme; zinzyme; DNzyme; cancer; breast cancer; Alzheimer's disease;
XX diabetes; obesity; cardiac disease; heart disease; age-related disease;
XX hepatitis B infection; hepatocellular carcinoma; genetic drift; human;

```

```

KW ss.
XX Homo sapiens.
XX
XX WO200116312-A2.
XX
XX 08-MAR-2001.
XX
XX 30-AUG-2000; 2000WO-US023998.
XX
XX 31-AUG-1999; 99US-0151713P.
XX 27-SEP-1999; 99US-00408643.
XX 27-SEP-1999; 99US-0156236P.
XX 27-SEP-1999; 99US-0156467P.
XX 08-NOV-1999; 99US-00436430.
XX 06-DEC-1999; 99US-0169100P.
XX 23-DEC-1999; 99US-00474432.
XX 29-DEC-1999; 99US-0173612P.
XX 30-DEC-1999; 99US-00476387.
XX 04-FEB-2000; 2000US-00498824.
XX 20-MAR-2000; 2000US-00531025.
XX 14-APR-2000; 2000US-0197769P.
XX 23-MAY-2000; 2000US-00578223.
XX 09-AUG-2000; 2000US-00636385.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Meswiggen J, Usman N, Blatt L, Beigelman L, Burgin A;
XX Karpelsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
XX Stinchcomb D, Beaudry A, Zinnen S, Lugwig J, Sproat BS;
XX
XX WPI; 2001-244406/25.
XX
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules
XX are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
XX obesity and heart disease.
XX
XX Example 2; Page 211; 717pp; English.
XX
XX The present invention relates to the use of enzymatic nucleic acid
XX molecules (e.g. ribozymes) to modulate gene expression. The invention
XX also methods for their use to down regulate or inhibit the expression of
XX genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine
XX C
XX aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase
XX alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
XX receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
XX presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
XX nucleic acid molecules used to inhibit the expression of the said genes
XX include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,
XX zinzyme, and/or DNzyme motifs. The methods of the invention are useful
XX for treating cancer, in particular breast cancer, Alzheimer's disease,
XX diabetes, obesity, cardiac diseases e.g. heart disease, age-related
XX diseases, hepatitis B infections, and hepatitis and hepatocellular
XX carcinoma. The enzymatic nucleic acid molecules can also be used as
XX diagnostic tools to examine genetic drift and mutations within diseased
XX cells and to detect the presence of specific RNA in a cell. The present
XX sequence represents a ribozyme used in the examples of the present
XX invention. Note: Some SEQ ID Nos are repeated more than once in the
XX specification, but these have different sequences associated with them.
XX
XX Sequence 36 BP; 8 A; 5 C; 15 G; 0 T; 8 U; 0 Other;
XX
XX Query Match 55.8%; Score 15.8; DB 5; Length 36;
XX Best Local Similarity 78.9%; Pred. No. 1.4e+03;
XX Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 5 GGAGTGATGGCAAGCAGCA 23
XX Db 2 GGAGUGAUGGCAUGCAGCA 20
XX
XX RESULT 29
XX ADU85545

```

ID ADU85545 standard; RNA; 36 BP.  
AC ADU85545;  
XX  
DT 10-FEB-2005 (first entry)  
XX  
DE Human MetAP-2 G-cleaver ribozyme substrate sequence #133.  
XX  
KW Enzymatic nucleic acid molecule; gene expression; down regulation;  
KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;  
KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;  
KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;  
KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;  
KW amberyne; zinzyme; DNzyme; cancer; breast cancer; Alzheimer's disease;  
KW diabetes; obesity; cardiac disease; heart disease; age-related disease;  
KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;  
KW ss.  
XX  
OS Homo sapiens.  
XX  
FN WO200116312-A2.  
XX  
PD 08-MAR-2001.  
XX  
PF 30-AUG-2000; 2000WO-US023998.  
XX  
PR 31-AUG-1999; 99US-0151713P.  
PR 27-SEP-1999; 99US-00406643.  
PR 27-SEP-1999; 99US-0156236P.  
PR 27-SEP-1999; 99US-0156467P.  
PR 08-NOV-1999; 99US-00436430.  
PR 06-DEC-1999; 99US-0169100P.  
PR 29-DEC-1999; 99US-00474432.  
PR 29-DEC-1999; 99US-0173612P.  
PR 30-DEC-1999; 99US-00476387.  
PR 04-FEB-2000; 2000US-00498824.  
PR 20-MAR-2000; 2000US-00531025.  
PR 14-APR-2000; 2000US-0197769P.  
PR 23-MAY-2000; 2000US-00578223.  
PR 09-AUG-2000; 2000US-00636385.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Mcswiggen J, Usman N, Beigelman L, Burgin A;  
PI Karpeisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;  
PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;  
XX  
DR WPI; 2001-244406/25.  
XX  
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules  
XX are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,  
XX obesity and heart disease.  
XX  
PS Example 3; Page 264; 717pp; English.  
XX  
CC The present invention relates to the use of enzymatic nucleic acid  
CC molecules (e.g. ribozymes) to modulate gene expression. The invention  
CC also methods for their use to down regulate or inhibit the expression of  
CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine  
CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C  
CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor  
CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),  
CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic  
CC nucleic acid molecules used to inhibit the expression of the said genes  
CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberyne,  
CC zinzyme, and/or DNzyme motifs. The methods of the invention are useful  
CC for treating cancer, in particular breast cancer, Alzheimer's disease,  
CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related  
CC diseases, hepatitis B infections, and hepatitis and hepatocellular  
CC carcinoma. The enzymatic nucleic acid molecules can also be used as  
CC diagnostic tools to examine genetic drift and mutations within diseased  
CC cells and to detect the presence of specific RNA in a cell. The present

CC sequence represents a substrate/target sequence for a ribozyme used in  
CC the examples of the present invention. Note: Some SEQ ID Nos are repeated  
CC more than once in the specification, but these have different sequences  
CC associated with them.  
XX  
SQ Sequence 36 BP; 8 A; 6 C; 13 G; 0 T; 9 U; 0 Other;  
XX  
Query Match 65.8%; Score 15.8; DB 5; Length 36;  
Best Local Similarity 78.9%; Pred. No. 1.4e+03;  
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 5 GGAGTGATGGCAAGCACGA 23  
DB 2 GGAGUGAGGCAUGACACUA 20  
RESULT 30  
ADM90361  
ID ADM90361 standard; RNA; 36 BP.  
XX  
AC ADM90361;  
XX  
DT 10-FEB-2005 (first entry)  
XX  
DE Human PTP-1B G-cleaver ribozyme sequence #108.  
XX  
KW Enzymatic nucleic acid molecule; gene expression; down regulation;  
KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;  
KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;  
KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;  
KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;  
KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;  
KW amberyne; zinzyme; DNzyme; cancer; breast cancer; Alzheimer's disease;  
KW diabetes; obesity; cardiac disease; heart disease; age-related disease;  
KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;  
KW ss.  
XX  
OS Homo sapiens.  
XX  
FN WO200116312-A2.  
XX  
PD 08-MAR-2001.  
XX  
PF 30-AUG-2000; 2000WO-US023998.  
XX  
PR 31-AUG-1999; 99US-0151713P.  
PR 27-SEP-1999; 99US-00406643.  
PR 27-SEP-1999; 99US-0156236P.  
PR 27-SEP-1999; 99US-0156467P.  
PR 08-NOV-1999; 99US-00436430.  
PR 06-DEC-1999; 99US-0169100P.  
PR 29-DEC-1999; 99US-00474432.  
PR 29-DEC-1999; 99US-0173612P.  
PR 30-DEC-1999; 99US-00476387.  
PR 04-FEB-2000; 2000US-00498824.  
PR 20-MAR-2000; 2000US-00531025.  
PR 14-APR-2000; 2000US-0197769P.  
PR 23-MAY-2000; 2000US-00578223.  
PR 09-AUG-2000; 2000US-00636385.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Mcswiggen J, Usman N, Beigelman L, Burgin A;  
PI Karpeisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;  
PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;  
XX  
DR WPI; 2001-244406/25.  
XX  
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules  
XX are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,  
XX obesity and heart disease.  
XX  
PS Example 2; Page 211; 717pp; English.



PA (RIBO-) RIBOZYME PHARM INC.  
 PA (FATT/) FATTAEY A R.  
 XX  
 PI Fattaey AR, Jarvis T, Mcswiggen J, Booher RN, Holman PS;  
 XX  
 DR WPI; 2001-496922/54.  
 XX  
 DR Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid  
 PT molecules, which downregulate expression of a checkpoint kinase-1 gene,  
 PT useful for treating colorectal, lung, breast or prostate cancers.  
 XX  
 PS Claim 5; Page 67; 115pp; English.  
 XX  
 CC The present invention provides nucleic acid molecules capable of  
 CC downregulating the expression of the human checkpoint kinase-1 (Chk1)  
 CC gene. These may be antisense or ribozyme sequences, and are useful in the  
 CC treatment of diseases associated with conditions affected by Chk1 levels,  
 CC including cancer. The present sequence is an oligonucleotide described in  
 CC the exemplification of the invention  
 XX  
 XX Sequence 37 BP; 9 A; 7 C; 11 G; 0 T; 10 U; 0 Other;  
 SQ

Query Match 65.8%; Score 15.8; DB 4; Length 37;  
 Best Local Similarity 78.9%; Pred. No. 1.4e+03;  
 Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCACGA 23  
 ||||:|||||  
 Db 5 GGAGUGAUGGCAUGCACUA 23

RESULT 33  
 ABK05427  
 ID ABK05427 standard; RNA; 37 BP.  
 XX  
 AC ABK05427;  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX  
 DE Human NOGO G-Cleaver substrate sequence #90.  
 XX  
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;  
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;  
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
 KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;  
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
 KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;  
 KW inflammatory arthropathy; central nervous system injury;  
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
 KW Parkinson's disease; ataxia; Huntington's disease; substrate sequence;  
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200159103-A2.  
 XX  
 PD 16-AUG-2001.  
 XX  
 XX 09-FEB-2001; 2001WO-US004273.  
 PF  
 XX 11-FEB-2000; 2000US-0181797P.  
 PR 28-FEB-2000; 2000US-0185516P.  
 PR 06-MAR-2000; 2000US-0187128P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (CHOW/) CHOWRIRA B M.  
 XX  
 XX Blatt L, Mcswiggen J, Chowrira BM;  
 PI

XX WPI; 2001-607195/69.  
 DR  
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
 PT constructs, which down regulate expression of a CD20 gene or neurite  
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
 PT central nervous system injury.  
 XX  
 PS Claim 89; Page 93; 200pp; English.  
 XX  
 CC The invention relates to a nucleic acid molecule which down regulates  
 CC expression of a CD20 gene and a nucleic acid molecule which down  
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The  
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving a an RNA molecule  
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr  
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA  
 CC with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA  
 CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
 CC the cell and treat a patient having a condition associated with the level  
 CC of CD20. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the CD20 targetting nucleic acid may be used to  
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-  
 CC targetting nucleic acid is used to cleave RNA of the NOGO gene in the  
 CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the  
 CC cell and treat a patient having a condition associated with the level of  
 CC NOGO. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the NOGO-targetting nucleic acid may be used to  
 CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NOGO expression. The present  
 CC sequence is a substrate sequence for a nucleic acid of the invention  
 CC based on the human NOGO sequence  
 XX  
 SQ Sequence 37 BP; 11 A; 6 C; 13 G; 0 T; 7 U; 0 Other;  
 Query Match 65.8%; Score 15.8; DB 4; Length 37;  
 Best Local Similarity 78.9%; Pred. No. 1.4e+03;  
 Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCACGA 23  
 ||||:|||||  
 Db 5 GGAGUGAUGGCAUGCACUA 23

RESULT 34  
 ABK08475  
 ID ABK08475 standard; RNA; 37 BP.  
 XX  
 AC ABK08475;  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX  
 DE Human CD20 G-Cleaver substrate #34.  
 XX  
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;  
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;  
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
 KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;  
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
 KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;  
 KW inflammatory arthropathy; central nervous system injury;  
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
 KW Parkinson's disease; ataxia; Huntington's disease; substrate sequence;  
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.



RESULT 36  
ABK59178  
ID ABK59178 standard; RNA; 37 BP.  
XX AC ABK59178;  
XX AC ABK59178;  
XX 02-JUL-2002 (first entry)  
XX Human CLCA1 gene enzymatic nucleic acid #3549.  
XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;  
KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;  
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;  
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;  
KW acetylcysteine.  
XX Homo sapiens.  
XX WO200211674-A2.  
XX 14-FEB-2002.  
XX 09-AUG-2001; 2001WO-US024970.  
XX 09-AUG-2000; 2000US-0224383P.  
XX (RIBO-) RIBOZYME PHARM INC.  
PA (SYNT ) SYNTEX USA LLC.  
PA (THOM/) THOMPSON J.  
XX Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;  
PI Grupe A;  
XX WPI; 2002-217145/27.  
XX Enzymatic polynucleotide that down regulates expression of chloride  
PT channel calcium activated gene, useful for treating Chronic obstructive  
PT pulmonary disease (COPD), chronic bronchitis and asthma.  
XX Claim 5; Page 88; 152pp; English.  
XX The invention relates to enzymatic nucleic acid molecules that down  
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes  
CC by cleaving RNA derived from the genes. The nucleic acid sequences are  
CC useful as pharmaceutical agents for treating conditions such as chronic  
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic  
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions  
CC that are related to or will respond to the levels of CLCA1 in a cell or  
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,  
CC hence, are useful for treatment of a patient having a condition  
CC associated with the level of CLCA1, where the invention further comprises  
CC the use of one or more therapies under conditions suitable for the  
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,  
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The  
CC nucleic acids of the invention are also used as diagnostic tools to  
CC examine genetic drift and mutations within diseased cells or to detect  
CC the presence of CLCA1 RNA in a cell. This sequence represents an  
CC enzymatic nucleic acid molecule of the invention  
XX Sequence 37 BP; 10 A; 7 C; 12 G; 0 T; 8 U; 0 Other;  
SQ Query Match 65.8%; Score 15.8; DB 6; Length 37;  
Best Local Similarity 78.9%; Pred. No. 1.4e+03;  
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 5 GGAGTGATGGCAAGCACGA 23  
||||:|||||  
DB 5 GGAGUGAUGGCAUGCACUA 23  
RESULT 37  
ABK59155  
ID ABK59155 standard; RNA; 37 BP.  
XX AC ABK59155;  
XX 02-JUL-2002 (first entry)  
XX Human CLCA1 gene enzymatic nucleic acid #3526.  
XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;  
KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;  
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;  
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;  
KW acetylcysteine.  
XX Homo sapiens.  
XX WO200211674-A2.  
XX 14-FEB-2002.  
XX 09-AUG-2001; 2001WO-US024970.  
XX 09-AUG-2000; 2000US-0224383P.  
XX (RIBO-) RIBOZYME PHARM INC.  
PA (SYNT ) SYNTEX USA LLC.  
PA (THOM/) THOMPSON J.  
XX Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;  
PI Grupe A;  
XX WPI; 2002-217145/27.  
XX Enzymatic polynucleotide that down regulates expression of chloride  
PT channel calcium activated gene, useful for treating Chronic obstructive  
PT pulmonary disease (COPD), chronic bronchitis and asthma.  
XX Claim 5; Page 87; 152pp; English.  
XX The invention relates to enzymatic nucleic acid molecules that down  
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes  
CC by cleaving RNA derived from the genes. The nucleic acid sequences are  
CC useful as pharmaceutical agents for treating conditions such as chronic  
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic  
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions  
CC that are related to or will respond to the levels of CLCA1 in a cell or  
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,  
CC hence, are useful for treatment of a patient having a condition  
CC associated with the level of CLCA1, where the invention further comprises  
CC the use of one or more therapies under conditions suitable for the  
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,  
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The  
CC nucleic acids of the invention are also used as diagnostic tools to  
CC examine genetic drift and mutations within diseased cells or to detect  
CC the presence of CLCA1 RNA in a cell. This sequence represents an  
CC enzymatic nucleic acid molecule of the invention  
XX Sequence 37 BP; 8 A; 5 C; 14 G; 0 T; 10 U; 0 Other;  
SQ Query Match 65.8%; Score 15.8; DB 6; Length 37;  
Best Local Similarity 78.9%; Pred. No. 1.4e+03;  
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 5 GGAGTGATGGCAAGCACGA 23  
||||:|||||  
DB 5 GGAGUGAUGGCAUGCACUA 23  
RESULT 38  
ABK05394  
ID ABK05394 standard; RNA; 37 BP.  
XX AC ABK05394;  
XX ABK05394;

XX 12-MAR-2002 (first entry)  
 DE Human NOGO G-Cleaver substrate sequence #57.  
 XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;  
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;  
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
 KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;  
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
 KW MCL; immunocytooma; IMC; immune thrombocytopaenia; stroke; dementia;  
 KW inflammatory arthropathy; central nervous system injury;  
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
 KW Parkinson's disease; ataxia; Huntington's disease; substrate sequence;  
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX WO200159103-A2.  
 XX  
 XX 16-AUG-2001.  
 XX  
 XX 09-FEB-2001; 2001WO-US004273.  
 XX  
 XX 11-FEB-2000; 2000US-0181797P.  
 XX 28-FEB-2000; 2000US-0185516P.  
 XX 06-MAR-2000; 2000US-0187128P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (CHOW/) CHOWRIRA B M.  
 XX  
 XX Blatt L, Mcswiggen J, Chowrira BM;  
 XX WPI; 2001-607195/69.  
 XX  
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
 PT constructs, which down regulate expression of a CD20 gene or neurite  
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
 PT central nervous system injury.  
 XX  
 XX Claim 89; Page 92; 200pp; English.  
 XX  
 XX The invention relates to a nucleic acid molecule which down regulates  
 CC expression of a CD20 gene and a nucleic acid molecule which down  
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The  
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule  
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or  
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA  
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
 CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
 CC the cell and treat a patient having a condition associated with the level  
 CC of CD20. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
 CC lymphoma (MCL), immunocytooma (IMC), small B-cell lymphocytic lymphoma,  
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-  
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the  
 CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the  
 CC cell and treat a patient having a condition associated with the level of  
 CC NOGO. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to  
 CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),

CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NOGO expression. The present  
 CC sequence is a substrate sequence for a nucleic acid of the invention  
 CC based on the human NOGO sequence  
 XX  
 SQ Sequence 37 BP; 8 A; 9 C; 12 G; 0 T; 8 U; 0 Other;  
 Query Match 65.0%; Score 15.6; DB 4; Length 37;  
 Best Local Similarity 72.7%; Pred. No. 1.8e+03;  
 Matches 16; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 AGCGGAGTGATGGCAAGCAGA 23  
 ||||| :||:|||||  
 DB 2 AGCGUAUGAUGGCAUGACACUA 23  
 ||||| :||:|||||  
 RESULT 39  
 ABK05401  
 ID ABK05401 standard; RNA; 37 BP.  
 XX  
 AC ABK05401;  
 XX  
 XX 12-MAR-2002 (first entry)  
 XX  
 XX Human NOGO G-Cleaver substrate sequence #64.  
 XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;  
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;  
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
 KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;  
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
 KW MCL; immunocytooma; IMC; immune thrombocytopaenia; stroke; dementia;  
 KW inflammatory arthropathy; central nervous system injury;  
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
 KW Parkinson's disease; ataxia; Huntington's disease; substrate sequence;  
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX WO200159103-A2.  
 XX  
 XX 16-AUG-2001.  
 XX  
 XX 09-FEB-2001; 2001WO-US004273.  
 XX  
 XX 11-FEB-2000; 2000US-0181797P.  
 XX 28-FEB-2000; 2000US-0185516P.  
 XX 06-MAR-2000; 2000US-0187128P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (CHOW/) CHOWRIRA B M.  
 XX  
 XX Blatt L, Mcswiggen J, Chowrira BM;  
 XX WPI; 2001-607195/69.  
 XX  
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
 PT constructs, which down regulate expression of a CD20 gene or neurite  
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
 PT central nervous system injury.  
 XX  
 XX Claim 89; Page 93; 200pp; English.  
 XX  
 XX The invention relates to a nucleic acid molecule which down regulates  
 CC expression of a CD20 gene and a nucleic acid molecule which down  
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The  
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule  
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or  
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA  
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
 CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
 CC the cell and treat a patient having a condition associated with the level  
 CC of CD20. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
 CC lymphoma (MCL), immunocytooma (IMC), small B-cell lymphocytic lymphoma,  
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-  
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the  
 CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the  
 CC cell and treat a patient having a condition associated with the level of  
 CC NOGO. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to  
 CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),

CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving a an RNA molecule  
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NIN motif) pr  
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA  
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
 CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
 CC the cell and treat a patient having a condition associated with the level  
 CC of CD20. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-  
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the  
 CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the  
 CC cell and treat a patient having a condition associated with the level of  
 CC NOGO. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to  
 CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NOGO expression. The present  
 CC sequence is a substrate sequence for a nucleic acid of the invention  
 CC based on the human NOGO sequence

XX Sequence 37 BP; 11 A; 6 C; 12 G; 0 T; 8 U; 0 Other;

Query Match 65.0%; Score 15.6; DB 4; Length 37;

Best Local Similarity 72.7%; Pred. No. 1.8e+03;

Matches 16; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 AGCGAGTGTATGGCAAGCACA 23

DB 2 AGAGAAGUGAUGGCAUGCACUA 23

RESULT 40

ABK05385

ID ABK05385 standard; RNA; 37 BP.

AC ABK05385;

XX

DT 12-MAR-2002 (first entry)

XX

DE Human NOGO G-Cleaver substrate sequence #48.

XX

Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;  
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;  
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
 KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;  
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;  
 KW inflammatory arthropathy; central nervous system injury;  
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
 KW Parkinson's disease; ataxia; Huntington's disease; substrate sequence;  
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

OS Homo sapiens.

OS Synthetic.

XX

PN WO200159103-A2.

XX

PD 16-AUG-2001.

XX

PF 09-FEB-2001; 2001WO-US004273.

XX

PR 11-FEB-2000; 2000US-0181797P.  
 PR 26-FEB-2000; 2000US-0185516P.  
 PR 06-MAR-2000; 2000US-0187128P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (CHOW/) CHOWRIRA B M.

XX Blatt L, Mcswiggen J, Chowrira BM;

PI WPI; 2001-607195/69.

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense

PT constructs, which down regulate expression of a CD20 gene or neurite

PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and

PT central nervous system injury.

XX Claim 89; Page 92; 200pp; English.

CC The invention relates to a nucleic acid molecule which down regulates  
 CC expression of a CD20 gene and a nucleic acid molecule which down  
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The  
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving a an RNA molecule  
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NIN motif) pr  
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA  
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
 CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
 CC the cell and treat a patient having a condition associated with the level  
 CC of CD20. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-  
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the  
 CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the  
 CC cell and treat a patient having a condition associated with the level of  
 CC NOGO. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to  
 CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NOGO expression. The present  
 CC sequence is a substrate sequence for a nucleic acid of the invention  
 CC based on the human NOGO sequence

XX Sequence 37 BP; 5 A; 7 C; 20 G; 0 T; 5 U; 0 Other;

Query Match 65.0%; Score 15.6; DB 4; Length 37;

Best Local Similarity 72.7%; Pred. No. 1.8e+03;

Matches 16; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 AGCGAGTGTATGGCAAGCACA 23

DB 2 AGGGGGGUGAUGGCAUGCACUA 23

Search completed: December 13, 2005, 13:34:14

Job time : 370.5 secs



Result No.	Score	Query %			DB	ID	Description
		Match	Length				
1	24	100.0	24	6	CS101222	Sequence CS101222	
2	18.2	75.8	37	6	AX2119953	Sequence AX2119953	
3	17.2	71.7	37	6	AX228569	Sequence AX228569	
4	16.6	69.2	37	6	AX2119916	Sequence AX2119916	
5	16.6	69.2	37	6	AX581664	Sequence AX581664	
6	16.2	67.5	37	6	AX2119924	Sequence AX2119924	
7	16.2	67.5	37	6	AX425032	Sequence AX425032	
8	15.8	65.8	36	6	AR335577	Sequence AR335577	
9	15.8	65.8	36	6	AR335598	Sequence AR335598	
10	15.8	65.8	36	6	AR436338	Sequence AR436338	
11	15.8	65.8	37	6	AX2119985	Sequence AX2119985	
12	15.8	65.8	37	6	AX223033	Sequence AX223033	
13	15.8	65.8	37	6	AX228555	Sequence AX228555	
14	15.8	65.8	37	6	AX581654	Sequence AX581654	
15	15.8	65.8	37	6	AX581688	Sequence AX581688	
16	15.8	65.8	37	6	AX581711	Sequence AX581711	
17	15.6	65.0	37	6	AX2119943	Sequence AX2119943	
18	15.6	65.0	37	6	AX2119952	Sequence AX2119952	

other sequences; artificial sequences.

1  
**REFERENCE**  
**AUTHORS** Blatt, L., McSwiggen, J. and Chowrira, B.M.  
**TITLE** Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression  
**JOURNAL** Patent: WO 0159103-A 5395 16-AUG-2001;  
 RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
 McSwiggen, James (US) ; Chowrira, Bharat M. (US)

**FEATURES**  
 source  
 1. .37  
 /organism="synthetic construct"  
 /mol\_type="unassigned RNA"  
 /db\_xref="taxon:32630"  
 /note="Nucleic Acid"

**ORIGIN**

Query Match 75.8%; Score 18.2; DB 6; Length 37;  
 Best Local Similarity 87.0%; Pred. No. 2e+03;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAGCGAGTGTGGCAAGCAGCA 23  
 ||| ||||| ||||| ||||| |||||  
 Db 1 CAGAGGAGTGTGGCATGCACTA 23

**RESULT 3**  
**LOCUS** AX228569 37 bp RNA linear PAT 10-SEP-2001.  
**DEFINITION** Sequence 1941 from Patent WO0157206.  
**ACCESSION** AX228569  
**VERSION** AX228569.1 GI:15557710  
**KEYWORDS**  
 .  
**SOURCE** synthetic construct  
**ORGANISM** synthetic construct  
 other sequences; artificial sequences.

**REFERENCE**  
 1  
**AUTHORS** Fattaey, A.R., Jarvis, T., McSwiggen, J., Booher, R.N. and Holman, P.S.  
**TITLE** Method and reagent for the inhibition of checkpoint kinase-1 (chk 1) enzyme  
**JOURNAL** Patent: WO 0157206-A 1941 09-AUG-2001;  
 RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)

**FEATURES**  
 source  
 1. .37  
 /organism="synthetic construct"  
 /mol\_type="unassigned RNA"  
 /db\_xref="taxon:32630"

**ORIGIN**

Query Match 71.7%; Score 17.2; DB 6; Length 37;  
 Best Local Similarity 86.4%; Pred. No. 5.9e+03;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AGCGGAGTGTGGCAAGCAGCA 23  
 ||| ||||| ||||| ||||| |||||  
 Db 2 AGAGGAGTGTGGCATGCACTA 23

**RESULT 4**  
**LOCUS** AX219916 37 bp RNA linear PAT 07-SEP-2001  
**DEFINITION** Sequence 5358 from Patent WO0159103.  
**ACCESSION** AX219916  
**VERSION** AX219916.1 GI:15547640  
**KEYWORDS**  
 .  
**SOURCE** synthetic construct  
**ORGANISM** synthetic construct  
 other sequences; artificial sequences.

**REFERENCE**  
 1  
**AUTHORS** Blatt, L., McSwiggen, J. and Chowrira, B.M.  
**TITLE** Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression  
**JOURNAL** Patent: WO 0159103-A 5358 16-AUG-2001;  
 RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;

**FEATURES**  
 source  
 1. .37  
 /organism="synthetic construct"  
 /mol\_type="unassigned RNA"  
 /db\_xref="taxon:32630"  
 /note="Nucleic Acid"

**ORIGIN**

Query Match 69.2%; Score 16.6; DB 6; Length 37;  
 Best Local Similarity 82.6%; Pred. No. 1.1e+04;  
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGTGGCAAGCAGCA 23  
 ||| ||||| ||||| ||||| |||||  
 Db 1 CAGGGCGGTGATGCATGCACTA 23

**RESULT 5**  
**LOCUS** AX581664 37 bp RNA linear PAT 10-JAN-2003  
**DEFINITION** Sequence 3502 from Patent WO0211674.  
**ACCESSION** AX581664  
**VERSION** AX581664.1 GI:27653474  
**KEYWORDS**  
 .  
**SOURCE** synthetic construct  
**ORGANISM** synthetic construct  
 other sequences; artificial sequences.

**REFERENCE**  
 1  
**AUTHORS** Thompson, J., McSwiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E. and Grupe, A.  
**TITLE** Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)  
**JOURNAL** Patent: WO 0211674-A 3502 14-FEB-2002;  
 RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;  
 Thompson, James (US)

**FEATURES**  
 source  
 1. .37  
 /organism="synthetic construct"  
 /mol\_type="unassigned RNA"  
 /db\_xref="taxon:32630"  
 /note="Enzymatic Nucleic Acid"

**ORIGIN**

Query Match 69.2%; Score 16.6; DB 6; Length 37;  
 Best Local Similarity 82.6%; Pred. No. 1.1e+04;  
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAGCGGAGTGTGGCAAGCAGCA 23  
 ||| ||||| ||||| ||||| |||||  
 Db 1 CAGGGTAGTGATGCATGCACTA 23

**RESULT 6**  
**LOCUS** AX219924 37 bp RNA linear PAT 07-SEP-2001  
**DEFINITION** Sequence 5366 from Patent WO0159103.  
**ACCESSION** AX219924  
**VERSION** AX219924.1 GI:15547648  
**KEYWORDS**  
 .  
**SOURCE** synthetic construct  
**ORGANISM** synthetic construct  
 other sequences; artificial sequences.

**REFERENCE**  
 1  
**AUTHORS** Blatt, L., McSwiggen, J. and Chowrira, B.M.  
**TITLE** Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression  
**JOURNAL** Patent: WO 0159103-A 5366 16-AUG-2001;  
 RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
 McSwiggen, James (US) ; Chowrira, Bharat M. (US)

**FEATURES**  
 source  
 1. .37  
 /organism="synthetic construct"

```
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

ORIGIN
Query Match          67.5%; Score 16.2; DB 6; Length 37;
Best Local Similarity 85.7%; Pred. No. 1.7e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  3 GCGGAGTGATGGCAAGCAGCA 23
    |||||
Db   3 GCGGAGTGATGGCATGCACTA 23
    |||||

RESULT 7
AX425032          37 bp RNA linear PAT 18-JUN-2002
LOCUS
DEFINITION
Sequence 3368 from Patent WO0188124.
ACCESSION
AX425032
VERSION
AX425032.1 GI:21528414
KEYWORDS
.
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1 Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and
  Randi,A.M.
TITLE
Method and reagent for the inhibition of erg
JOURNAL
PATENT: WO 0188124-A 3368 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
1. .37
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"

ORIGIN
Query Match          67.5%; Score 16.2; DB 6; Length 37;
Best Local Similarity 85.7%; Pred. No. 1.7e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  3 GCGGAGTGATGGCAAGCAGCA 23
    |||||
Db   3 GCGTAGTGATGGCATGCACTA 23
    |||||

RESULT 8
AR335577          36 bp RNA linear PAT 17-AUG-2003
LOCUS
DEFINITION
Sequence 12979 from patent US 6566127.
ACCESSION
AR335577
VERSION
AR335577.1 GI:33721385
KEYWORDS
.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 36)
AUTHORS
Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL
Patent: US 6566127-A 12979 20-MAY-2003;
Ribozyne Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO
FEATURES
source
1. .36
/organism="unknown"
/mol_type="unassigned RNA"

ORIGIN
Query Match          65.8%; Score 15.8; DB 6; Length 36;
Best Local Similarity 89.5%; Pred. No. 2.6e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  5 GCGAGTGATGGCAAGCAGCA 23
    |||||
Db   2 GCGAGTGATGGCATGCACTA 20
    |||||

RESULT 9
AR335598          36 bp RNA linear PAT 17-AUG-2003
LOCUS
DEFINITION
Sequence 13000 from patent US 6566127.
ACCESSION
AR335598
VERSION
AR335598.1 GI:33721406
KEYWORDS
.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 36)
AUTHORS
Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL
Patent: US 6566127-A 13000 20-MAY-2003;
Ribozyne Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO
FEATURES
source
1. .36
/organism="unknown"
/mol_type="unassigned RNA"

ORIGIN
Query Match          65.8%; Score 15.8; DB 6; Length 36;
Best Local Similarity 89.5%; Pred. No. 2.6e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  5 GCGAGTGATGGCAAGCAGCA 23
    |||||
Db   2 GCGAGTGATGGCATGCACTA 20
    |||||

RESULT 10
AR436338          36 bp RNA linear PAT 18-DEC-2003
LOCUS
DEFINITION
Sequence 597 from patent US 6656731.
ACCESSION
AR436338
VERSION
AR436338.1 GI:40199422
KEYWORDS
.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 36)
AUTHORS
Eckstein,F., Ludwig,J. and Beigelman,L.
TITLE
Nucleic acid catalysts with endonuclease activity
JOURNAL
Patent: US 6656731-A 597 02-DEC-2003;
Max Planck Gesellschaft zur Forderung der Wissenschaften E.V. and
Sirna Therapeutics; Munich;
DEX;
FEATURES
Location/Qualifiers
source
1. .36
/organism="unknown"
/mol_type="unassigned RNA"

ORIGIN
Query Match          65.8%; Score 15.8; DB 6; Length 36;
Best Local Similarity 89.5%; Pred. No. 2.6e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  5 GCGAGTGATGGCAAGCAGCA 23
    |||||
Db   2 GCGAGTGATGGCATGCACTA 20
    |||||

RESULT 11
AX219985          37 bp RNA linear PAT 07-SEP-2001
LOCUS
DEFINITION
Sequence 5427 from Patent WO0159103.
ACCESSION
AX219985
```

```

VERSION      AX219985.1  GI:15547709
KEYWORDS     .
SOURCE       synthetic construct
ORGANISM     other sequences; artificial sequences.
REFERENCE    1
AUTHORS      Blatt L., McSwiggen,J. and Chowrira,B.M.
TITLE        Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL      nogo gene expression
              Patent: WO 0159103-A 5427 16-AUG-2001;
              RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
              McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES     Location/Qualifiers
              source
                1..37
                /organism="synthetic construct"
                /mol_type="unassigned RNA"
                /db_xref="taxon:32630"
                /note="Nucleic Acid"
ORIGIN
Query Match      65.8%; Score 15.8; DB 6; Length 37;
Best Local Similarity 89.5%; Pred. No. 2.6e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GGAGTGATGGCAAGCACGA 23
    |||||
Db 5 GGAGTGATGGCATGCACTA 23

RESULT 12
AX223033      AX223033      37 bp  RNA      linear      PAT 07-SEP-2001
LOCUS         Sequence 8475 from Patent WO0159103.
DEFINITION    AX223033
ACCESSION     AX223033
VERSION       AX223033.1  GI:15550757
KEYWORDS      .
SOURCE        synthetic construct
ORGANISM      synthetic construct
              other sequences; artificial sequences.
REFERENCE     1
AUTHORS       Blatt L., McSwiggen,J. and Chowrira,B.M.
TITLE         Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL       nogo gene expression
              Patent: WO 0159103-A 8475 16-AUG-2001;
              RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
              McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES      Location/Qualifiers
              source
                1..37
                /organism="synthetic construct"
                /mol_type="unassigned RNA"
                /db_xref="taxon:32630"
                /note="Nucleic Acid"
ORIGIN
Query Match      65.8%; Score 15.8; DB 6; Length 37;
Best Local Similarity 89.5%; Pred. No. 2.6e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GGAGTGATGGCAAGCACGA 23
    |||||
Db 5 GGAGTGATGGCATGCACTA 23

RESULT 13
AX228555      AX228555      37 bp  RNA      linear      PAT 10-SEP-2001
LOCUS         Sequence 1927 from Patent WO0157206.
DEFINITION    AX228555
ACCESSION     AX228555
VERSION       AX228555.1  GI:15557696
KEYWORDS      .
SOURCE        synthetic construct
ORGANISM      synthetic construct
              other sequences; artificial sequences.

```

```

REFERENCE     1
AUTHORS       Fattaey,A.R., Jarvis,T., Mcswiggen,J., Boher,R.N. and Holman,P.S.
TITLE         Method and reagent for the inhibition of checkpoint kinase-1 (chk
JOURNAL       1) enzyme
              Patent: WO 0157206-A 1927 09-AUG-2001;
              RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES      Location/Qualifiers
              source
                1..37
                /organism="synthetic construct"
                /mol_type="unassigned RNA"
                /db_xref="taxon:32630"
ORIGIN
Query Match      65.8%; Score 15.8; DB 6; Length 37;
Best Local Similarity 89.5%; Pred. No. 2.6e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GGAGTGATGGCAAGCACGA 23
    |||||
Db 5 GGAGTGATGGCATGCACTA 23

RESULT 14
AX581654      AX581654      37 bp  RNA      linear      PAT 10-JAN-2003
LOCUS         Sequence 3492 from Patent WO0211674.
DEFINITION    AX581654
ACCESSION     AX581654
VERSION       AX581654.1  GI:27653464
KEYWORDS      .
SOURCE        synthetic construct
ORGANISM      synthetic construct
              other sequences; artificial sequences.
REFERENCE     1
AUTHORS       Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
              and Grupe,A.
TITLE         Method and reagent for the inhibition of calcium activated chloride
JOURNAL       channel-1 (clca-1)
              Patent: WO 0211674-A 3492 14-FEB-2002;
              RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
              Thompson, James (US)
FEATURES      Location/Qualifiers
              source
                1..37
                /organism="synthetic construct"
                /mol_type="unassigned RNA"
                /db_xref="taxon:32630"
                /note="Enzymatic Nucleic Acid"
ORIGIN
Query Match      65.8%; Score 15.8; DB 6; Length 37;
Best Local Similarity 89.5%; Pred. No. 2.6e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GGAGTGATGGCAAGCACGA 23
    |||||
Db 5 GGAGTGATGGCATGCACTA 23

RESULT 15
AX581688      AX581688      37 bp  RNA      linear      PAT 10-JAN-2003
LOCUS         Sequence 3526 from Patent WO0211674.
DEFINITION    AX581688
ACCESSION     AX581688
VERSION       AX581688.1  GI:27653498
KEYWORDS      .
SOURCE        synthetic construct
ORGANISM      synthetic construct
              other sequences; artificial sequences.
REFERENCE     1
AUTHORS       Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
              and Grupe,A.
TITLE         Method and reagent for the inhibition of calcium activated chloride
JOURNAL       channel-1 (clca-1)
              Patent: WO 0211674-A 3526 14-FEB-2002;

```

FEATURES  
source  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;  
Thompson, James (US)  
Location/Qualifiers  
1. .37  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Enzymatic Nucleic Acid"

ORIGIN  
Query Match 65.8%; Score 15.8; DB 6; Length 37;  
Best Local Similarity 89.5%; Pred. No. 2.6e+04;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCACGA 23  
|||||  
Db 5 GGAGTGATGGCATGCACTA 23

RESULT 16  
AX581711  
LOCUS AX581711 37 bp RNA linear PAT 10-JAN-2003  
DEFINITION Sequence 3549 from Patent WO0211674.  
ACCESSION AX581711  
VERSION AX581711.1 GI:27653521  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Thompson, J., McSwiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.  
and Grupe, A.  
TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (cica-1)  
JOURNAL Patent: WO 0211674-A 3549 14-FEB-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;  
Thompson, James (US)  
FEATURES  
source  
Location/Qualifiers  
1. .37  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Enzymatic Nucleic Acid"

ORIGIN  
Query Match 65.8%; Score 15.8; DB 6; Length 37;  
Best Local Similarity 89.5%; Pred. No. 2.6e+04;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GGAGTGATGGCAAGCACGA 23  
|||||  
Db 5 GGAGTGATGGCATGCACTA 23

RESULT 17  
AX219943  
LOCUS AX219943 37 bp RNA linear PAT 07-SEP-2001  
DEFINITION Sequence 5385 from Patent WO0159103.  
ACCESSION AX219943  
VERSION AX219943.1 GI:15547667  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression  
JOURNAL Patent: WO 0159103-A 5385 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
McSwiggen, James (US) ; Chowrira, Bharat M. (US)  
FEATURES  
source  
Location/Qualifiers  
1. .37

ORIGIN  
Query Match 65.0%; Score 15.6; DB 6; Length 37;  
Best Local Similarity 81.8%; Pred. No. 3.2e+04;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AGCGGAGTGATGGCAAGCACGA 23  
|||||  
Db 2 AGCGGGGTGATGGCATGCACTA 23

RESULT 18  
AX219952  
LOCUS AX219952 37 bp RNA linear PAT 07-SEP-2001  
DEFINITION Sequence 5394 from Patent WO0159103.  
ACCESSION AX219952  
VERSION AX219952.1 GI:15547676  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression  
JOURNAL Patent: WO 0159103-A 5394 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
McSwiggen, James (US) ; Chowrira, Bharat M. (US)  
FEATURES  
source  
Location/Qualifiers  
1. .37  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"

ORIGIN  
Query Match 65.0%; Score 15.6; DB 6; Length 37;  
Best Local Similarity 81.8%; Pred. No. 3.2e+04;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AGCGGAGTGATGGCAAGCACGA 23  
|||||  
Db 2 AGCGTATTGATGGCATGCACTA 23

RESULT 19  
AX219959  
LOCUS AX219959 37 bp RNA linear PAT 07-SEP-2001  
DEFINITION Sequence 5401 from Patent WO0159103.  
ACCESSION AX219959  
VERSION AX219959.1 GI:15547683  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression  
JOURNAL Patent: WO 0159103-A 5401 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
McSwiggen, James (US) ; Chowrira, Bharat M. (US)  
FEATURES  
source  
Location/Qualifiers  
1. .37  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"

ORIGIN

Query Match 65.0%; Score 15.6; DB 6; Length 37;  
Best Local Similarity 81.8%; Pred. No. 3.2e+04;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AGCGAGTGATGGCAAGCACGA 23  
||| ||||| ||||| |||||  
Db 2 AGAGAGTGATGGCATGCACTA 23

RESULT 20  
AR335309  
LOCUS AR335309 36 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 12711 from patent US 6566127.  
ACCESSION AR335309  
VERSION AR335309.1 GI:33721117  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
UNCLASSIFIED.

REFERENCE 1 (bases 1 to 36)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 12711 20-MAY-2003;  
Ribozyne Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO  
FEATURES  
source  
1..36  
/organism="unknown"  
/mol\_type="unassigned RNA"

## ORIGIN

Query Match 63.3%; Score 15.2; DB 6; Length 36;  
Best Local Similarity 85.0%; Pred. No. 4.9e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CGGAGTGATGGCAAGCACGA 23  
| | | | | | | | | | | | | | | |  
Db 1 CTGAGTGATGGCATGCACTA 20

RESULT 21  
AR335323  
LOCUS AR335323 36 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 12725 from patent US 6566127.  
ACCESSION AR335323  
VERSION AR335323.1 GI:33721131  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
UNCLASSIFIED.

REFERENCE 1 (bases 1 to 36)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 12725 20-MAY-2003;  
Ribozyne Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO  
FEATURES  
source  
1..36  
/organism="unknown"  
/mol\_type="unassigned RNA"

## ORIGIN

Query Match 63.3%; Score 15.2; DB 6; Length 36;  
Best Local Similarity 85.0%; Pred. No. 4.9e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CGGAGTGATGGCAAGCACGA 23  
| | | | | | | | | | | | | | | |  
Db 1 CTGAGTGATGGCATGCACTA 20

## RESULT 22

AR336775  
LOCUS AR336775 36 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 14177 from patent US 6566127.  
ACCESSION AR336775  
VERSION AR336775.1 GI:33722583  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
UNCLASSIFIED.

REFERENCE 1 (bases 1 to 36)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 14177 20-MAY-2003;  
Ribozyne Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO  
FEATURES  
source  
1..36  
/organism="unknown"  
/mol\_type="unassigned RNA"

## ORIGIN

Query Match 63.3%; Score 15.2; DB 6; Length 36;  
Best Local Similarity 85.0%; Pred. No. 4.9e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CGGAGTGATGGCAAGCACGA 23  
| | | | | | | | | | | | | | | |  
Db 1 CTGAGTGATGGCATGCACTA 20

## RESULT 23

AR336798  
LOCUS AR336798 36 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 14200 from patent US 6566127.  
ACCESSION AR336798  
VERSION AR336798.1 GI:33722606  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
UNCLASSIFIED.

REFERENCE 1 (bases 1 to 36)  
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor  
JOURNAL Patent: US 6566127-A 14200 20-MAY-2003;  
Ribozyne Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO  
FEATURES  
source  
1..36  
/organism="unknown"  
/mol\_type="unassigned RNA"

## ORIGIN

Query Match 63.3%; Score 15.2; DB 6; Length 36;  
Best Local Similarity 85.0%; Pred. No. 4.9e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CGGAGTGATGGCAAGCACGA 23  
| | | | | | | | | | | | | | | |  
Db 1 CTGAGTGATGGCATGCACTA 20

## RESULT 24

AR436566  
LOCUS AR436566 36 bp RNA linear PAT 18-DEC-2003  
DEFINITION Sequence 825 from patent US 6656731.  
ACCESSION AR436566  
VERSION AR436566.1 GI:40199650  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
UNCLASSIFIED.

REFERENCE 1 (bases 1 to 36)  
AUTHORS Eckstein,F., Ludwig,J. and Beigelman,L.

TITLE Nucleic acid catalysts with endonuclease activity  
JOURNAL Patent: US 6656731-A 825 02-DEC-2003;  
Max Planck Gesellschaft zur Forderung der Wissenschaften E.V. and  
Sirna Therapeutics; Munich;  
DEX;

FEATURES source Location/Qualifiers  
1. .36  
/organism="unknown"  
/mol\_type="unassigned RNA"

ORIGIN  
Query Match 63.3%; Score 15.2; DB 6; Length 36;  
Best Local Similarity 85.0%; Pred. No. 4.9e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CGGAGTGATGGCAAGCACGA 23  
||| ||||| ||||| |||||  
Db 1 CGTAGTGATGGCATGCACTA 20

RESULT 25  
LOCUS AR436755 36 bp RNA linear PAT 18-DEC-2003  
DEFINITION Sequence 1014 from patent US 6656731.  
ACCESSION AR436755  
VERSION AR436755.1 GI:40199839  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 36)  
AUTHORS Eckstein, F., Ludwig, J. and Beigelman, L.  
TITLE Nucleic acid catalysts with endonuclease activity  
JOURNAL Patent: US 6656731-A 1014 02-DEC-2003;  
Max Planck Gesellschaft zur Forderung der Wissenschaften E.V. and  
Sirna Therapeutics; Munich;  
DEX;

FEATURES source Location/Qualifiers  
1. .36  
/organism="unknown"  
/mol\_type="unassigned RNA"

ORIGIN  
Query Match 63.3%; Score 15.2; DB 6; Length 36;  
Best Local Similarity 85.0%; Pred. No. 4.9e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CGGAGTGATGGCAAGCACGA 23  
||| ||||| ||||| |||||  
Db 1 CGGGGTGATGGCATGCACTA 20

RESULT 26  
LOCUS AX219922 37 bp RNA linear PAT 07-SEP-2001  
DEFINITION Sequence 5364 from Patent WO0159103.  
ACCESSION AX219922  
VERSION AX219922.1 GI:15547646  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and  
nogo gene expression  
JOURNAL Patent: WO 0159103-A 5364 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);  
McSwiggen, James (US); Chowrira, Bharat M. (US)  
Location/Qualifiers  
1. .37  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"

FEATURES source

/db\_xref="taxon:32630"  
/note="Nucleic Acid"

ORIGIN  
Query Match 63.3%; Score 15.2; DB 6; Length 37;  
Best Local Similarity 85.0%; Pred. No. 4.9e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CGGAGTGATGGCAAGCACGA 23  
||| ||||| ||||| |||||  
Db 4 CGGGGTGATGGCATGCACTA 23

RESULT 27  
LOCUS AX219925 37 bp RNA linear PAT 07-SEP-2001  
DEFINITION Sequence 5367 from Patent WO0159103.  
ACCESSION AX219925  
VERSION AX219925.1 GI:15547649  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and  
nogo gene expression  
JOURNAL Patent: WO 0159103-A 5367 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);  
McSwiggen, James (US); Chowrira, Bharat M. (US)  
Location/Qualifiers  
1. .37  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"

FEATURES source

ORIGIN  
Query Match 63.3%; Score 15.2; DB 6; Length 37;  
Best Local Similarity 85.0%; Pred. No. 4.9e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CGGAGTGATGGCAAGCACGA 23  
||| ||||| ||||| |||||  
Db 4 CGGGGTGATGGCATGCACTA 23

RESULT 28  
LOCUS AX220062 37 bp RNA linear PAT 07-SEP-2001  
DEFINITION Sequence 5504 from Patent WO0159103.  
ACCESSION AX220062  
VERSION AX220062.1 GI:15547786  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and  
nogo gene expression  
JOURNAL Patent: WO 0159103-A 5504 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);  
McSwiggen, James (US); Chowrira, Bharat M. (US)  
Location/Qualifiers  
1. .37  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"

FEATURES source

ORIGIN  
Query Match 63.3%; Score 15.2; DB 6; Length 37;

```

Best Local Similarity 85.0%; Pred. No. 4.9e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CCGAGTGATGGCAAGCACA 23
Db 4 CCGGGTGATGGCATGCACTA 23
|||||

RESULT 29
AX228522
LOCUS AX228522 37 bp RNA linear PAT 10-SEP-2001
DEFINITION Sequence 1894 from Patent WO0157206.
ACCESSION AX228522
VERSION AX228522.1 GI:15557663
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Fattaey,A.R., Jarvis,T., Mcswiggen,J., Booher,R.N. and Holman,P.S.
TITLE Method and reagent for the inhibition of checkpoint kinase-1 (chk
1) enzyme
JOURNAL Patent: WO 0157206-A 1894 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES
source
1. 37
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 63.3%; Score 15.2; DB 6; Length 37;
Best Local Similarity 85.0%; Pred. No. 4.9e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CCGAGTGATGGCAAGCACA 23
Db 4 CCGAGTGATGGCATGCACTA 23
|||||

RESULT 30
AX228545
LOCUS AX228545 37 bp RNA linear PAT 10-SEP-2001
DEFINITION Sequence 1917 from Patent WO0157206.
ACCESSION AX228545
VERSION AX228545.1 GI:15557686
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Fattaey,A.R., Jarvis,T., Mcswiggen,J., Booher,R.N. and Holman,P.S.
TITLE Method and reagent for the inhibition of checkpoint kinase-1 (chk
1) enzyme
JOURNAL Patent: WO 0157206-A 1917 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES
source
1. 37
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 63.3%; Score 15.2; DB 6; Length 37;
Best Local Similarity 85.0%; Pred. No. 4.9e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CTGAGTGATGGCATGCACTA 23
Db 4 CTGAGTGATGGCATGCACTA 23
|||||

RESULT 31

```

```

AX424952
LOCUS AX424952 37 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 3288 from Patent WO0188124.
ACCESSION AX424952
VERSION AX424952.1 GI:21528334
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,P.G. and
Randi,A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 3288 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
1. 37
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"

ORIGIN
Query Match 63.3%; Score 15.2; DB 6; Length 37;
Best Local Similarity 85.0%; Pred. No. 4.9e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CCGAGTGATGGCAAGCACA 23
Db 4 CCGGGTGATGGCATGCACTA 23
|||||

RESULT 32
AX581615
LOCUS AX581615 37 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 3453 from Patent WO0211674.
ACCESSION AX581615
VERSION AX581615.1 GI:27653425
KEYWORDS .
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Thompson,J., Mcswiggen,J., McKenzie,T., Ayers,D., Szymkowski,D.E.
and Grupe,A.
TITLE Method and reagent for the inhibition of calcium activated chloride
channel-1 (clca-1)
JOURNAL Patent: WO 0211674-A 3453 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
FEATURES
source
1. 37
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"

ORIGIN
Query Match 63.3%; Score 15.2; DB 6; Length 37;
Best Local Similarity 85.0%; Pred. No. 4.9e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CCGAGTGATGGCAAGCACA 23
Db 4 CCGATTGATGGCATGCACTA 23
|||||

RESULT 33
AX219897
LOCUS AX219897 37 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 5339 from Patent WO0159103.
ACCESSION AX219897
VERSION AX219897.1 GI:15547621

```



AUTHORS	Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE	Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL	Patient: WO 0159103-A 5453 16-AUG-2001; RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES	Location/Qualifiers 1..37 /organism="synthetic construct" /mol_type="unassigned RNA" /db_xref="taxon:32630" /note="Nucleic Acid"
SOURCE	
ORIGIN	
Query Match	62.5%; Score 15; DB 6; Length 37;
Best Local Similarity	78.3%; Pred. No. 6.1e+04;
Matches	18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY	1 CACGGGAGTGATGCCAAGCACGA 23 
DB	1 CACGGAAGTGATGGCATGCCTA 23 
RESULT 36	
AX220100	AX220100 37 bp RNA linear PAT 07-SEP-2001
LOCUS	Sequence 5542 from Patent W00159103.
DEFINITION	AX220100
ACCESSION	AX220100.1 GI:15547824
VERSION	
KEYWORDS	synthetic construct
SOURCE	synthetic construct
ORGANISM	other sequences; artificial sequences.
REFERENCE	1
AUTHORS	Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE	Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL	Patient: WO 0159103-A 5542 16-AUG-2001; RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES	Location/Qualifiers 1..37 /organism="synthetic construct" /mol_type="unassigned RNA" /db_xref="taxon:32630" /note="Nucleic Acid"
SOURCE	
ORIGIN	
Query Match	62.5%; Score 15; DB 6; Length 37;
Best Local Similarity	78.3%; Pred. No. 6.1e+04;
Matches	18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY	1 CACGGGAGTGATGCCAAGCACGA 23 
DB	1 CAGAGAATTGATGGCATGCCTA 23 
RESULT 37	
AX220111	AX220111 37 bp RNA linear PAT 07-SEP-2001
LOCUS	Sequence 5553 from Patent W00159103.
DEFINITION	AX220111
ACCESSION	AX220111.1 GI:15547835
VERSION	
KEYWORDS	synthetic construct
SOURCE	synthetic construct
ORGANISM	other sequences; artificial sequences.
REFERENCE	1
AUTHORS	Blatt, L., Mcswiggen, J. and Chowrira, B.M.
TITLE	Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL	Patient: WO 0159103-A 5553 16-AUG-2001; RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;

```

FEATURES
  source
    McSwiggen, James (US) ; Chowrira, Bharat M. (US)
    Location/Qualifiers
      1..37
        /organism="synthetic construct"
        /mol_type="unassigned RNA"
        /db_xref="taxon:32630"
        /note="Nucleic Acid"
ORIGIN
  Query Match      62.5%; Score 15; DB 6; Length 37;
  Best Local Similarity 78.3%; Pred. No. 6.1e+04;
  Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
  Qy 1 CAGCGAGTGATGGCAAGCAGCA 23
  Db 1 CAGCTTTGTGATGGCATGCACTA 23
  RESULT 38
  LOCUS AX220120 37 bp RNA linear PAT 07-SEP-2001
  DEFINITION Sequence 5562 from Patent WO0159103.
  ACCESSION AX220120
  VERSION AX220120.1 GI:15547844
  KEYWORDS
  SOURCE
    synthetic construct
    other sequences; artificial sequences.
  ORGANISM
  1
  REFERENCE
    1
  AUTHORS
    Blatt L., McSwiggen, J. and Chowrira, B.M.
  TITLE
    Method and reagent for the modulation and diagnosis of cd20 and
    nogo gene expression
  JOURNAL
    Patent: WO 0159103-A 5562 16-AUG-2001;
    RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
    McSwiggen, James (US) ; Chowrira, Bharat M. (US)
  FEATURES
    source
      1..37
        /organism="synthetic construct"
        /mol_type="unassigned RNA"
        /db_xref="taxon:32630"
        /note="Nucleic Acid"
ORIGIN
  Query Match      62.5%; Score 15; DB 6; Length 37;
  Best Local Similarity 78.3%; Pred. No. 6.1e+04;
  Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
  Qy 1 CAGCGAGTGATGGCAAGCAGCA 23
  Db 1 CAACAGTGTGATGGCATGCACTA 23
  RESULT 39
  LOCUS AX228609 37 bp RNA linear PAT 10-SEP-2001
  DEFINITION Sequence 1981 from Patent WO0157206.
  ACCESSION AX228609
  VERSION AX228609.1 GI:15557750
  KEYWORDS
  SOURCE
    synthetic construct
    other sequences; artificial sequences.
  ORGANISM
  1
  REFERENCE
    1
  AUTHORS
    Fattaey, A.R., Jarvis, T., McSwiggen, J., Booher, R.N. and Holman, P.S.
  TITLE
    Method and reagent for the inhibition of checkpoint kinase-1 (chk
    1) enzyme
  JOURNAL
    Patent: WO 0157206-A 1981 09-AUG-2001;
    RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
  FEATURES
    Location/Qualifiers
      1..37
        /organism="synthetic construct"
        /mol_type="unassigned RNA"
        /db_xref="taxon:32630"

```

```

ORIGIN
  Query Match      62.5%; Score 15; DB 6; Length 37;
  Best Local Similarity 78.3%; Pred. No. 6.1e+04;
  Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
  Qy 1 CAGCGAGTGATGGCAAGCAGCA 23
  Db 1 CATAGCAGTGATGGCATGCACTA 23
  RESULT 40
  LOCUS AX228610 37 bp RNA linear PAT 10-SEP-2001
  DEFINITION Sequence 1982 from Patent WO0157206.
  ACCESSION AX228610
  VERSION AX228610.1 GI:15557751
  KEYWORDS
  SOURCE
    synthetic construct
    other sequences; artificial sequences.
  ORGANISM
  1
  REFERENCE
    1
  AUTHORS
    Fattaey, A.R., Jarvis, T., McSwiggen, J., Booher, R.N. and Holman, P.S.
  TITLE
    Method and reagent for the inhibition of checkpoint kinase-1 (chk
    1) enzyme
  JOURNAL
    Patent: WO 0157206-A 1982 09-AUG-2001;
    RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
  FEATURES
    source
      1..37
        /organism="synthetic construct"
        /mol_type="unassigned RNA"
        /db_xref="taxon:32630"
ORIGIN
  Query Match      62.5%; Score 15; DB 6; Length 37;
  Best Local Similarity 78.3%; Pred. No. 6.1e+04;
  Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
  Qy 1 CAGCGAGTGATGGCAAGCAGCA 23
  Db 1 CAACATAGTGTGATGGCATGCACTA 23

```

Search completed: December 13, 2005, 14:11:38  
 Job time : 1118.5 secs



```
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 253506
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-253506
```

```
Query Match 61.7%; Score 14.8; DB 9; Length 19;
Best Local Similarity 77.8%; Pred. No. 4.1e+02;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 3 TGCACAGCTGGGGAACAA 20
Db 2 UGCACAGCUGGGGACAA 19
```

```
RESULT 3
US-11-101-244-126494
; Sequence 126494, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 126494
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-126494
```

```
Query Match 60.0%; Score 14.4; DB 8; Length 19;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 4 GCACAGCTGGGGAACA 19
Db 3 GCACAGCUGGGGGAAGA 18
```

```
RESULT 4
US-11-083-784-126494
; Sequence 126494, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
```

```
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 126494
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-126494
```

```
Query Match 60.0%; Score 14.4; DB 9; Length 19;
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 4 GCACAGCTGGGGAACA 19
Db 3 GCACAGCUGGGGGAAGA 18
```

```
RESULT 5
US-10-508-932-36/C
; Sequence 36, Application US/10508932
; Publication No. US20050260586A1
; GENERAL INFORMATION:
; APPLICANT: Medical College of Ohio
; APPLICANT: Willey, James C.
; APPLICANT: Weaver, David A.
; APPLICANT: Warner, Kristy A.
; APPLICANT: Graves, Timothy G.
; APPLICANT: Demuth, Jeffrey P.
; APPLICANT: Crawford, Erin L.
; TITLE OF INVENTION: Method and Compositions for the Diagnosis and Treatment of Non-Si.
; TITLE OF INVENTION: Lung Cancer Using Gene Expression Profiles
; FILE REFERENCE: 9050
; CURRENT APPLICATION NUMBER: US/10/508,932
; CURRENT FILING DATE: 2004-09-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-508-932-36
```

```
Query Match 60.0%; Score 14.4; DB 6; Length 42;
Best Local Similarity 75.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

```
QY 1 GATGACAGCTGGGGAACAAGACG 24
Db 37 GATGAGAGGAGGGGACCAAGAG 14
```

```
RESULT 6
US-11-101-244-314817
; Sequence 314817, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
```

; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 314817  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-314817

Query Match 59.2%; Score 14.2; DB 8; Length 19;  
Best Local Similarity 78.9%; Pred. No. 7.6e+02;  
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCACAGCTGGGGAACAAGA 22  
|||||||: |||||  
Db 1 GCACAGCTCAGGAACUAGA 19

RESULT 7  
US-11-083-784-314817  
; Sequence 314817, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmakon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 314817  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-314817

Query Match 59.2%; Score 14.2; DB 9; Length 19;  
Best Local Similarity 78.9%; Pred. No. 7.6e+02;  
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCACAGCTGGGGAACAAGA 22  
|||||||: |||||  
Db 1 GCACAGCTCAGGAACUAGA 19

RESULT 8  
US-11-101-244-253501  
; Sequence 253501, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmakon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin

; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 253501  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-253501

Query Match 57.5%; Score 13.8; DB 8; Length 19;  
Best Local Similarity 82.4%; Pred. No. 1.2e+03;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GCACAGCTGGGGAACAA 20  
|||||||: |||||  
Db 1 GCACAGCTCAGGAGGACAA 17

RESULT 9  
US-11-101-244-452572  
; Sequence 452572, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmakon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 452572  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-452572

Query Match 57.5%; Score 13.8; DB 8; Length 19;  
Best Local Similarity 82.4%; Pred. No. 1.2e+03;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GCACAGCTGGGGAACAA 20  
|||||||: |||||  
Db 3 GCACAGCTCAGGAGGACAA 19

RESULT 10  
US-11-101-244-452581  
; Sequence 452581, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmakon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William

```

; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 452581
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-452581

```

```

Query Match      57.5%; Score 13.8; DB 8; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      4 GCACAGCTGGGGAACAA 20
      |||||:|||||
Db      1 GCACAGCUGGUAUCAA 17

```

```

RESULT 11
US-11-101-244-639666
; Sequence 639666, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 639666
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-639666

```

```

Query Match      57.5%; Score 13.8; DB 8; Length 19;
Best Local Similarity 76.5%; Pred. No. 1.2e+03;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      3 TGCACAGCTGGGGAACA 19
      |||||:|||||
Db      2 UGCACACUGGAGAACAA 18

```

```

RESULT 12
US-11-101-244-940716
; Sequence 940716, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen

```

```

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 940716
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-940716

```

```

Query Match      57.5%; Score 13.8; DB 8; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      6 ACAGCTGGGGAACAAGA 22
      |||||:|||||
Db      2 AAAGCUGAGGAACAAGA 18

```

```

RESULT 13
US-11-101-244-940758
; Sequence 940758, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 940758
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-940758

```

```

Query Match      57.5%; Score 13.8; DB 8; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      6 ACAGCTGGGGAACAAGA 22
      |||||:|||||
Db      3 AAAGCUGAGGAACAAGA 19

```

```

RESULT 14
US-11-101-244-987947
; Sequence 987947, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA

```

```
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 987947
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-987947
```

```
Query Match 57.5%; Score 13.8; DB 8; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 6 ACAGCTGGGGGAACAGA 22
    |||||:|||||
Db 3 ACAGCUGGUAUAAGA 19
```

```
RESULT 15
US-11-083-784-253501
; Sequence 253501, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 253501
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-253501
```

```
Query Match 57.5%; Score 13.8; DB 9; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 4 GCACAGCTGGGGGAACAA 20
    |||||:|||||
Db 1 GCACAGCUGAGGGACAA 17
```

```
RESULT 16
US-11-083-784-452572
; Sequence 452572, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
```

```
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 452572
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-452572
```

```
Query Match 57.5%; Score 13.8; DB 9; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 4 GCACAGCTGGGGGAACAA 20
    |||||:|||||
Db 3 GCACAGCUGGUAUCAA 19
```

```
RESULT 17
US-11-083-784-452581
; Sequence 452581, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 452581
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-452581
```

```
Query Match 57.5%; Score 13.8; DB 9; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 4 GCACAGCTGGGGGAACAA 20
    |||||:|||||
Db 1 GCACAGCUGGUAUCAA 17
```

```
RESULT 18
US-11-083-784-639666
; Sequence 639666, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
```

```
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 639666
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-639666
```

```
Query Match 57.5%; Score 13.8; DB 9; Length 19;
Best Local Similarity 76.5%; Pred. No. 1.2e+03;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 3 TGCACAGCTGGGGAACA 19
   :|||||:|||||
Db 2 UGCACACCTUGGAGACA 18
```

## RESULT 19

```
US-11-083-784-940716
; Sequence 940716, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 940716
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-940716
```

```
Query Match 57.5%; Score 13.8; DB 9; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 6 ACAGCTGGGGAACAAGA 22
   :|||||:|||||
Db 2 AAAGCUGAGGACACA 18
```

## RESULT 20

```
US-11-083-784-940758
; Sequence 940758, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 940758
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-940758
```

```
Query Match 57.5%; Score 13.8; DB 9; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 6 ACAGCTGGGGAACAAGA 22
   :|||||:|||||
Db 3 AAAGCUGAGGACACA 19
```

## RESULT 21

```
US-11-083-784-987947
; Sequence 987947, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 987947
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-987947
```

```
Query Match 57.5%; Score 13.8; DB 9; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.2e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 6 ACAGCTGGGGAACAAGA 22
   :|||||:|||||
Db 3 ACAGCUGGGAUAAAGA 19
```

## RESULT 22

```
US-10-770-726-10883/c
```



```
; Sequence 10883, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/107707,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10883
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-770-726-10883

Query Match      56.7%; Score 13.6; DB 6; Length 21;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      3  TGCACAGCTGGGGAACAAGA 22
Db      20  TCCACAGCTGTGGAATATA 1

RESULT 23
US-11-101-244-387702
; Sequence 387702, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 1349US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 387702
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-387702

Query Match      55.8%; Score 13.4; DB 8; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.7e+03;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      5  CACAGCTGGGGAACA 19
Db      4  CACAGCUGGUGAACA 18

RESULT 24
US-11-101-244-387807
; Sequence 387807, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 1349US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 387807
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-387807

Query Match      55.8%; Score 13.4; DB 8; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.7e+03;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      5  CACAGCTGGGGAACA 19
Db      4  CACAGCUGGUGAACA 18

RESULT 25
US-11-101-244-387902
; Sequence 387902, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 1349US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 387902
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-387902

Query Match      55.8%; Score 13.4; DB 8; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.7e+03;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      5  CACAGCTGGGGAACA 19
Db      4  CACAGCUGGUGAACA 18

RESULT 26
US-11-101-244-503486
; Sequence 503486, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 1349US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 503486
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-503486

Query Match      55.8%; Score 13.4; DB 8; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.7e+03;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      5  CACAGCTGGGGAACA 19
Db      4  CACAGCUGGUGAACA 18
```

```
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 503486
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-503486
```

```
Query Match 55.8%; Score 13.4; DB 8; Length 19;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 TGACAGCTGGGCAA 17
    |||||:|||||
Db 2 UGCACGCGUGGAGAA 16
```

```
RESULT 27
US-11-083-784-387702
; Sequence 387702, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 387702
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-387702
```

```
Query Match 55.8%; Score 13.4; DB 9; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.7e+03;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 5 CACAGCTGGGGAACA 19
    |||||:|||||
Db 4 CACAGCUGGUGAACA 18
```

```
RESULT 28
US-11-083-784-387807
; Sequence 387807, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
```

```
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 387807
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-387807
```

```
Query Match 55.8%; Score 13.4; DB 9; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.7e+03;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 5 CACAGCTGGGGAACA 19
    |||||:|||||
Db 4 CACAGCUGGUGAACA 18
```

```
RESULT 29
US-11-083-784-387902
; Sequence 387902, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 387902
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-387902
```

```
Query Match 55.8%; Score 13.4; DB 9; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.7e+03;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 5 CACAGCTGGGGAACA 19
    |||||:|||||
Db 4 CACAGCUGGUGAACA 18
```

```
RESULT 30
US-11-083-784-503486
; Sequence 503486, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
```

; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/083,784  
 ; CURRENT FILING DATE: 2005-03-18  
 ; PRIOR APPLICATION NUMBER: US/10/714,333  
 ; PRIOR FILING DATE: 2003-11-14  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 503486  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 ; US-11-083-784-503486

Query Match 55.8%; Score 13.4; DB 9; Length 19;  
 Best Local Similarity 80.0%; Pred. No. 1.7e+03;  
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TGCACAGCTGGGGAA 17  
 :|||||:||||  
 Db 2 UGCACAGCUGGAGAA 16

RESULT 31  
 US-11-101-244-92175/c  
 ; Sequence 92175, Application US/11101244  
 ; Publication No. US20050246794A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmakon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/101,244  
 ; CURRENT FILING DATE: 2005-04-07  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 92175  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 ; US-11-101-244-92175

Query Match 55.0%; Score 13.2; DB 8; Length 19;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+03;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 ACAGCTGGGGAAACAAGAC 23  
 :|||||:|||||  
 Db 19 AAATCTGGGAAACAAGAC 2

RESULT 32  
 US-11-101-244-624295  
 ; Sequence 624295, Application US/11101244  
 ; Publication No. US20050246794A1  
 ; GENERAL INFORMATION:

; APPLICANT: Dharmakon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/101,244  
 ; CURRENT FILING DATE: 2005-04-07  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 624295  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 ; US-11-101-244-624295

Query Match 55.0%; Score 13.2; DB 8; Length 19;  
 Best Local Similarity 72.2%; Pred. No. 2.2e+03;  
 Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TGCACAGCTGGGGAAACAA 20  
 :|||||:|||||  
 Db 2 UGCACACUGUGAGAGAA 19

RESULT 33  
 US-11-101-244-1302115  
 ; Sequence 1302115, Application US/11101244  
 ; Publication No. US20050246794A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dharmakon, Inc.  
 ; APPLICANT: Khvorova, Anastasia  
 ; APPLICANT: Reynolds, Angela  
 ; APPLICANT: Leake, Devin  
 ; APPLICANT: Marshall, William  
 ; APPLICANT: Scaringe, Stephen  
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 ; FILE REFERENCE: 13499US  
 ; CURRENT APPLICATION NUMBER: US/11/101,244  
 ; CURRENT FILING DATE: 2005-04-07  
 ; PRIOR APPLICATION NUMBER: 60/502,050  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: 60/426,137  
 ; PRIOR FILING DATE: 2002-11-14  
 ; NUMBER OF SEQ ID NOS: 1591911  
 ; SOFTWARE: Proprietary  
 ; SEQ ID NO 1302115  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens  
 ; US-11-101-244-1302115

Query Match 55.0%; Score 13.2; DB 8; Length 19;  
 Best Local Similarity 72.2%; Pred. No. 2.2e+03;  
 Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TGCACAGCTGGGGAAACAA 20  
 :|||:|||||:|||||  
 Db 2 UGCACAGCUGGGAAACCAA 19

RESULT 34  
 US-11-101-244-1313799  
 ; Sequence 1313799, Application US/11101244  
 ; Publication No. US20050246794A1  
 ; GENERAL INFORMATION:

; APPLICANT: Dharmakon, Inc.

```

; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1313799
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-1313799

```

Query Match 55.0%; Score 13.2; DB 8; Length 19;  
Best Local Similarity 72.2%; Pred. NO. 2.2e+03;  
Matches 13; Conservative 2; Mismatches 3 Indels

Qy 3 TGCACAGCTGGGGAACAA 20  
: : : : : : : : : :  
Db 2 UGCUCUGCUGAGGGAACAA 19

```

RESULT 35
US-11-101-244-1313893
; Sequence 1313893, Application US/1101244
; Publication NO. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Khormaccon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 1349SUS
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1313893
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1313893

```

Query Match	55.0%	Score 13.2;	DB 8;
Best Local Similarity	72.2%	Pred. No. 2.2e+03;	
Matches 13; Conservative	2;	Mismatches 3	Indels

Qy 3 TGCACAGCTGGGGAACAA 20  
:| | | | | | | | | |  
Db 2 UGCUCUGCUGAGGGAACAA 19

RESULT 36  
US-11-101-244-1345869  
; Sequence 1345869, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia

```

; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1345869
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1345869

```

Query Match	55.0%	Score 13.2;	DB 8;	Length 19;
Best Local Similarity	77.8%;	Pred. No. 2.2e+03;		
Matches 14;	Conservative 1;	Mismatches 3;	Indels 0;	Gaps 0;
Qy	5	CACAGCTGGGGAACAAGA	22	
Db	2	CACAGCTUGGUGAGGAAGA	19	

```

RESULT 37
US-11-101-244-1360531
; Sequence 1360531, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 159111
; SOFTWARE: Proprietary
; SEQ ID NO 1360531
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1360531

```

Query Match	55.0%	Score 13.2;	DB 8;	Length 19;
Best Local Similarity	77.8%;	Pred. No. 2.2e+03;		
Matches 14;	Conservative	1;	Mismatches 3;	Indels 0;
			Gaps	0;

Qy 5 CACAGCTGGGGAACAAGA 22  
|||||: |||| ||||  
pb 2 CACAGCTAGGGGAGAAAGA 19

RESULT 38  
US-11-101-244-1526049  
; Sequence 1526049, Application US/11101244  
; Publication No. US200502467941  
; GENERAL INFORMATION:  
; APPLICANT: Pharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela

```
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1526049
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1526049
```

```
Query Match 55.0%; Score 13.2; DB 8; Length 19;
Best Local Similarity 77.8%; Pred. No. 2.2e+03;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 6 ACAGCTGGGGAACAAGAC 23
Db 2 AAAGUUGGAGAACAAAGAC 19
```

## RESULT 39

```
US-11-101-244-1529226
; Sequence 1529226, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1529226
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1529226
```

```
Query Match 55.0%; Score 13.2; DB 8; Length 19;
Best Local Similarity 72.2%; Pred. No. 2.2e+03;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 3 TGCACAGCTGGGGAACAA 20
Db 2 UGAACAGCGUGGAAUAA 19
```

## RESULT 40

```
US-11-083-784-92175/c
; Sequence 92175, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
```

```
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 92175
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-92175
```

```
Query Match 55.0%; Score 13.2; DB 9; Length 19;
Best Local Similarity 83.3%; Pred. No. 2.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 6 ACAGCTGGGGAACAAGAC 23
Db 19 AAATCTGGGAACAAGAC 2
```

```
Search completed: December 13, 2005, 16:24:35
Job time : 215.5 secs
```

**THIS PAGE BLANK (USPTO)**